SEQUENCE LISTING

<110> The Trustees of the University of Pennsylvania

<120> COMPOSITIONS COMPRISING AAV EXPRESSIONG DUAL ANTIBODY CONSTRUCTS AND USES THEREOF

<130> UPN-14-7032PCT

<150> 61/992649
<151> 2014-05-13

<160> 50

<170> PatentIn version 3.5

<210> 1
<211> 705
<212> DNA
<213> Artificial sequence

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<223> Synthetic sequence encoding FI6 heavy chain

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<221> CDS
<222> (1)..(705)
<223> FI6 constant

<400> 1

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gcg gcg cct aag agc tgc gac aag acc cac acc tgt ccc ccc tgc cct         48
Ala Ala Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
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gcc cct gaa ctg ctg gga ggc ccc agc gtg ttc ctg ttc ccc cca aag         96
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            20                  25                  30

ccc aag gac acc ctg atg atc agc cgg acc ccc gaa gtg acc tgc gtg        144
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        35                  40                  45

gtg gtg gac gtg tcc cac gag gac cct gaa gtg aag ttc aat tgg tac        192
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    50                  55                  60

gtg gac ggc gtg gaa gtg cac aac gcc aag acc aag ccc aga gag gaa        240
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65                  70                  75                  80

cag tac aac agc acc tac cgg gtg gtg tcc gtg ctg acc gtg ctg cac        288
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                85                  90                  95

cag gac tgg ctg aac ggc aaa gag tac aag tgc aag gtg tcc aac aag        336
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            100                 105                 110
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gcc ctg cct gcc ccc atc gag aaa acc atc agc aag gcc aag ggc cag        384
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        115                 120                 125

ccc cgc gag cct cag gtg tgc aca ctg ccc ccc agc cgg gaa gag atg        432
Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
    130                 135                 140

acc aag aac cag gtg tcc ctg acc tgc ctg gtc aag ggc ttc tac ccc        480
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145                 150                 155                 160

agc gat atc gcc gtg gaa tgg gag agc aac ggc cag ccc gag aac aac        528
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                165                 170                 175

tac aag acc acc ccc cct gtg ctg gac agc gac ggc tca ttc ttc ctg        576
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            180                 185                 190

tac agc aag ctg acc gtg gac aag agc cgg tgg cag cag ggc aac gtg        624
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        195                 200                 205

ttc agc tgc agc gtg atg cac gag gcc ctg cac aac cac tac acc cag        672
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    210                 215                 220

aag tcc ctg agc ctg agc ccc ggc aag tga tga                            705
Lys Ser Leu Ser Leu Ser Pro Gly Lys
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Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        35                  40                  45


Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    50                  55                  60
```

```
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65                  70                  75                  80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                85                  90                  95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            100                 105                 110

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        115                 120                 125

Pro Arg Glu Pro Gln Val Cys Thr Leu Pro Pro Ser Arg Glu Glu Met
    130                 135                 140

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

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                165                 170                 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            180                 185                 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        195                 200                 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
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Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<222> (915)..(1235)
<223> complement - CH'1

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<222> (1236)..(1598)
<223> complement - 1A6\VH

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<222> (1599)..(1655)
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<222> (1734)..(2202)
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<222> (2445)..(2777)
<223> FI6\VL

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<222> (3951)..(4619)
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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

aggaagatct cacacaaaaa accaacacac agatgtaatg aaaataaaga tattttattt 240

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ttgctataca ggaagaatga gccgtcgctg tccagcacag ggggggtggt cttgtagttg 420

ttctcgggct ggccgttgct ctcccattcc acggcgatct cgctggggta gaagcccttg 480

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cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc ccattgacgt     1860

caataatgac gtatgttccc atagtaacgc caatagggac tttccattga cgtcaatggg     1920

tggagtattt acggtaaact gcccacttgg cagtacatca agtgtatcat atgccaagta     1980

cgcccccctat tgacgtcaat gacggtaaat ggcccgcctg gcattatgcc cagtacatga     2040

ccttatggga ctttcctact tggcagtaca tctacgtatt agtcatcgct attaccatgg     2100

tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca cggggatttc     2160

caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat caacgggact     2220

ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt     2280

gggaggtcta tataagcaga gctggtttag tgaaccgtca gatccgctgg gcactttgca     2340

ctggaactta caacacccga gcaaggacgc gactctgccg ccccaccatg cgcatgcagc     2400

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                                                  Asp Ile Val Met
                                                  1

acc cag agc cca gat agc ctg gcc gtg agc ctg gga gag cgg gcc acc       2504
Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr
5                   10                  15                  20

atc aac tgc aag agc agc cag agc gtg acc ttc aac tac aag aac tac       2552
Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr Lys Asn Tyr
                25                  30                  35

ctg gcc tgg tac cag cag aag cca gga cag cca cca aag ctg ctg atc       2600
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
            40                  45                  50

tac tgg gcc agc acc cgg gag agc gga gtg cca gat cgg ttc agc gga       2648
Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
        55                  60                  65

agc gga agc gga acc gat ttc acc ctg acc atc agc agc ctg cag gcc       2696
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
    70                  75                  80

gag gat gtg gcc gtg tac tac tgc cag cag cac tac cgg acc cca cca       2744
Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro Pro
85                  90                  95                  100

acc ttc gga cag gga acc aag gtg gag atc aag cgtacggtgg ccgccccaag     2797
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                105                 110
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cgtgttcatc ttcccaccaa gcgatgagca gctgaagagc ggaaccgcca gcgtggtgtg     2857

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gcagagcgga aacagccagg agagcgtgac cgagcaggat agcaaggata gcacctacag     2977

cctgagcagc accctgaccc tgagcaaggc cgattacgag aagcacaagg tgtacgcctg     3037

cgaggtgacc caccagggac tgagcagccc agtgaccaag agcttcaacc gcggagagtg     3097

ccggaagcgg cgggccccag tgaagcagac cctgaacttc gatctgctga agctggccgg     3157

agatgtggag agcaacccag gaccaatgta cagaatgcag ctgctgagct gcatcgccct     3217

gagcctggcc ctggtgacca acagc cag gtg caa cta gtg gag agc gga gga       3269
                           Gln Val Gln Leu Val Glu Ser Gly Gly
                                           115                 120

gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc gcc agc       3317
Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser
                125                 130                 135

gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag gcc cca       3365
Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln Ala Pro
            140                 145                 150

gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc aac tac       3413
Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala Asn Tyr
        155                 160                 165

aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc cgg gat       3461
Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
    170                 175                 180

aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg gcc gag       3509
Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
185                 190                 195                 200

gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg agc ctg       3557
Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg Ser Leu
                205                 210                 215

ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg gga cag       3605
Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp Gly Gln
            220                 225                 230

gga acc ctg gtg acc gtg agc agc gct agc acc aag gga cca agc gtg       3653
Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
        235                 240                 245

ttc cca ctg gcc cca agc agc aag agc acc agc gga gga acc gcc gcc       3701
Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
    250                 255                 260

ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg acc gtg agc       3749
Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
265                 270                 275                 280

tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc cca gcc gtg       3797
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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
                285                 290                 295

ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg acc gtg cca      3845
Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
            300                 305                 310

agc agc agc ctg gga acc cag acc tac atc tgc aac gtg aac cac aag      3893
Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
        315                 320                 325

cca agc aac acc aag gtg gat aag aag gtg gag cca aag agc tgc gat      3941
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
    330                 335                 340

aag acc cac acg tgc cct cct tgt cca gcc ccc gaa ctg ctg ggc ggg      3989
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
345                 350                 355                 360

cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca ctg atg att      4037
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
                365                 370                 375

agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg tcc cac gaa      4085
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            380                 385                 390

gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg gag gtg cac      4133
Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        395                 400                 405

aat gct aag act aaa cca cgc gaa gag cag tat aat agt aca tac cga      4181
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
    410                 415                 420

gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg aac ggc aag      4229
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
425                 430                 435                 440

gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc cct atc gag      4277
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
                445                 450                 455

aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc cag gtc tac      4325
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
            460                 465                 470

act ctg cca ccc tca aga gat gaa ctg act aag aac cag gtc agc ctg      4373
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
        475                 480                 485

acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc gtg gag tgg      4421
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
    490                 495                 500

gaa agt aac ggc cag cct gag aat aac tac aag act acc cct cca gtg      4469
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
505                 510                 515                 520
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ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg aca gtg gac      4517
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aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct gtg atg cat      4565
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
            540                 545                 550

gag gcc ctg cac aat cat tac acc cag aag agt ctg tca ctg agc ccc      4613
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        555                 560                 565

ggc aaa tgataaaagg aacccgcgct atgacggcaa taaaaagaca gaataaaacc       4669
Gly Lys
    570

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gctacgtaga taagtagcat ggcgggttaa tcattaacta caaggaaccc ctagtgatgg    4789

agttggccac tccctctctg cgcgctcgct cgctcactga ggccgggcga ccaaaggtcg    4849

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<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 4

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
20 25 30

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

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
50 55 60

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
85 90 95

Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 5
<211> 129
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 5

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

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

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
            100                 105                 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

Ser
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<210> 6
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 6

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95
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Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
100 105

<210> 7
<211> 223
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 7

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
20 25 30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50 55 60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65 70 75 80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
85 90 95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
100 105 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
115 120 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
130 135 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145 150 155 160

