FIG. 1A

Humanized 2A4 IgG1 Heavy Chain Variant 2 (G1m3 allotype):

```
      EVQLVESGGG LVQPGGSLRL SCAASGFTFN TYAMYWIRQA PGKGLEWVAR
 51   IRSKSNNYAI YYADSVKDRF TISRDDSKNS LYLQMNSLKT EDTAVYYCAR
101   PYSDSFAYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD
151   YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
201   ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK
251   DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
301   TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV
351   YTLPPSREEM TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL
401   DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
(SEQ ID NO: 15)
```

Humanized 2A4 Kappa Light Chain:

```
      DVVMTQSPLS LPVTPGEPAS ISCRSSQSLV HSTGNTYLHW YLQKPGQSPQ
 51   LLIYKVSNRF SGVPDRFSGS GSGTDFTLKI SRVEAEDVGV YYCSQSTHVP
101   FTFGGGTKVE IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK
151   VQWKVDNALQ SGNSQESVTE QDSKDSTYSL SSTLTLSKAD YEKHKVYACE
201   VTHQGLSSPV TKSFNRGEC
(SEQ ID NO: 13)
```

FIG. 1B

Humanized 2A4 IgG1 heavy chain variant 1 (G1m1 allotype)

```
  1  EVQLVESGGG LVQPGGSLRL SCAASGFTFN TYAMYWIRQA PGKGLEWVAR
 51  IRSKSNNYAI YYADSVKDRF TISRDDSKNS LYLQMNSLKT EDTAVYYCAR
101  PYSDSFAYWG QGTLVTVSSA STKGPSVFPL APSSKSTSGG TAALGCLVKD
151  YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSSLGTQTY
201  ICNVNHKPSN TKVDKRVEPK SCDKTHTCPP CPAPELLGGP SVFLFPPKPK
251  DTLMISRTPE VTCVVVDVSH EDPEVKFNWY VDGVEVHNAK TKPREEQYNS
301  TYRVVSVLTV LHQDWLNGKE YKCKVSNKAL PAPIEKTISK AKGQPREPQV
351  YTLPPSRDEL TKNQVSLTCL VKGFYPSDIA VEWESNGQPE NNYKTTPPVL
401  DSDGSFFLYS KLTVDKSRWQ QGNVFSCSVM HEALHNHYTQ KSLSLSPGK
(SEQ ID NO: 14)
```

Humanized 2A4 IgG2 heavy chain

```
  1  EVQLVESGGG LVQPGGSLRL SCAASGFTFN TYAMYWIRQA PGKGLEWVAR
 51  IRSKSNNYAI YYADSVKDRF TISRDDSKNS LYLQMNSLKT EDTAVYYCAR
101  PYSDSFAYWG QGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD
151  YFPEPVTVSW NSGALTSGVH TFPAVLQSSG LYSLSSVVTV PSSNFGTQTY
201  TCNVDHKPSN TKVDKTVERK CCVECPPCPA PPVAGPSVFL FPPKPKDTLM
251  ISRTPEVTCV VVDVSHEDPE VQFNWYVDGV EVHNAKTKPR EEQFNSTFRV
301  VSVLTVVHQD WLNGKEYKCK VSNKGLPAPI EKTISKTKGQ PREPQVYTLP
351  PSREEMTKNQ VSLTCLVKGF YPSDIAVEWE SNGQPENNYK TTPPMLDSDG
401  SFFLYSKLTV DKSRWQQGNV FSCSVMHEAL HNHYTQKSLS LSPGK
(SEQ ID NO: 16)
```

FIG. 2

Murine VL 2A4

MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSTGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGS
GSGTYFTLKISRVEAEDLGVYFCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 1)

Murine VL7D8

MKLPVRLLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSLSLVHSTGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGS
GSGTYFTLKISRVEAEDLGVYFCSQSTHVPFTFGGGTKLEIK (SEQ ID NO: 2)

Murine VH (2A4 and 7D8)

MVLGLKWVFFVVFYQGVHCEVQLVESGGRLVQPKGSLKLSCAASGFTFNTYAMYWIRQAPGKGLEWVARIRSKSNNYAIYYADSVKDRF
TIFRDDSQSMLYLQMNNLKTEDTAMYYCVRPYSDSFAYWGQGTLVTVSA (SEQ ID NO: 3)

FIG. 3

Hum2A4 VL Version 3

DVVMTQSPLSLPVTPGEPASISCRSSQSLVHSTGNTYLHWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVG
VYYCSQSTHVPFTFGGGTKVEIK (SEQ ID NO: 4)

Hum2A4/7D8/8G9 VH Version 3

EVQLVESGGGLVQPGGSLRLSCAASGFTFNTYAMYWiRQAPGKGLEWVaRIRSKSNNYAIYYADSVKDRFTISRDDSKNSLYLQMNSLK
TEDTAVYYCARPYSDSFAYWGQGTLVTVSS (SEQ ID NO: 5)