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

```
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190


Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205


His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215                 220


<210>  8
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<220>
<223>  Plasmid encoding FI6 and C05 monoclonal antibodies


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<222>  (204)..(252)
<223>  synthetic\polyA

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<222>  (259)..(927)
<223>  complement - CH'2-3

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<222>  (928)..(1248)
<223>  complement - CH'1

<220>
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<222>  (1251)..(1668)
<223>  complement - C05\VH

<220>
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<222>  (1669)..(1719)
<223>  complement - leader

<220>
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<222>  (1729)..(1979)
<223>  complement - CMV\mp2

<220>
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<222>  (1798)..(2266)
<223>  Enhancer

<220>
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<222>  (2267)..(2392)
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<223> CMV\mp2

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<222> (2509)..(2841)
<223> FI6\VL

<220>
<221> CDS
<222> (2842)..(3162)
<223> CL

<220>
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<222> (3247)..(3306)
<223> leader

<220>
<221> CDS
<222> (3307)..(3693)
<223> FI6\VH

<220>
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<222> (3694)..(4014)
<223> CH1

<220>
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<222> (4015)..(4683)
<223> CH2-3

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<222> (4690)..(4767)
<223> TKpAshort

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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac 180

gtagccatgc tctaggaaga tctcacacaa aaaaccaaca cacagatgta atgaaaataa 240

agatatttta ttttatcact tcccggggct caggctcagg gacttctggg tgtagtggtt 300

gtgcagggcc tcgtgcatca cgctgcagct gaacacgttg ccctgctgcc accggctctt 360

gtccacggtc agcttgctat acaggaagaa tgagccgtcg ctgtccagca cagggggggt 420

ggtcttgtag ttgttctcgg gctggccgtt gctctcccat tccacggcga tctcgctggg 480

gtagaagccc ttgaccaggc aggtcaggga cacctggttc ttggtcatct cttcccggct 540

gggggggcagt gtgtagacct gaggctcgcg gggctggccc ttggccttgc tgatggtttt 600

ctcgatgggg gcaggcaggg ccttgttgga caccttgcac ttgtactctt tgccgttcag 660

ccagtcctgg tgcagcacgg tcagcacgga caccacccgg taggtgctgt tgtactgttc 720

ctctctgggc ttggtcttgg cgttgtgcac ttccacgccg tccacgtacc aattgaactt 780

cacttcaggg tcctcgtggg acacgtccac caccacgcag gtcacttcgg gggtccggct 840

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gctcagccac tccagtccct ttcctggggc ctgccgcacc cagctcacgg cgtagtagct 1560

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atggtgatgc ggttttggca gtacatcaat gggcgtggat agcggtttga ctcacgggga 2220

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gactttccaa aatgtcgtaa caactccgcc ccattgacgc aaatgggcgg taggcgtgta 2340

cggtgggagg tctatataag cagagctggt ttagtgaacc gtcagatccg ctgggcactt 2400

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tgcactggaa cttacaacac ccgagcaagg acgcgactct gccgccccac catgcgcatg     2460

cagctgctgc tgctgatcgc cctgagcctg gccctggtga ccaacagc gat atc gtc      2517
                                                    Asp Ile Val
                                                    1

atg acc cag agc cca gat agc ctg gcc gtg agc ctg gga gag cgg gcc       2565
Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala
    5                  10                  15

acc atc aac tgc aag agc agc cag agc gtg acc ttc aac tac aag aac       2613
Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr Lys Asn
20                 25                  30                  35

tac ctg gcc tgg tac cag cag aag cca gga cag cca cca aag ctg ctg       2661
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
                40                  45                  50

atc tac tgg gcc agc acc cgg gag agc gga gtg cca gat cgg ttc agc       2709
Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser
            55                  60                  65

gga agc gga agc gga acc gat ttc acc ctg acc atc agc agc ctg cag       2757
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
        70                  75                  80

gcc gag gat gtg gcc gtg tac tac tgc cag cag cac tac cgg acc cca       2805
Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro
    85                  90                  95

cca acc ttc gga cag gga acc aag gtg gag atc aag cgt acg gtg gcc       2853
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
100                 105                 110                 115

gcc cca agc gtg ttc atc ttc cca cca agc gat gag cag ctg aag agc       2901
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
                120                 125                 130

gga acc gcc agc gtg gtg tgc ctg ctg aac aac ttc tac cca cgg gag       2949
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
            135                 140                 145

gcc aag gtg cag tgg aag gtg gat aac gcc ctg cag agc gga aac agc       2997
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
        150                 155                 160

cag gag agc gtg acc gag cag gat agc aag gat agc acc tac agc ctg       3045
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
    165                 170                 175

agc agc acc ctg acc ctg agc aag gcc gat tac gag aag cac aag gtg       3093
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180                 185                 190                 195

tac gcc tgc gag gtg acc cac cag gga ctg agc agc cca gtg acc aag       3141
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
                200                 205                 210

agc ttc aac cgc gga gag tgc cggaagcggc gggccccagt gaagcagacc          3192
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Ser Phe Asn Arg Gly Glu Cys
            215

ctgaacttcg atctgctgaa gctggccgga gatgtggaga gcaacccagg accaatgtac     3252

agaatgcagc tgctgagctg catcgccctg agcctggccc tggtgaccaa cagc cag       3309
                                                            Gln


gtg caa cta gtg gag agc gga gga gga gtg gtg cag cca gga cgg agc       3357
Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser
220                 225                 230                 235

ctg cgg ctg agc tgc gcc gcc agc gga ttc acc ttc agc acc tac gcc       3405
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala
                240                 245                 250

atg cac tgg gtg cgg cag gcc cca gga aag gga ctg gag tgg gtg gcc       3453
Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
            255                 260                 265

gtg atc agc tac gat gcc aac tac aag tac tac gcc gat agc gtg aag       3501
Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys
        270                 275                 280

gga cgg ttc acc atc agc cgg gat aac agc aag aac acc ctg tac ctg       3549
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
    285                 290                 295

cag atg aac agc ctg cgg gcc gag gat acc gcc gtg tac tac tgc gcc       3597
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
300                 305                 310                 315

aag gat agc cag ctg cgg agc ctg ctg tac ttc gag tgg ctg agc cag       3645
Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln
                320                 325                 330

gga tac ttc gat tac tgg gga cag gga acc ctg gtg acc gtg agc agc       3693
Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
            335                 340                 345

gct agc acc aag gga cca agc gtg ttc cca ctg gcc cca agc agc aag       3741
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
        350                 355                 360

agc acc agc gga gga acc gcc gcc ctg gga tgc ctg gtg aag gat tac       3789
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
    365                 370                 375

ttc cca gag cca gtg acc gtg agc tgg aac agc gga gcc ctg acc agc       3837
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
380                 385                 390                 395

gga gtg cac acc ttc cca gcc gtg ctg cag agc agc gga ctg tat agc       3885
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
                400                 405                 410

ctg agc agc gtg gtg acc gtg cca agc agc agc ctg gga acc cag acc       3933
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
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            415                 420                 425

tac atc tgc aac gtg aac cac aag cca agc aac acc aag gtg gat aag       3981
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
        430                 435                 440

aag gtg gag cca aag agc tgc gat aag acc cac acg tgc cct cca tgt       4029
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
    445                 450                 455

cca gcc ccc gaa ctg ctg ggc ggg cct agc gtg ttc ctg ttt ccc cct       4077
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
460                 465                 470                 475

aag cct aaa gat aca ctg atg att agt aga acc cca gag gtc aca tgc       4125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
                480                 485                 490

gtg gtc gtg gac gtg tcc cac gaa gag cct gac gtg aag ttc aac tgg       4173
Val Val Val Asp Val Ser His Glu Glu Pro Asp Val Lys Phe Asn Trp
            495                 500                 505

tac gtg gat ggc gtg gag gtg cac aat gct aag act aaa cca cgc gaa       4221
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
        510                 515                 520

gag cag tat aat agt aca tac cga gtc gtg tca gtc ctg aca gtg ctg       4269
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
    525                 530                 535

cac cag gat tgg ctg aac ggc aag gag tat aag tgc aag gtg tct aac       4317
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
540                 545                 550                 555

aag gcc ctg ccc gcc cct atc gag aaa aca att agc aag gcc aaa ggg       4365
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
                560                 565                 570

cag cca cgg gaa ccc cag gtc tac act ctg cca ccc tca aga gat gaa       4413
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
            575                 580                 585

ctg act aag aac cag gtc agc ctg acc tgt ctg gtg aaa ggc ttc tac       4461
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
        590                 595                 600

ccc agc gac atc gcc gtg gag tgg gaa agt aac ggc cag cct gag aat       4509
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
    605                 610                 615

aac tac aag act acc cct cca gtg ctg gat agc gac ggg tcc ttc ttc       4557
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
620                 625                 630                 635

ctg tat agc aag ctg aca gtg gac aaa tcc cgc tgg cag cag gga aac       4605
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
                640                 645                 650

gtc ttt tcc tgt tct gtg atg cat gag gcc ctg cac aat cat tac acc       4653
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Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
            655                 660                 665

cag aag agt ctg tca ctg agc ccc ggc aaa tgataaaagg aacccgcgct        4703
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
        670                 675

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cgggatcgat aaggatcttc ctagagcatg gctacgtaga taagtagcat ggcgggttaa    4823

tcattaacta caaggaaccc ctagtgatgg agttggccac tccctctctg cgcgctcgct    4883

cgctcactga ggccgggcga ccaaaggtcg cccgacgccc gggctttgcc cgggcggcct    4943

cagtgagcga gcgagcgcgc agccttaatt aacctaattc actggccgtc gttttacaac    5003

gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catcccccctt    5063

tcgccagctg gcgtaatagc gaagaggccc gcaccgatcg cccttcccaa cagttgcgca    5123

gcctgaatgg cgaatgggac gcgccctgta gcggcgcatt aagcgcggcg ggtgtggtgg    5183

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cacttttcgg ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa    5663

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gagtatgagt attcaacatt tccgtgtcgc ccttattccc ttttttgcgg cattttgcct    5783

tcctgttttt gctcacccag aaacgctggt gaaagtaaaa gatgctgaag atcagttggg    5843

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atcccgtatt gacgccgggc aagagcaact cggtcgccgc atacactatt ctcagaatga    6023

cttggttgag tactcaccag tcacagaaaa gcatcttacg gatggcatga cagtaagaga    6083

attatgcagt gctgccataa ccatgagtga taacactgcg gccaacttac ttctgacaac    6143

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ccttgatcgt tgggaaccgg agctgaatga agccatacca aacgacgagc gtgacaccac    6263
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atagttaccg gataaggcgc agcggtcggg ctgaacgggg ggttcgtgca cacagcccag 7103

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cacgcttccc gaagggagaa aggcggacag gtatccggta agcggcaggg tcggaacagg 7223

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gaaaaacgcc agcaacgcgg cctttttacg gttcctggcc ttttgctggc cttttgctca 7403

catgttcttt cctgcgttat cccctgattc tgtggataac cgtattaccg cctttgagtg 7463

agctgatacc gctcgccgca gccgaacgac cgagcgcagc gagtcagtga gcgaggaagc 7523

ggaagagcgc ccaatacgca aaccgcctct ccccgcgcgt tggccgattc attaatgcag 7583

ctggcacgac aggtttcccg actggaaagc gggcagtgag cgcaacgcaa ttaatgtgag 7643

ttagctcact cattaggcac cccaggcttt acactttatg cttccggctc gtatgttgtg 7703

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atttaattaa 7773

<210> 9
<211> 111
<212> PRT
<213> Artificial sequence

<220>

<223> Synthetic Construct

<400> 9

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
20 25 30

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

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
50 55 60

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
85 90 95

Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu

65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
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Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
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Ser

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
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Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
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Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
100 105

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
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Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

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    50                  55                  60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65                  70                  75                  80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                 135                 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                 150                 155                 160

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190

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


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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

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cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc ccattgacgt     1860

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caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat caacgggact     2220

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atcggttcag cggaagcgga agcggaaccg atttcaccct gaccatcagc agcctgcagg     2700

ccgaggatgt ggccgtgtac tactgccagc agtactacag caccccactg accttcggac     2760

agggaaccaa ggtggagatc aag cgt acg gtg gcc gcc cca agc gtg ttc atc     2813
                          Arg Thr Val Ala Ala Pro Ser Val Phe Ile
                          1               5                  10

ttc cca cca agc gat gag cag ctg aag agc gga acc gcc agc gtg gtg      2861
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
               15                  20                  25

tgc ctg ctg aac aac ttc tac cca cgg gag gcc aag gtg cag tgg aag      2909
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
           30                  35                  40
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gtg gat aac gcc ctg cag agc gga aac agc cag gag agc gtg acc gag       2957
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
        45                  50                  55

cag gat agc aag gat agc acc tac agc ctg agc agc acc ctg acc ctg       3005
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
    60                  65                  70

agc aag gcc gat tac gag aag cac aag gtg tac gcc tgc gag gtg acc       3053
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
75                  80                  85                  90

cac cag gga ctg agc agc cca gtg acc aag agc ttc aac cgc gga gag       3101
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                95                  100                 105

tgc cggaagcggc gggccccagt gaagcagacc ctgaacttcg atctgctgaa            3154
Cys


gctggccgga gatgtggaga gcaacccagg accaatgtac agaatgcagc tgctgagctg     3214

catcgccctg agcctggccc tggtgaccaa cagc cag gtg caa cta gtg gag agc     3269
                                      Gln Val Gln Leu Val Glu Ser
                                              110

gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc       3317
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
115                 120                 125                 130

gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag       3365
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln
                135                 140                 145

gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc       3413
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala
            150                 155                 160

aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc       3461
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
        165                 170                 175

cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg       3509
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
    180                 185                 190

gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg       3557
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg
195                 200                 205                 210

agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg       3605
Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp
                215                 220                 225

gga cag gga acc ctg gtg acc gtg agc agc gct agc acc aag gga cca       3653
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
            230                 235                 240
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agc gtg ttc cca ctg gcc cca agc agc aag agc acc agc gga gga acc       3701
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
        245                 250                 255

gcc gcc ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg acc       3749
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
    260                 265                 270

gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc cca       3797
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
275                 280                 285                 290

gcc gtg ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg acc       3845
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                295                 300                 305

gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg aac       3893
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
            310                 315                 320

cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag agc       3941
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
        325                 330                 335

tgc gat aag acc cac acg tgc cct cct tgt cca gcc ccc gaa ctg ctg       3989
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
    340                 345                 350

ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca ctg       4037
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
355                 360                 365                 370

atg att agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg tcc       4085
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                375                 380                 385

cac gaa gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg gag       4133
His Glu Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
            390                 395                 400

gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt aca       4181
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
        405                 410                 415

tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg aac       4229
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
    420                 425                 430

ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc cct       4277
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
435                 440                 445                 450

atc gag aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc cag       4325
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                455                 460                 465

gtc tac act ctg cca ccc tca aga gat gaa ctg act aag aac cag gtc       4373
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
            470                 475                 480
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agc ctg acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc gtg       4421
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
        485                 490                 495

gag tgg gaa agt aac ggc cag cct gag aat aac tac aag act acc cct       4469
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    500                 505                 510

cca gtg ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg aca       4517
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
515                 520                 525                 530

gtg gac aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct gtg       4565
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                535                 540                 545

atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca ctg       4613
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            550                 555                 560

agc ccc ggc aaa tgataaaagg aacccgcgct atgacggcaa taaaaagaca           4665
Ser Pro Gly Lys
        565

gaataaaacc cacgggtgtt gggtcgtttg ttcataaacc cgggatcgat aaggatcttc     4725

ctagagcatg gctacgtaga taagtagcat ggcgggttaa tcattaacta caaggaaccc     4785

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<223> Synthetic Construct

<400> 15

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
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Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 16
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<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 16

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

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

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
            100                 105                 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

Ser
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<210> 17
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 17

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                  10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45
```

```
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
            100                 105
```

<210> 18
<211> 223
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 18

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1               5                   10                  15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            20                  25                  30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
        35                  40                  45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    50                  55                  60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65                  70                  75                  80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
```

```
    130                 135                 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                 150                 155                 160

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215                 220
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<210> 19
<211> 7746
<212> DNA
<213> Artificial sequence

<220>
<223> Plasmid carrying FI6 and CR8033 monoclonals

<220>
<221> polyA_signal
<222> (173)..(221)
<223> synthetic\polyA

<220>
<221> misc_feature
<222> (228)..(896)
<223> complement - CH'2-3

<220>
<221> misc_feature
<222> (897)..(1217)
<223> complement - CH'1

<220>
<221> misc_feature
<222> (1218)..(1604)
<223> complement - CR8033\VH

<220>
<221> misc_feature
<222> (1605)..(1655)
<223> complement - leader

<220>
<221> misc_feature

<222> (1665)..(1733)
<223> complement - CMV\mp2

<220>
<221> misc_feature
<222> (1734)..(2202)
<223> Enhancer

<220>
<221> misc_feature
<222> (2203)..(2328)
<223> CMV\mp1

<220>
<221> misc_feature
<222> (2445)..(2789)
<223> KGL

<220>
<221> CDS
<222> (2784)..(3104)
<223> CL

<220>
<221> misc_feature
<222> (3189)..(3248)
<223> leader

<220>
<221> CDS
<222> (3249)..(3635)
<223> FI6\VH

<220>
<221> CDS
<222> (3636)..(3956)
<223> CH1

<220>
<221> CDS
<222> (3957)..(4625)
<223> CH2-3

<220>
<221> misc_feature
<222> (3968)..(3968)
<223> A -> T

<220>
<221> polyA_signal
<222> (4632)..(4709)
<223> TKpAshort

<400> 19
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agcgagcgag cgcgcagaga gggagtggcc aactccatca ctaggggttc cttgtagtta 120

atgattaacc cgccatgcta cttatctacg tagccatgct ctaggaagat ctcacacaaa 180

aaaccaacac acagatgtaa tgaaaataaa gatattttat tttatcactt cccggggctc 240

aggctcaggg acttctgggt gtagtggttg tgcagggcct cgtgcatcac gctgcagctg 300

aacacgttgc cctgctgcca ccggctcttg tccacggtca gcttgctata caggaagaat 360

gagccgtcgc tgtccagcac agggggggtg gtcttgtagt tgttctcggg ctggccgttg 420

ctctcccatt ccacggcgat ctcgctgggg tagaagccct tgaccaggca ggtcagggac 480

acctggttct tggtcatctc ttcccggctg gggggcagtg tgtagacctg aggctcgcgg 540

ggctggccct tggccttgct gatggttttc tcgatggggg caggcagggc cttgttggac 600

accttgcact tgtactcttt gccgttcagc cagtcctggt gcagcacggt cagcacggac 660

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aacaggaaca cgctggggcc tcccagcagt tcaggggcag ggcaggggg acacgtgtgg 900

gtcttgtcgc agctcttagg ttccacccgc ttgtccacct tggtgttgct gggcttgtgg 960

ttcacgttgc agatgtaggt ctgggtgccc aggctgctgc tgggcacggt gaccacgctg 1020

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ggtcccttgg tgctggcgct cgagacggtc accatggttc cctgtcccca gatatcgaag 1260

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agggcggtat cctcggcccg caggctgttc atctgcaggt acaggctgtt ctttccgtta 1380

tcccggctga tggtgaaccg tccctgcacg ctatcggcgt atcccatgaa gtttcccttc 1440

cagttgattc cggccaccca ctccagtccc tttcctgggg cctgccgcac ccagtgcatg 1500

gtgtactcat cgaagctgaa tccgctggcg gcgcagctca gccgcaggct ccgtcctggc 1560

tgcaccagtc ctcctccggt ctccaccagc tgcacctctg aattcgtcac cagggccagg 1620

ctcagggcga tcagcagcag cagctgcatg cgcatggtgg cggcgcgatc tgacggttca 1680

ctaaacgagc tctgcttata taggcctccc accgtacacg ccacctcgac atacctagtt 1740

attaatagta atcaattacg gggtcattag ttcatagccc atatatggag ttccgcgtta 1800

cataacttac ggtaaatggc ccgcctggct gaccgcccaa cgacccccgc ccattgacgt 1860

caataatgac gtatgttccc atagtaacgc caatagggac tttccattga cgtcaatggg 1920

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tggagtattt acggtaaact gcccacttgg cagtacatca agtgtatcat atgccaagta     1980

cgcccccctat tgacgtcaat gacggtaaat ggcccgcctg gcattatgcc cagtacatga     2040

ccttatggga ctttcctact tggcagtaca tctacgtatt agtcatcgct attaccatgg     2100

tgatgcggtt ttggcagtac atcaatgggc gtggatagcg gtttgactca cggggatttc     2160

caagtctcca ccccattgac gtcaatggga gtttgttttg gcaccaaaat caacgggact     2220

ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat gggcggtagg cgtgtacggt     2280