FIG. 4A

Hu2A4 VH3VL3 hcg1,k cDNA sequence / Heavy Chain

```
ATGGAGTTCGGCCTGTCCTGGCTGTTCCTGGTGGCCATCCTGAAGGGCGTGCAGTGCGAG   60
GTGCAGCTGGTCGAGTCCGGCGGAGGCCTGGTGCAGCCTGGCGGCTCCCTGAGACTGTCC  120
TGCGCCGCCTCCGGCTTCACCTTCAACACCTACGCCATGTACTGGATCAGGCAGGCTCCT  180
GGCAAGGGACTGGAGTGGGTGGCCCGGATCAGGTCCAAGTCCAACAACTACGCTATCTAC  240
TACGCCGACTCCGTGAAGGACCGGTTCACCATCTCCCGGGACGACTCCAAGAACTCCCTG  300
TATCTGCAGATGAACTCCCTGAAAACCGAGGACACCGCCGTGTACTACTGCGCTCGGCCT  360
TACTCCGACTCCTTCGCCTACTGGGGCCAGGGCACCCTGGTGACCGTGTCCAGCGCCTCC  420
ACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCACA  480
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAAC  540
TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTC  600
TACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATC  660
TGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGCCCAAATCT  720
TGTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCA  780
GTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTC  840
ACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTG  900
GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG  960
TACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC 1020
AAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAGCC 1080
AAAGGGCAGCCCCGAGAACCACAGGTGTACACGCTGCCCCCATCCCGGGAGGAGATGACC 1140
AAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTG 1200
GAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGAC 1260
TCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAG 1320
GGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG 1380
AGCCTCTCCCTGTCCCCGGGTAAATGA                                    1407
```

(SEQ ID NO: 23)

FIG. 4B

Hu2A4 VH3VL3 hcg1,k cDNA sequence / Light Chain

```
ATGGACATGCGGGTGCCCGCACAGCTGCTGGGCCTGCTGATGCTGTGGGTGTCCGGCTCC 60
TCCGGCGACGTGGTGATGACCCAGTCCCCTCTGTCCCTGCCTGTGACCCCTGGCGAGCCT 120
GCCTCCATCTCCTGCCGGTCCTCCCAGTCCCTGGTGCACTCCACCGGCAACACCTATCTG 180
CACTGGTATCTGCAGAAGCCTGGCCAGTCTCCTCAGCTGCTGATCTACAAGGTGTCCAAC 240
CGGTTCTCCGGCGTGCCTGACCGGTTCTCTGGCTCCGGCTCCGGCACCGACTTCACCCTG 300
AAGATCTCCCGGGTGGAGGCCGAGGACGTGGGCGTGTACTACTGCTCCCAGTCCACCCAC 360
GTGCCTTTCACCTTCGGCGGAGGCACCAAGGTGGAGATCAAGCGAACTGTGGCTGCACCA 420
TCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTG 480
TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC 540
CTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTAC 600
AGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC 660
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAG 720
TGTTAG                                                        726
(SEQ ID NO: 20)
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```
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
               -15                 -10                 -5

Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
        -1  1               5                   10
```

```
Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
    15                  20                  25

Val His Ser Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
30                  35                  40                  45

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

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr
            65                  70                  75

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
        80                  85                  90

Ser Gln Ser Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu
    95                  100                 105

Glu Ile Lys
110
```

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```
Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
                -15                 -10                 -5


Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val
        -1  1               5                   10


Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Leu Ser Leu
    15                  20                  25


Val His Ser Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro
30                  35                  40                  45


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


Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Tyr Phe Thr
            65                  70                  75


Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys
        80                  85                  90


Ser Gln Ser Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu
    95                  100                 105


Glu Ile Lys
110
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```
Met Val Leu Gly Leu Lys Trp Val Phe Phe Val Val Phe Tyr Gln Gly
                -15                 -10                  -5


Val His Cys Glu Val Gln Leu Val Glu Ser Gly Gly Arg Leu Val Gln
        -1  1               5                   10


Pro Lys Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                  20                  25


Asn Thr Tyr Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45


Glu Trp Val Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr
                50                  55                  60


Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Phe Arg Asp Asp Ser
            65                  70                  75


Gln Ser Met Leu Tyr Leu Gln Met Asn Asn Leu Lys Thr Glu Asp Thr
        80                  85                  90


Ala Met Tyr Tyr Cys Val Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp
    95                  100                 105
```

```
Gly Gln Gly Thr Leu Val Thr Val Ser Ala
110                 115


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       (humanized 2A4 light chain variable region version 3)

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


Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30


Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


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


Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
                85                  90                  95


Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


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       (humanized 2A4 heavy chain variable region version 3)

<400>  5
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```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

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

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
    50                  55                  60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
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Arg Ser Ser Gln Ser Leu Val His Ser Thr Gly Asn Thr Tyr Leu His
1               5                   10                  15
```

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Lys Val Ser Asn Arg Phe Ser
1 5

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Ser Gln Ser Thr His Val Pro Phe Thr
1 5

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Gly Phe Thr Phe Asn Thr Tyr Ala Met Tyr
1 5 10

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<400> 10

Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp Ser
1 5 10 15

Val Lys Asp

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<213> Mus musculus

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Pro Tyr Ser Asp Ser Phe Ala Tyr
1 5

<210> 12
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<213> Mus musculus

<400> 12

Lys Val Ser Asn Arg Phe Ser
1 5

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<400> 13

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

```
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
            20                  25                  30

Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45

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

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
                85                  90                  95

Thr His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

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

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
    50                  55                  60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

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

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175
```

```
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380
```

```
Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

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

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
    50                  55                  60
```

```
Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

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

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
                245                 250                 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
        275                 280                 285
```

```
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
    290                 295                 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
                325                 330                 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
            340                 345                 350

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
        355                 360                 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
    370                 375                 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
385                 390                 395                 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
            420                 425                 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445

Lys
```

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1               5                  10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
            20                  25                  30

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

Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr Tyr Ala Asp
    50                  55                  60

Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65                  70                  75                  80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
    130                 135                 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145                 150                 155                 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
                165                 170                 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
            180                 185                 190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
        195                 200                 205
```

```
Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu
    210                 215                 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
            340                 345                 350

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415
```

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 17
<211> 7
<212> PRT
<213> Homo sapiens

<400> 17

Cys Gly Gly His Glu Asp Thr
1 5

<210> 18
<211> 4
<212> PRT
<213> Homo sapiens

<400> 18

Ala Glu Asp Ser
1

<210> 19
<211> 660
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence containing murine and human residues (Hu2A4 VH3VL3 hcg1,k cDNA sequence - light chain without signal sequence)

<400> 19
gacgtggtga tgacccagtc ccctctgtcc ctgcctgtga cccctggcga gcctgcctcc 60

atctcctgcc ggtcctccca gtccctggtg cactccaccg gcaacaccta tctgcactgg 120

tatctgcaga agcctggcca gtctcctcag ctgctgatct acaaggtgtc caaccggttc 180

tccggcgtgc ctgaccggtt ctctggctcc ggctccggca ccgacttcac cctgaagatc 240

tcccgggtgg aggccgagga cgtgggcgtg tactactgct cccagtccac ccacgtgcct 300

ttcaccttcg gcggaggcac caaggtggag atcaagcgaa ctgtggctgc accatctgtc 360

ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420

```
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa      480

tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc      540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa      600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttag      660


<210>  20
<211>  726
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Humanized antibody sequence containing murine and human residues
       (Hu2A4 VH3VL3 hcg1,k cDNA sequence - light chain)


<220>
<221>  sig_peptide
<222>  (1)..(66)

<220>
<221>  CDS
<222>  (1)..(726)

<220>
<221>  V_region
<222>  (67)..(402)

<220>
<221>  C_region
<222>  (403)..(726)

<400>  20
atg gac atg cgg gtg ccc gca cag ctg ctg ggc ctg ctg atg ctg tgg         48
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
1               5                   10                  15

gtg tcc ggc tcc tcc ggc gac gtg gtg atg acc cag tcc cct ctg tcc         96
Val Ser Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser
            20                  25                  30

ctg cct gtg acc cct ggc gag cct gcc tcc atc tcc tgc cgg tcc tcc        144
Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
        35                  40                  45

cag tcc ctg gtg cac tcc acc ggc aac acc tat ctg cac tgg tat ctg        192
Gln Ser Leu Val His Ser Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu
    50                  55                  60
```

```
cag aag cct ggc cag tct cct cag ctg ctg atc tac aag gtg tcc aac        240
Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn
65                  70                  75                  80

cgg ttc tcc ggc gtg cct gac cgg ttc tct ggc tcc ggc tcc ggc acc        288
Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
                85                  90                  95

gac ttc acc ctg aag atc tcc cgg gtg gag gcc gag gac gtg ggc gtg        336
Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
            100                 105                 110

tac tac tgc tcc cag tcc acc cac gtg cct ttc acc ttc ggc gga ggc        384
Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Phe Thr Phe Gly Gly Gly
        115                 120                 125

acc aag gtg gag atc aag cga act gtg gct gca cca tct gtc ttc atc        432
Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile
    130                 135                 140

ttc ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg        480
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
145                 150                 155                 160

tgc ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag        528
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
                165                 170                 175

gtg gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag        576
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
            180                 185                 190

cag gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg        624
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

agc aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc        672
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
    210                 215                 220

cat cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag        720
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225                 230                 235                 240

tgt tag                                                               726
Cys
```