gggaggtcta tataagcaga gctggtttag tgaaccgtca gatccgctgg gcactttgca     2340

ctggaactta caacacccga gcaaggacgc gactctgccg ccccaccatg cgcatgcagc     2400

tgctgctgct gatcgccctg agcctggccc tggtgaccaa cagcgatatc gtcatgaccc     2460

agagcccaga tagcctggcc gtgagcctgg gagagcgggc caccatcaac tgcaagagca     2520

gccagagcgt gctgtacagc agcaacaaca agaactacct ggcctggtac cagcagaagc     2580

caggacagcc accaaagctg ctgatctact gggccagcac ccgggagagc ggagtgccag     2640

atcggttcag cggaagcgga agcggaaccg atttcaccct gaccatcagc agcctgcagg     2700

ccgaggatgt ggccgtgtac tactgccagc agtactacag caccccactg accttcggac     2760

agggaaccaa ggtggagatc aag cgt acg gtg gcc gcc cca agc gtg ttc atc     2813
                          Arg Thr Val Ala Ala Pro Ser Val Phe Ile
                          1               5                   10

ttc cca cca agc gat gag cag ctg aag agc gga acc gcc agc gtg gtg      2861
Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val
                15                  20                  25

tgc ctg ctg aac aac ttc tac cca cgg gag gcc aag gtg cag tgg aag      2909
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys
            30                  35                  40

gtg gat aac gcc ctg cag agc gga aac agc cag gag agc gtg acc gag      2957
Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu
        45                  50                  55

cag gat agc aag gat agc acc tac agc ctg agc agc acc ctg acc ctg      3005
Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu
    60                  65                  70

agc aag gcc gat tac gag aag cac aag gtg tac gcc tgc gag gtg acc      3053
Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
75                  80                  85                  90

cac cag gga ctg agc agc cca gtg acc aag agc ttc aac cgc gga gag      3101
His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
                95                  100                 105

tgc cggaagcggc gggccccagt gaagcagacc ctgaacttcg atctgctgaa           3154
Cys
```

```
gctggccgga gatgtggaga gcaacccagg accaatgtac agaatgcagc tgctgagctg     3214

catcgccctg agcctggccc tggtgaccaa cagc cag gtg caa cta gtg gag agc     3269
                                      Gln Val Gln Leu Val Glu Ser
                                              110

gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc       3317
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
115                 120                 125                 130

gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag       3365
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln
                135                 140                 145

gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc       3413
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala
            150                 155                 160

aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc       3461
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
        165                 170                 175

cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg       3509
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
    180                 185                 190

gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg       3557
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg
195                 200                 205                 210

agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg       3605
Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp
                215                 220                 225

gga cag gga acc ctg gtg acc gtg agc agc gct agc acc aag gga cca       3653
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
            230                 235                 240

agc gtg ttc cca ctg gcc cca agc agc aag agc acc agc gga gga acc       3701
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
        245                 250                 255

gcc gcc ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg acc       3749
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
    260                 265                 270

gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc cca       3797
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
275                 280                 285                 290

gcc gtg ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg acc       3845
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
                295                 300                 305

gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg aac       3893
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
            310                 315                 320
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cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag agc       3941
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
        325                 330                 335

tgc gat aag acc cac acg tgc cct cct tgt cca gcc ccc gaa ctg ctg       3989
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
    340                 345                 350

ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca ctg       4037
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
355                 360                 365                 370

atg att agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg tcc       4085
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
                375                 380                 385

cac gaa gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg gag       4133
His Glu Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
            390                 395                 400

gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt aca       4181
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
        405                 410                 415

tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg aac       4229
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
    420                 425                 430

ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc cct       4277
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
435                 440                 445                 450

atc gag aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc cag       4325
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
                455                 460                 465

gtc tac act ctg cca ccc tca aga gat gaa ctg act aag aac cag gtc       4373
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
            470                 475                 480

agc ctg acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc gtg       4421
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
        485                 490                 495

gag tgg gaa agt aac ggc cag cct gag aat aac tac aag act acc cct       4469
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
    500                 505                 510

cca gtg ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg aca       4517
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
515                 520                 525                 530

gtg gac aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct gtg       4565
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
                535                 540                 545

atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca ctg       4613
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
            550                 555                 560
```

agc ccc ggc aaa tgataaaagg aacccgcgct atgacggcaa taaaaagaca 4665
Ser Pro Gly Lys
565

gaataaaacc cacgggtgtt gggtcgtttg ttcataaacc cgggatcgat aaggatcttc 4725

ctagagcatg gctacgtaga taagtagcat ggcgggttaa tcattaacta caaggaaccc 4785

ctagtgatgg agttggccac tccctctctg cgcgctcgct cgctcactga ggccgggcga 4845

ccaaaggtcg cccgacgccc gggctttgcc cgggcggcct cagtgagcga gcgagcgcgc 4905

agccttaatt aacctaattc actggccgtc gttttacaac gtcgtgactg ggaaaaccct 4965

ggcgttaccc aacttaatcg ccttgcagca catccccctt tcgccagctg gcgtaatagc 5025

gaagaggccc gcaccgatcg cccttcccaa cagttgcgca gcctgaatgg cgaatgggac 5085

gcgccctgta gcggcgcatt aagcgcggcg ggtgtggtgg ttacgcgcag cgtgaccgct 5145

acacttgcca gcgccctagc gcccgctcct ttcgctttct tcccttcctt tctcgccacg 5205

ttcgccggct ttccccgtca agctctaaat cgggggctcc ctttagggtt ccgatttagt 5265

gctttacggc acctcgaccc caaaaaactt gattagggtg atggttcacg tagtgggcca 5325

tcgccctgat agacggtttt tcgccctttg acgttggagt ccacgttctt taatagtgga 5385

ctcttgttcc aaactggaac aacactcaac cctatctcgg tctattcttt tgatttataa 5445

gggattttgc cgatttcggc ctattggtta aaaaatgagc tgatttaaca aaaatttaac 5505

gcgaatttta acaaaatatt aacgcttaca atttaggtgg cacttttcgg ggaaatgtgc 5565

gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg ctcatgagac 5625

aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt attcaacatt 5685

tccgtgtcgc ccttattccc ttttttgcgg cattttgcct tcctgttttt gctcacccag 5745

aaacgctggt gaaagtaaaa gatgctgaag atcagttggg tgcacgagtg ggttacatcg 5805

aactggatct caacagcggt aagatccttg agagttttcg ccccgaagaa cgttttccaa 5865

tgatgagcac ttttaaagtt ctgctatgtg gcgcggtatt atcccgtatt gacgccgggc 5925

aagagcaact cggtcgccgc atacactatt ctcagaatga cttggttgag tactcaccag 5985

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taaccgcttt tttgcacaac atgggggatc atgtaactcg ccttgatcgt tgggaaccgg 6165

agctgaatga agccatacca aacgacgagc gtgacaccac gatgcctgta gcaatggcaa 6225

caacgttgcg caaactatta actggcgaac tacttactct agcttcccgg caacaattaa 6285

tagactggat ggaggcggat aaagttgcag gaccacttct gcgctcggcc cttccggctg 6345

gctggtttat tgctgataaa tctggagccg gtgagcgtgg gtctcgcggt atcattgcag 6405

cactggggcc agatggtaag ccctcccgta tcgtagttat ctacacgacg gggagtcagg 6465

caactatgga tgaacgaaat agacagatcg ctgagatagg tgcctcactg attaagcatt 6525

ggtaactgtc agaccaagtt tactcatata tactttagat tgatttaaaa cttcattttt 6585

aatttaaaag gatctaggtg aagatccttt ttgataatct catgaccaaa atcccttaac 6645

gtgagttttc gttccactga gcgtcagacc ccgtagaaaa gatcaaagga tcttcttgag 6705

atccttttt tctgcgcgta atctgctgct tgcaaacaaa aaaaccaccg ctaccagcgg 6765

tggtttgttt gccggatcaa gagctaccaa ctctttttcc gaaggtaact ggcttcagca 6825

gagcgcagat accaaatact gttcttctag tgtagccgta gttaggccac cacttcaaga 6885

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actggaaagc gggcagtgag cgcaacgcaa ttaatgtgag ttagctcact cattaggcac 7605

cccaggcttt acactttatg cttccggctc gtatgttgtg tggaattgtg agcggataac 7665

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aggctgcgcg ctcgctcgct c 7746

<210> 20
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 20

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 21
<211> 129
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 21

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

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

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser

<210> 22
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 22

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
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Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
100 105

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
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20 25 30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50 55 60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65 70 75 80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
85 90 95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
100 105 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
115 120 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
130 135 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145 150 155 160

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
180 185 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
195 200 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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aggggttcct tgtagttaat gattaacccg ccatgctact tatctacgta gccatgctct 180

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tatcacttcc cggggctcag gctcagggac ttctgggtgt agtggttgtg cagggcctcg 300

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accaaaatca acgggacttt ccaaaatgtc gtaacaactc cgccccattg acgcaaatgg 2280

gcggtaggcg tgtacggtgg gaggtctata taagcagagc tggtttagtg aaccgtcaga 2340

tccgctgggc actttgcact ggaacttaca acacccgagc aaggacgcga ctctgccgcc 2400

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ccaccatgcg catgcagctg ctgctgctga tcgccctgag cctggccctg gtgaccaaca     2460

gc gat atc gtc atg acc cag agc cca gat agc ctg gcc gtg agc ctg        2507
   Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
   1               5                  10                  15

gga gag cgg gcc acc atc aac tgc aag agc agc cag agc gtg acc ttc       2555
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe
                20                  25                  30

aac tac aag aac tac ctg gcc tgg tac cag cag aag cca gga cag cca       2603
Asn Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro
            35                  40                  45

cca aag ctg ctg atc tac tgg gcc agc acc cgg gag agc gga gtg cca       2651
Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro
        50                  55                  60

gat cgg ttc agc gga agc gga agc gga acc gat ttc acc ctg acc atc       2699
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
    65                  70                  75

agc agc ctg cag gcc gag gat gtg gcc gtg tac tac tgc cag cag cac       2747
Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His
80                  85                  90                  95

tac cgg acc cca cca acc ttc gga cag gga acc aag gtg gag atc aag       2795
Tyr Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                100                 105                 110

cgt acg gtg gcc gcc cca agc gtg ttc atc ttc cca cca agc gat gag       2843
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
            115                 120                 125

cag ctg aag agc gga acc gcc agc gtg gtg tgc ctg ctg aac aac ttc       2891
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
        130                 135                 140

tac cca cgg gag gcc aag gtg cag tgg aag gtg gat aac gcc ctg cag       2939
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
    145                 150                 155

agc gga aac agc cag gag agc gtg acc gag cag gat agc aag gat agc       2987
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
160                 165                 170                 175

acc tac agc ctg agc agc acc ctg acc ctg agc aag gcc gat tac gag       3035
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
                180                 185                 190

aag cac aag gtg tac gcc tgc gag gtg acc cac cag gga ctg agc agc       3083
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
            195                 200                 205

cca gtg acc aag agc ttc aac cgc gga gag tgc cggaagcggc gggccccagt     3136
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
        210                 215
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gaagcagacc ctgaacttcg atctgctgaa gctggccgga gatgtggaga gcaacccagg     3196

accaatgtac agaatgcagc tgctgagctg catcgccctg agcctggccc tggtgaccaa     3256

cagc cag gtg caa cta gtg gag agc gga gga gga gtg gtg cag cca gga      3305
     Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
         220                 225                 230

cgg agc ctg cgg ctg agc tgc gcc gcc agc gga ttc acc ttc agc acc      3353
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr
    235                 240                 245

tac gcc atg cac tgg gtg cgg cag gcc cca gga aag gga ctg gag tgg      3401
Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
250                 255                 260                 265

gtg gcc gtg atc agc tac gat gcc aac tac aag tac tac gcc gat agc      3449
Val Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser
                270                 275                 280

gtg aag gga cgg ttc acc atc agc cgg gat aac agc aag aac acc ctg      3497
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
            285                 290                 295

tac ctg cag atg aac agc ctg cgg gcc gag gat acc gcc gtg tac tac      3545
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
        300                 305                 310

tgc gcc aag gat agc cag ctg cgg agc ctg ctg tac ttc gag tgg ctg      3593
Cys Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu
    315                 320                 325

agc cag gga tac ttc gat tac tgg gga cag gga acc ctg gtg acc gtg      3641
Ser Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
330                 335                 340                 345

agc agc gct agc acc aag gga cca agc gtg ttc cca ctg gcc cca agc      3689
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
                350                 355                 360

agc aag agc acc agc gga gga acc gcc gcc ctg gga tgc ctg gtg aag      3737
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
            365                 370                 375

gat tac ttc cca gag cca gtg acc gtg agc tgg aac agc gga gcc ctg      3785
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
        380                 385                 390

acc agc gga gtg cac acc ttc cca gcc gtg ctg cag agc agc gga ctg      3833
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
    395                 400                 405

tat agc ctg agc agc gtg gtg acc gtg cca agc agc agc ctg gga acc      3881
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
410                 415                 420                 425

cag acc tac atc tgc aac gtg aac cac aag cca agc aac acc aag gtg      3929
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
                430                 435                 440
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gat aag aag gtg gag cca aag agc tgc gat aag acc cac acg tgc cct       3977
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
            445                 450                 455

cct tgt cca gcc ccc gaa ctg ctg ggc ggg cct agc gtg ttc ctg ttt       4025
Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
        460                 465                 470

ccc cct aag cct aaa gat aca ctg atg att agt aga acc cca gag gtc       4073
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
    475                 480                 485

aca tgc gtg gtc gtg gac gtg tcc cac gaa gag cct gac gtg aag ttc       4121
Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp Val Lys Phe
490                 495                 500                 505

aac tgg tac gtg gat ggc gtg gag gtg cac aat gct aag act aaa cca       4169
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                510                 515                 520

cgc gaa gag cag tat aat agt aca tac cga gtc gtg tca gtc ctg aca       4217
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
            525                 530                 535

gtg ctg cac cag gat tgg ctg aac ggc aag gag tat aag tgc aag gtg       4265
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
        540                 545                 550

tct aac aag gcc ctg ccc gcc cct atc gag aaa aca att agc aag gcc       4313
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
    555                 560                 565

aaa ggg cag cca cgg gaa ccc cag gtc tac act ctg cca ccc tca aga       4361
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
570                 575                 580                 585

gat gaa ctg act aag aac cag gtc agc ctg acc tgt ctg gtg aaa ggc       4409
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                590                 595                 600

ttc tac ccc agc gac atc gcc gtg gag tgg gaa agt aac ggc cag cct       4457
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
            605                 610                 615

gag aat aac tac aag act acc cct cca gtg ctg gat agc gac ggg tcc       4505
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
        620                 625                 630

ttc ttc ctg tat agc aag ctg aca gtg gac aaa tcc cgc tgg cag cag       4553
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
    635                 640                 645

gga aac gtc ttt tcc tgt tct gtg atg cat gag gcc ctg cac aat cat       4601
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
650                 655                 660                 665

tac acc cag aag agt ctg tca ctg agc ccc ggc aaa tgataaaagg            4647
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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670 675

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<213> Artificial sequence

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<400> 25

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
20 25 30

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

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
50 55 60

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
85 90 95

Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 26
<211> 107
<212> PRT
<213> Artificial sequence

<220>
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<400> 26

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95

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Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210>  27
<211>  129
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic Construct

<400>  27

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


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


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


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


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


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


Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
            100                 105                 110


Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125


Ser



<210>  28
<211>  107
<212>  PRT
<213>  Artificial sequence

<220>
<223>  Synthetic Construct
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<400> 28

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
100 105

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
20 25 30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
35 40 45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
50 55 60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65 70 75 80

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Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                 135                 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                 150                 155                 160

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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<222> (589)..(909)
<223> complement - TCN032\VL

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<223> complement - leader

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<223> CH2-3

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<222> (4693)..(4770)
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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac 180

gtagccatgc tctaggaaga tctcacacaa aaaaccaaca cacagatgta atgaaaataa 240

agatatttta ttgcggccgc tttatcagca ctctccgcgg ttgaagctct tggtcactgg 300

gctgctcagt ccctggtggg tcacctcgca ggcgtacacc ttgtgcttct cgtaatcggc 360

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cacgctctcc tggctgtttc cgctctgcag ggcgttatcc accttccact gcaccttggc 480

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tagtcatcgc tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc 1500

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ggtttgactc acggggattt ccaagtctcc accccattga cgtcaatggg agtttgtttt     1560

ggcaccaaaa tcaacgggac tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa     1620

tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctggttta gtgaaccgtc     1680

agatccgctg ctagcgggca ctttgcactg gaacttacaa cacccgagca aggacgcgac     1740

tctccaccat gcgcatgcag ctgctgctgc tgatcgccct gagcctggcc ctggtgacca     1800

acagc cag gtg cag ctg cag gag agc gga cca gga ctg gtg aag cca agc      1850
      Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
      1               5                  10                  15

gag acc ctg agc ctg acc tgc acc gtg agc gga agc agc atc agc aac       1898
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn
                 20                  25                  30

tac tac tgg agc tgg atc cgg cag agc cca gga aag gga ctg gag tgg       1946
Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
            35                  40                  45

atc gga ttc atc tac tac gga gga aac acc aag tac aac cca agc ctg       1994
Ile Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu
        50                  55                  60

aag agc cgg gtg acc atc agc cag gat acc agc aag agc cag gtg agc       2042
Lys Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser
    65                  70                  75

ctg acc atg agc agc gtg acc gcc gcc gag agc gcc gtg tac ttc tgc       2090
Leu Thr Met Ser Ser Val Thr Ala Ala Glu Ser Ala Val Tyr Phe Cys
80                  85                  90                  95

gcc cgg gcc agc tgc agc gga gga tac tgc atc ctg gat tac tgg gga       2138
Ala Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly
                100                 105                 110

cag gga acc ctg gtg acc gtg agc agc gcg tcg acc aag gga cct tcg       2186
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
            115                 120                 125

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg       2234
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
        130                 135                 140

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg       2282
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
    145                 150                 155

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct       2330
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
160                 165                 170                 175

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg       2378
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
                180                 185                 190
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ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac      2426
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
            195                 200                 205

aag ccc agc aac acc aag gtg gac aag aaa gtt gaaccaaaga gctgcgacaa     2479
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
        210                 215

gacccacacg tgtcccccct gccctgcccc tgaactgctg ggaggcccca gcgtgttcct     2539

gttcccccca aagcccaagg acaccctgat gatcagccgg acccccgaag tgacctgcgt     2599

ggtggtggac gtgtcccacg aggaccctga agtgaagttt aattggtacg tggacggcgt     2659

ggaagtgcac aacgccaaga ccaagcccag agaggaacag tacaacagca cctaccgggt     2719

ggtgtccgtg ctgaccgtgc tgcaccagga ctggctgaac ggcaaagagt acaagtgcaa     2779

ggtgtccaac aaggccctgc ctgcccccat cgagaaaacc atcagcaagg ccaagggcca     2839

gccccgcgag cctcaggtct acacactgcc ccccagccgg gaagagatga ccaagaacca     2899

ggtgtccctg acctgcctgg tcaagggctt ctaccccagc gacatcgccg tggaatggga     2959

gagcaacggc cagcccgaga acaactacaa gaccaccccc cctgtgctgg acagcgacgg     3019

ctcattcttc ctgtatagca agctgaccgt ggacaagagc cggtggcagc agggcaacgt     3079

gttcagctgc agcgtgatgc acgaggccct gcacaaccac tacacccaga agtccctgag     3139

cctgagcccc ggcagaaagc ggagagcccc cgtgaagcag accctgaact tcgacctgct     3199

gaagctggcc ggcgacgtgg aaagcaaccc tggccctatg tacagaatgc agctgctgag     3259

ctgcatcgcc ctgagcctgg ccctggtgac caacagc cag gtg caa cta gtg gag      3314
                                      Gln Val Gln Leu Val Glu
                                          220

agc gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc      3362
Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys
225                 230                 235                 240

gcc gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg      3410
Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg
                245                 250                 255

cag gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat      3458
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp
            260                 265                 270

gcc aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc      3506
Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile
        275                 280                 285

agc cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg      3554
Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
    290                 295                 300

cgg gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg      3602
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Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu
305                 310                 315                 320

cgg agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac      3650
Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr
                325                 330                 335

tgg gga cag gga acc ctg gtg acc gtg agc agc gcc agc acc aag ggg      3698
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
            340                 345                 350

ccc agc gtg ttc cca ctg gcc cca agc agc aag agc acc agc gga gga      3746
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
        355                 360                 365

acc gcc gcc ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg      3794
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
    370                 375                 380

acc gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc      3842
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
385                 390                 395                 400

cca gcc gtg ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg      3890
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
                405                 410                 415

acc gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg      3938
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
            420                 425                 430

aac cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag      3986
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
        435                 440                 445

agc tgc gat aag acc cac acg tgc cct cca tgt cca gcc ccc gaa ctg      4034
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu
    450                 455                 460

ctg ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca      4082
Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
465                 470                 475                 480

ctg atg att agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg      4130
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
                485                 490                 495

tcc cac gaa gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg      4178
Ser His Glu Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val
            500                 505                 510

gag gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt      4226
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
        515                 520                 525

aca tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg      4274
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
    530                 535                 540
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aac ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc      4322
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
545                 550                 555                 560

cct atc gag aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc      4370
Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
                565                 570                 575

cag gtc tac act ctg cca ccc tca aga gat gaa ctg act aag aac cag      4418
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
            580                 585                 590

gtc agc ctg acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc      4466
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
        595                 600                 605

gtg gag tgg gaa agt aac ggc cag cct gag aat aac tac aag act acc      4514
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
    610                 615                 620

cct cca gtg ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg      4562
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
625                 630                 635                 640

aca gtg gac aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct      4610
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
                645                 650                 655

gtg atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca      4658
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            660                 665                 670

ctg agc ccc ggc aaa tgataaaaag cttctcgaga aggaacccgc gctatgacgg      4713
Leu Ser Pro Gly Lys
        675

caataaaaag acagaataaa acccacgggt gttgggtcgt ttgttcataa acccgggaag     4773

cttatcgata aggatcttcc tagagcatgg ctacgtagat aagtagcatg gcgggttaat     4833

cattaactac aaggaacccc tagtgatgga gttggccact ccctctctgc gcgctcgctc     4893

gctcactgag gccgggcgac caaaggtcgc ccgacgcccg ggctttgccc gggcggcctc     4953

agtgagcgag cgagcgcgca gccttaatta acctaattca ctggccgtcg ttttacaacg     5013

tcgtgactgg gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt     5073

cgccagctgg cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag     5133

cctgaatggc gaatgggacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt     5193

tacgcgcagc gtgaccgcta cacttgccag cgccctagcg cccgctcctt tcgctttctt     5253

cccttccttt ctcgccacgt tcgccggctt tccccgtcaa gctctaaatc gggggctccc     5313

tttagggttc cgatttagtg ctttacggca cctcgacccc aaaaaacttg attagggtga     5373

tggttcacgt agtgggccat cgccctgata gacggttttt cgccctttga cgttggagtc     5433
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cacgttcttt aatagtggac tcttgttcca aactggaaca acactcaacc ctatctcggt 5493

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cgccacctct gacttgagcg tcgatttttg tgatgctcgt caggggggcg gagcctatgg 7353

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<400> 31

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser Leu
65 70 75 80

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

Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 32
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<212> PRT
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<220>
<223> Synthetic Construct

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1   5   10   15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20   25   30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35   40   45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50   55   60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65   70   75   80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85   90   95

Lys Val

<210> 33
<211> 129
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 33

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr

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            20                  25                  30

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
            100                 105                 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

Ser
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<210> 34
<211> 107
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 34

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
```