<210> 21
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 21

```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp
1               5                  10                  15

Val Ser Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser
            20                  25                  30

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

Gln Ser Leu Val His Ser Thr Gly Asn Thr Tyr Leu His Trp Tyr Leu
    50                  55                  60

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

Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
                85                  90                  95

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
            100                 105                 110

Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Phe Thr Phe Gly Gly Gly
        115                 120                 125

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

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

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

Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
            180                 185                 190
```

```
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
        195                 200                 205

Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
    210                 215                 220

His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
225                 230                 235                 240

Cys
```

<210> 22
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence containing murine and human residues (Hu2A4 VH3VL3 hcg1,k cDNA sequence - heavy chain without signal sequence)

<400> 22

```
gaggtgcagc tggtcgagtc cggcggaggc ctggtgcagc ctggcggctc cctgagactg       60

tcctgcgccg cctccggctt caccttcaac acctacgcca tgtactggat caggcaggct      120

cctggcaagg gactggagtg ggtggcccgg atcaggtcca agtccaacaa ctacgctatc      180

tactacgccg actccgtgaa ggaccggttc accatctccc gggacgactc caagaactcc      240

ctgtatctgc agatgaactc cctgaaaacc gaggacaccg ccgtgtacta ctgcgctcgg      300

ccttactccg actccttcgc ctactggggc cagggcaccc tggtgaccgt gtccagcgcc      360

tccaccaagg gcccatcggt cttccccctg gcaccctcct ccaagagcac ctctgggggc      420

acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg      480

aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga      540

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac ccagacctac      600

atctgcaacg tgaatcacaa gcccagcaac accaaggtgg acaagagagt tgagcccaaa      660

tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct gggggggaccg      720

tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctcccg gacccctgag      780

gtcacatgcg tggtggtgga cgtgagccac gaagaccctg aggtcaagtt caactggtac      840
```

```
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc      900

acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag      960

tacaagtgca aggtctccaa caaagccctc ccagccccca tcgagaaaac catctccaaa     1020

gccaaagggc agccccgaga accacaggtg tacacgctgc ccccatcccg ggaggagatg     1080

accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc     1140

gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg     1200

gactccgacg gctccttctt cctctatagc aagctcaccg tggacaagag caggtggcag     1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag     1320

aagagcctct ccctgtcccc gggtaaatga                                      1350
```

<210> 23
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> Humanized antibody sequence containing murine and human residues (Hu2A4 VH3VL3 hcg1,k cDNA sequence - heavy chain)

<220>
<221> sig_peptide
<222> (1)..(57)

<220>
<221> CDS
<222> (1)..(1407)

<220>
<221> V_region
<222> (58)..(414)

<220>
<221> C_region
<222> (415)..(1407)

<400> 23

```
atg gag ttc ggc ctg tcc tgg ctg ttc ctg gtg gcc atc ctg aag ggc        48
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1               5                  10                  15

gtg cag tgc gag gtg cag ctg gtc gag tcc ggc gga ggc ctg gtg cag        96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30
```

```
cct ggc ggc tcc ctg aga ctg tcc tgc gcc gcc tcc ggc ttc acc ttc        144
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

aac acc tac gcc atg tac tgg atc agg cag gct cct ggc aag gga ctg        192
Asn Thr Tyr Ala Met Tyr Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
    50                  55                  60

gag tgg gtg gcc cgg atc agg tcc aag tcc aac aac tac gct atc tac        240
Glu Trp Val Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr
65                  70                  75                  80

tac gcc gac tcc gtg aag gac cgg ttc acc atc tcc cgg gac gac tcc        288
Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
                85                  90                  95

aag aac tcc ctg tat ctg cag atg aac tcc ctg aaa acc gag gac acc        336
Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr
            100                 105                 110

gcc gtg tac tac tgc gct cgg cct tac tcc gac tcc ttc gcc tac tgg        384
Ala Val Tyr Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp
        115                 120                 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

tcc ccg ggt aaa tga                                                   1407
Ser Pro Gly Lys
465
```

<210> 24
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

```
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
1               5                   10                  15

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

Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
        35                  40                  45

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

Glu Trp Val Ala Arg Ile Arg Ser Lys Ser Asn Asn Tyr Ala Ile Tyr
65                  70                  75                  80

Tyr Ala Asp Ser Val Lys Asp Arg Phe Thr Ile Ser Arg Asp Asp Ser
                85                  90                  95

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

Ala Val Tyr Tyr Cys Ala Arg Pro Tyr Ser Asp Ser Phe Ala Tyr Trp
        115                 120                 125

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Ser Pro Gly Lys
465
```