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
            100                 105
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<210> 35
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<212> PRT
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<220>
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<400> 35

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1               5                  10                  15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            20                  25                  30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
        35                  40                  45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    50                  55                  60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65                  70                  75                  80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                 135                 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                 150                 155                 160
```

```
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                165                 170                 175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215                 220
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<220>
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<222> (453)..(1121)
<223> complement - CH'2-3

<220>
<221> misc_feature
<222> (1125)..(1457)
<223> complement - C05\VL

<220>
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<222> (1458)..(1502)
<223> SL\from\3bn201co

<220>
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<222> (1503)..(1916)
<223> complement - C05\VH

<220>
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<223> leader

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<222> (2371)..(2412)

<223> complement - CMV\mp2

<220>
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<222> (2413)..(2881)
<223> enhancer

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<222> (2882)..(3007)
<223> CMV\mp1

<220>
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<222> (3067)..(3055)
<223> leader

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<221> CDS
<222> (3124)..(3510)
<223> FI6\VH

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<222> (3511)..(3555)
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<222> (3556)..(3888)
<223> FI6\VL

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<222> (3892)..(4560)
<223> CH2-3

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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac 180

gtagccatgc tctaggaaga tcattttacc acatttgtag aggttttact tgctttaaaa 240

aacctcccac atctcccccc gaacctgaaa cataaaatga atgcaattgt tgttgttaac 300

ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat 360

aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat 420

catgtctgct cgaagcggcc gcaagcttat cacttcccgg ggctcaggct cagggacttc 480

tgggtgtagt ggttgtgcag ggcctcgtgc atcacgctgc agctgaacac gttgccctgc 540

tgccaccggc tcttgtccac ggtcagcttg ctatacagga agaatgagcc gtcgctgtcc 600

agcacagggg gggtggtctt gtagttgttc tcgggctggc cgttgctctc ccattccacg 660

gcgatctcgc tggggtagaa gcccttgacc aggcaggtca gggacacctg gttcttggtc 720

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ccgctcgaga cggtcaccag ggttccctgt ccccacacat cgaaggcatc tcccaccaga 1560

tcggcccgct cccatccggc gctcaccacc tgctgcatgg acatgtgctt ggcgcagtag 1620

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acggcgtagt agctcagggt gctctctccg aagctgcttc cgcttcccac gcagctcagc 1860

cgcaggctct ctcctggctg caccagtcct cctccgctct cctgcagctg cacctgtgaa 1920

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cggcagagtc gcgtccttgc tcgggtgttg taagttccag tgcaaagtgc cctagcctat 2040

agtgagtcgt attaagtact ctagccttaa gagctgtaat tgaactggga gtggacacct 2100

gtggagagaa aggcaaagtg gatgtcagta agaccaatag gtgcctatca gaaacgcaag 2160

agtcttctct gtctcgacaa gcccagtttc tattggtctc cttaaacctg tcttgtaacc 2220

ttgatactta cctgcccagt gcctcacgac caacttctgc agcttaagtt cgagactgtt 2280

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gtgtcagaag cactgactgc gttagcaatt taactgtgat aaactaccgc aataaagctt     2340

ctagtgatct gacggttcac taaacgagct ctgcttatat aggcctccca ccgtacacgc     2400

cacctcgaca tacctagtta ttaatagtaa tcaattacgg ggtcattagt tcatagccca     2460

tatatggagt tccgcgttac ataacttacg gtaaatggcc cgcctggctg accgcccaac     2520

gacccccgcc cattgacgtc aataatgacg tatgttccca tagtaacgcc aatagggact     2580

ttccattgac gtcaatgggt ggagtattta cggtaaactg cccacttggc agtacatcaa     2640

gtgtatcata tgccaagtac gccccctatt gacgtcaatg acggtaaatg gcccgcctgg     2700

cattatgccc agtacatgac cttatgggac tttcctactt ggcagtacat ctacgtatta     2760

gtcatcgcta ttaccatggt gatgcggttt tggcagtaca tcaatgggcg tggatagcgg     2820

tttgactcac ggggatttcc aagtctccac cccattgacg tcaatgggag tttgttttgg     2880

caccaaaatc aacgggactt tccaaaatgt cgtaacaact ccgccccatt gacgcaaatg     2940

ggcggtaggc gtgtacggtg ggaggtctat ataagcagag ctggtttagt gaaccgtcag     3000

atccgctggg cactttgcac tggaacttac aacacccgag caaggacgcg actctgccgc     3060

cccaccatgc gcatgcagct gctgctgctg atcgccctga gcctggccct ggtgaccaac     3120

agc cag gtg caa ttg gtg gag agc gga gga gga gtg gtg cag cca gga         3168
    Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
    1               5                   10                  15

cgg agc ctg cgg ctg agc tgc gcc gcc agc gga ttc acc ttc agc acc       3216
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr
                20                  25                  30

tac gcc atg cac tgg gtg cgg cag gcc cca gga aag gga ctg gag tgg       3264
Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
            35                  40                  45

gtg gcc gtg atc agc tac gat gcc aac tac aag tac tac gcc gat agc       3312
Val Ala Val Ile Ser Tyr Asp Ala Asn Tyr Lys Tyr Tyr Ala Asp Ser
        50                  55                  60

gtg aag gga cgg ttc acc atc agc cgg gat aac agc aag aac acc ctg       3360
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
    65                  70                  75

tac ctg cag atg aac agc ctg cgg gcc gag gat acc gcc gtg tac tac       3408
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
80                  85                  90                  95

tgc gcc aag gat agc cag ctg cgg agc ctg ctg tac ttc gag tgg ctg       3456
Cys Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu
                100                 105                 110

agc cag gga tac ttc gat tac tgg gga cag gga acc ctg gtg acc gtg       3504
Ser Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
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           115                 120                 125

agc agc ggcggaggag gcagcggagg aggagggtcc ggaggcgggg gatct gat atc     3561
Ser Ser                                                   Asp Ile
                                                          130

gtc atg acc cag agc cca gat agc ctg gcc gtg agc ctg gga gag cgg       3609
Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
           135                 140                 145

gcc acc atc aac tgc aag agc agc cag agc gtg acc ttc aac tac aag       3657
Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn Tyr Lys
       150                 155                 160

aac tac ctg gcc tgg tac cag cag aag cca gga cag cca cca aag ctg       3705
Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu
   165                 170                 175

ctg atc tac tgg gcc agc acc cgg gag agc gga gtg cca gat cgg ttc       3753
Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe
180                 185                 190                 195

agc gga agc gga agc gga acc gat ttc acc ctg acc atc agc agc ctg       3801
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                200                 205                 210

cag gcc gag gat gtg gcc gtg tac tac tgc cag cag cac tac cgg acc       3849
Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr Arg Thr
           215                 220                 225

cca cca acc ttc gga cag gga acc aag gtg gag atc aag gcc acg tgc       3897
Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys     Thr Cys
       230                 235                 240

cct cca tgt cca gcc ccc gaa ctg ctg ggc ggg cct agc gtg ttc ctg       3945
Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
       245                 250                 255

ttt ccc cct aag cct aaa gat aca ctg atg att agt aga acc cca gag       3993
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
   260                 265                 270

gtc aca tgc gtg gtc gtg gac gtg tcc cac gaa gag cct gac gtg aag       4041
Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp Val Lys
275                 280                 285                 290

ttc aac tgg tac gtg gat ggc gtg gag gtg cac aat gct aag act aaa       4089
Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
                295                 300                 305

cca cgc gaa gag cag tat aat agt aca tac cga gtc gtg tca gtc ctg       4137
Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
           310                 315                 320

aca gtg ctg cac cag gat tgg ctg aac ggc aag gag tat aag tgc aag       4185
Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
       325                 330                 335

gtg tct aac aag gcc ctg ccc gcc cct atc gag aaa aca att agc aag       4233
```

```
Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
    340                 345                 350

gcc aaa ggg cag cca cgg gaa ccc cag gtc tac act ctg cca ccc tca      4281
Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
355                 360                 365                 370

aga gat gaa ctg act aag aac cag gtc agc ctg acc tgt ctg gtg aaa      4329
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
                375                 380                 385

ggc ttc tac ccc agc gac atc gcc gtg gag tgg gaa agt aac ggc cag      4377
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
            390                 395                 400

cct gag aat aac tac aag act acc cct cca gtg ctg gat agc gac ggg      4425
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
        405                 410                 415

tcc ttc ttc ctg tat agc aag ctg aca gtg gac aaa tcc cgc tgg cag      4473
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
    420                 425                 430

cag gga aac gtc ttt tcc tgt tct gtg atg cat gag gcc ctg cac aat      4521
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
435                 440                 445                 450

cat tac acc cag aag agt ctg tca ctg agc ccc ggc aaa tgataagctt      4570
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
                455                 460

gcggccgctt cgagcagaca tgataagata cattgatgag tttggacaaa ccacaactag     4630

aatgcagtga aaaaaatgct ttatttgtga aatttgtgat gctattgctt tatttgtaac     4690

cattataagc tgcaataaac aagttaacaa caacaattgc attcatttta tgtttcaggt     4750

tcaggggggag atgtgggagg ttttttaaag caagtaaaac ctctacaaat gtggtaaaat     4810

cgataaggat cttcctagag catggctacg tagataagta gcatggcggg ttaatcatta     4870

actacaagga acccctagtg atggagttgg ccactccctc tctgcgcgct cgctcgctca     4930

ctgaggccgg gcgaccaaag gtcgcccgac gcccgggctt tgcccgggcg gcctcagtga     4990

gcgagcgagc gcgcagcctt aattaaccta attcactggc cgtcgtttta caacgtcgtg     5050

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gctggcgtaa tagcgaagag gcccgcaccg atcgcccttc ccaacagttg cgcagcctga     5170

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cctttctcgc cacgttcgcc ggctttcccc gtcaagctct aaatcggggg ctccctttag     5350

ggttccgatt tagtgcttta cggcacctcg accccaaaaa acttgattag ggtgatggtt     5410
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cacgtagtgg gccatcgccc tgatagacgg tttttcgccc tttgacgttg gagtccacgt 5470

tctttaatag tggactcttg ttccaaactg gaacaacact caaccctatc tcggtctatt 5530

cttttgattt ataagggatt ttgccgattt cggcctattg gttaaaaaat gagctgattt 5590

aacaaaaatt taacgcgaat tttaacaaaa tattaacgct tacaatttag gtggcacttt 5650

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gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt gccttcctgt 5830

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agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg tattatcccg 6010

tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga atgacttggt 6070

tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa gagaattatg 6130

cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga caacgatcgg 6190

aggaccgaag gagctaaccg ctttttttgca caacatgggg gatcatgtaa ctcgccttga 6250

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aactggcttc agcagagcgc agataccaaa tactgttctt ctagtgtagc cgtagttagg 6970

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cgacaggttt cccgactgga aagcgggcag tgagcgcaac gcaattaatg tgagttagct 7690

cactcattag gcaccccagg ctttacactt tatgcttccg gctcgtatgt tgtgtggaat 7750

tgtgagcgga taacaatttc acacaggaaa cagctatgac catgattacg ccagatttaa 7810

ttaa 7814

<210> 37
<211> 129
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 37

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

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

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser

100 105 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

Ser

<210> 38
<211> 111
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 38

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

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
20 25 30

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

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
50 55 60

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
85 90 95

Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 39
<211> 223
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 39

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Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1               5                  10                  15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            20                  25                  30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
        35                  40                  45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    50                  55                  60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65                  70                  75                  80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                 135                 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                 150                 155                 160

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

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215                 220
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<212> DNA

<213> Artificial sequence

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<222> (1125)..(1460)
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<223> complement - leader

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<222> (2341)..(2382)
<223> complement - CMV\mp2

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<222> (3094)..(3480)

<223> FI6\VH

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<223> SL\from\3bn201co

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<223> FI6\VL

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<223> CH2-3

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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac 180

gtagccatgc tctaggaaga tcattttacc acatttgtag aggttttact tgctttaaaa 240

aacctcccac atctcccccc gaacctgaaa cataaaatga atgcaattgt tgttgttaac 300

ttgtttattg cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat 360

aaagcatttt tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat 420

catgtctgct cgaagcggcc gcaagcttat cacttcccgg ggctcaggct cagggacttc 480

tgggtgtagt ggttgtgcag ggcctcgtgc atcacgctgc agctgaacac gttgccctgc 540

tgccaccggc tcttgtccac ggtcagcttg ctatacagga agaatgagcc gtcgctgtcc 600

agcacagggg gggtggtctt gtagttgttc tcgggctggc cgttgctctc ccattccacg 660

gcgatctcgc tggggtagaa gcccttgacc aggcaggtca gggacacctg gttcttggtc 720

atctcttccc ggctgggggg cagtgtgtag acctgaggct cgcggggctg gcccttggcc 780

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tctttgccgt tcagccagtc ctggtgcagc acggtcagca cggacaccac ccggtaggtg 900

ctgttgtact gttcctctct gggcttggtc ttggcgttgt gcacttccac gccgtccacg 960

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cctccggtct ccaccagctg cacctctgaa ttcgtcacca gggccaggct cagggcgatc 1920

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taagttccag tgcaaagtgc cctagcctat agtgagtcgt attaagtact ctagccttaa 2040

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agaccaatag gtgcctatca gaaacgcaag agtcttctct gtctcgacaa gcccagtttc 2160

tattggtctc cttaaacctg tcttgtaacc ttgatactta cctgcccagt gcctcacgac 2220

caacttctgc agcttaagtt cgagactgtt gtgtcagaag cactgactgc gttagcaatt 2280

taactgtgat aaactaccgc aataaagctt ctagtgatct gacggttcac taaacgagct 2340

ctgcttatat aggcctccca ccgtacacgc cacctcgaca tacctagtta ttaatagtaa 2400

tcaattacgg ggtcattagt tcatagccca tatatggagt tccgcgttac ataacttacg 2460

gtaaatggcc cgcctggctg accgcccaac gacccccgcc cattgacgtc aataatgacg 2520

tatgttccca tagtaacgcc aatagggact ttccattgac gtcaatgggt ggagtattta 2580

cggtaaactg cccacttggc agtacatcaa gtgtatcata tgccaagtac gccccctatt 2640

gacgtcaatg acggtaaatg gcccgcctgg cattatgccc agtacatgac cttatgggac 2700

tttcctactt ggcagtacat ctacgtatta gtcatcgcta ttaccatggt gatgcggttt 2760

tggcagtaca tcaatgggcg tggatagcgg tttgactcac ggggatttcc aagtctccac 2820

cccattgacg tcaatgggag tttgttttgg caccaaaatc aacgggactt tccaaaatgt 2880

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cgtaacaact ccgccccatt gacgcaaatg ggcggtaggc gtgtacggtg ggaggtctat     2940

ataagcagag ctggtttagt gaaccgtcag atccgctggg cactttgcac tggaacttac     3000

aacacccgag caaggacgcg actctgccgc cccaccatgc gcatgcagct gctgctgctg     3060

atcgccctga gcctggccct ggtgaccaac agc cag gtg caa ttg gtg gag agc      3114
                                      Gln Val Gln Leu Val Glu Ser
                                      1               5

gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc       3162
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
        10                  15                  20

gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag       3210
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln
    25                  30                  35

gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc       3258
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala
40                  45                  50                  55

aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc       3306
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
                60                  65                  70

cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg       3354
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
            75                  80                  85

gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg       3402
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg
        90                  95                  100

agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg       3450
Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp
    105                 110                 115

gga cag gga acc ctg gtg acc gtg agc agc ggcggaggag gcagcggagg        3500
Gly Gln Gly Thr Leu Val Thr Val Ser Ser
120                 125

aggagggtcc ggaggcgggg gatct gat atc gtc atg acc cag agc cca gat       3552
                           Asp Ile Val Met Thr Gln Ser Pro Asp
                           130                 135

agc ctg gcc gtg agc ctg gga gag cgg gcc acc atc aac tgc aag agc       3600
Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser
    140                 145                 150

agc cag agc gtg acc ttc aac tac aag aac tac ctg gcc tgg tac cag       3648
Ser Gln Ser Val Thr Phe Asn Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln
155                 160                 165                 170

cag aag cca gga cag cca cca aag ctg ctg atc tac tgg gcc agc acc       3696
Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr
                175                 180                 185
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cgg gag agc gga gtg cca gat cgg ttc agc gga agc gga agc gga acc      3744
Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
            190                 195                 200

gat ttc acc ctg acc atc agc agc ctg cag gcc gag gat gtg gcc gtg      3792
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val
        205                 210                 215

tac tac tgc cag cag cac tac cgg acc cca cca acc ttc gga cag gga      3840
Tyr Tyr Cys Gln Gln His Tyr Arg Thr Pro Pro Thr Phe Gly Gln Gly
    220                 225                 230

acc aag gtg gag atc aag gccacgtgcc ctccatgtcc agcccccgaa             3888
Thr Lys Val Glu Ile Lys
235                 240

ctgctgggcg ggcctagcgt gttcctgttt ccccctaagc ctaaagatac actgatgatt     3948

agtagaaccc cagaggtcac atgcgtggtc gtggacgtgt cccacgaaga gcctgacgtg     4008

aagttcaact ggtacgtgga tggcgtggag gtgcacaatg ctaagactaa accacgcgaa     4068

gagcagtata atagtacata ccgagtcgtg tcagtcctga cagtgctgca ccaggattgg     4128

ctgaacggca aggagtataa gtgcaaggtg tctaacaagg ccctgcccgc ccctatcgag     4188

aaaacaatta gcaaggccaa agggcagcca cgggaacccc aggtctacac tctgccaccc     4248

tcaagagatg aactgactaa gaaccaggtc agcctgacct gtctggtgaa aggcttctac     4308

cccagcgaca tcgccgtgga gtgggaaagt aacggccagc ctgagaataa ctacaagact     4368

acccctccag tgctggatag cgacgggtcc ttcttcctgt atagcaagct gacagtggac     4428

aaatcccgct ggcagcaggg aaacgtcttt tcctgttctg tgatgcatga ggccctgcac     4488

aatcattaca cccagaagag tctgtcactg agccccggca aatgataagc ttgcggccgc     4548

ttcgagcaga catgataaga tacattgatg agtttggaca aaccacaact agaatgcagt     4608

gaaaaaaatg ctttatttgt gaaatttgtg atgctattgc tttatttgta accattataa     4668

gctgcaataa acaagttaac aacaacaatt gcattcattt tatgtttcag gttcaggggg     4728

agatgtggga ggtttttaa agcaagtaaa acctctacaa atgtggtaaa atcgataagg     4788

atcttcctag agcatggcta cgtagataag tagcatggcg ggttaatcat taactacaag     4848

gaacccctag tgatggagtt ggccactccc tctctgcgcg ctcgctcgct cactgaggcc     4908

gggcgaccaa aggtcgcccg acgcccgggc tttgcccggg cggcctcagt gagcgagcga     4968

gcgcgcagcc ttaattaacc taattcactg gccgtcgttt tacaacgtcg tgactgggaa     5028

aaccctggcg ttacccaact taatcgcctt gcagcacatc ccccttcgc cagctggcgt     5088

aatagcgaag aggcccgcac cgatcgccct tcccaacagt tgcgcagcct gaatggcgaa     5148

tgggacgcgc cctgtagcgg cgcattaagc gcggcgggtg tggtggttac gcgcagcgtg     5208
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gccacgttcg ccggctttcc ccgtcaagct ctaaatcggg ggctcccttt agggttccga 5328

tttagtgctt tacggcacct cgaccccaaa aaacttgatt agggtgatgg ttcacgtagt 5388

gggccatcgc cctgatagac ggtttttcgc cctttgacgt tggagtccac gttctttaat 5448

agtggactct tgttccaaac tggaacaaca ctcaacccta tctcggtcta ttcttttgat 5508

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ttccaatgat gagcactttt aaagttctgc tatgtggcgc ggtattatcc cgtattgacg 5988

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cagcggtggt ttgtttgccg gatcaagagc taccaactct ttttccgaag gtaactggct 6888

tcagcagagc gcagatacca aatactgttc ttctagtgta gccgtagtta ggccaccact 6948

tcaagaactc tgtagcaccg cctacatacc tcgctctgct aatcctgtta ccagtggctg 7008

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ttgagcgtcg atttttgtga tgctcgtcag gggggcggag cctatggaaa aacgccagca 7368

acgcggcctt tttacggttc ctggcctttt gctggccttt tgctcacatg ttctttcctg 7428

cgttatcccc tgattctgtg gataaccgta ttaccgcctt tgagtgagct gataccgctc 7488

gccgcagccg aacgaccgag cgcagcgagt cagtgagcga ggaagcggaa gagcgcccaa 7548

tacgcaaacc gcctctcccc gcgcgttggc cgattcatta atgcagctgg cacgacaggt 7608

ttcccgactg gaaagcgggc agtgagcgca acgcaattaa tgtgagttag ctcactcatt 7668

aggcacccca ggctttacac tttatgcttc cggctcgtat gttgtgtgga attgtgagcg 7728

gataacaatt tcacacagga aacagctatg accatgatta cgccagattt aattaa 7784

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<223> Synthetic Construct

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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
            100                 105                 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
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Ser
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<210> 42
<211> 111
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 42

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Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Thr Phe Asn
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Tyr Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
    50                  55                  60

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

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln His Tyr
                85                  90                  95

Arg Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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<210> 43
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<223> stop cassette (complement)

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<222> (268)..(588)
<223> constant light (on complementary strand)

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<222> (967)..(971)
<223> Kozak (located on complementary strand)

<220>
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<223> c-myc 5' UTR (located on complementary strand)

<220>
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<223> CMV\mp2

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<222> (1026)..(1094)

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<222> (1564)..(1689)

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<222> (1696)..(1743)
<223> c-myc 5' UTR

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<222> (1744)..(1748)
<223> Kozak

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<222> (1749)..(1805)

<223> leader

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<223> TCN032 variable heavy

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<223> inverted terminal repeat

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<223> CH1

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<223> CH1

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<223> hinge-CH2'-CH3'

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<222> (3153)..(3164)
<223> furin cleavage site

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<222> (3165)..(3236)
<223> F2A linker

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<222> (3239)..(3296)

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<222> (3239)..(3296)

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<222> (3297)..(3683)
<223> FI6 VH

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<222> (3684)..(4004)
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<222> (4005)..(4673)
<223> CH2-3

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<222> (4674)..(4680)

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<222> (4693)..(4770)
<223> TKpAshort

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<222> (5151)..(5606)

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<222> (5737)..(6594)
<223> Amp-R

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<223> col\E1\origin

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caactccatc actaggggtt ccttgtagtt aatgattaac ccgccatgct acttatctac 180

gtagccatgc tctaggaaga tctcacacaa aaaaccaaca cacagatgta atgaaaataa 240

agatatttta ttgcggccgc tttatcagca ctctccgcgg ttgaagctct tggtcactgg 300

gctgctcagt ccctggtggg tcacctcgca ggcgtacacc ttgtgcttct cgtaatcggc 360

cttgctcagg gtcagggtgc tgctcaggct gtaggtgcta tccttgctat cctgctcggt 420

cacgctctcc tggctgtttc cgctctgcag ggcgttatcc accttccact gcaccttggc 480

ctcccgtggg tagaagttgt tcagcaggca caccacgctg gcggttccgc tcttcagctg 540

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ccgggttcct cctccgaagg tcagtggtgg gctgtagctc tgctggcagt agtaggtggc 660

gaaatcctct ggctgcaggc tggtgatggt cagggtgaaa tcggttccgc ttccgcttcc 720

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gctgaaccgg cttggcactc cgctctgcag tccgctggcg gcgctgatca gtccctttgg      780

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gcaggtgatg gtcacccgat ctcccacgct ggcgctcagg ctgcttgggc tctgggtcat      900

ctggatatcg ctgttggtca ccagggccag gctcagggcg atcagcagca gcagctgcat      960

tctcatggtg gagagtcgcg tccttgctcg ggtgttgtaa gttccagtgc aaagtgcccc     1020

aattggcgat ctgacggttc actaaacgag ctctgcttat ataggcctcc caccgtacac     1080

gccacctcga catacctagt tattaatagt aatcaattac ggggtcatta gttcatagcc     1140

catatatgga gttccgcgtt acataactta cggtaaatgg cccgcctggc tgaccgccca     1200

acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga     1260

ctttccattg acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc     1320

aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgcct     1380

ggcattatgc ccagtacatg accttatggg actttcctac ttggcagtac atctacgtat     1440

tagtcatcgc tattaccatg gtgatgcggt tttggcagta catcaatggg cgtggatagc     1500

ggtttgactc acggggattt ccaagtctcc accccattga cgtcaatggg agtttgtttt     1560

ggcaccaaaa tcaacgggac tttccaaaat gtcgtaacaa ctccgcccca ttgacgcaaa     1620

tgggcggtag gcgtgtacgg tgggaggtct atataagcag agctggttta gtgaaccgtc     1680

agatccgctg ctagcgggca ctttgcactg gaacttacaa cacccgagca aggacgcgac     1740

tctccaccat gcgcatgcag ctgctgctgc tgatcgccct gagcctggcc ctggtgacca     1800

acagc cag gtg cag ctg cag gag agc gga cca gga ctg gtg aag cca agc      1850
      Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
      1               5                  10                  15

gag acc ctg agc ctg acc tgc acc gtg agc gga agc agc atc agc aac       1898
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn
               20                  25                  30

tac tac tgg agc tgg atc cgg cag agc cca gga aag gga ctg gag tgg       1946
Tyr Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp
            35                  40                  45

atc gga ttc atc tac tac gga gga aac acc aag tac aac cca agc ctg       1994
Ile Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu
        50                  55                  60

aag agc cgg gtg acc atc agc cag gat acc agc aag agc cag gtg agc       2042
Lys Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser
    65                  70                  75

ctg acc atg agc agc gtg acc gcc gcc gag agc gcc gtg tac ttc tgc       2090
Leu Thr Met Ser Ser Val Thr Ala Ala Glu Ser Ala Val Tyr Phe Cys
80                  85                  90                  95
```

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gcc cgg gcc agc tgc agc gga gga tac tgc atc ctg gat tac tgg gga       2138
Ala Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly
                100                 105                 110

cag gga acc ctg gtg acc gtg agc agc gcg tcg acc aag gga cct tcg       2186
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
            115                 120                 125

gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggg ggc aca gcg       2234
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
        130                 135                 140

gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg       2282
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
    145                 150                 155

tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct       2330
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
160                 165                 170                 175

gtc cta cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg       2378
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
                180                 185                 190

ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac       2426
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
            195                 200                 205

aag ccc agc aac acc aag gtg gac aag aaa gtt gaa cca aag agc tgc       2474
Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
        210                 215                 220

gac aag acc cac acg tgt ccc ccc tgc cct gcc cct gaa ctg ctg gga       2522
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
    225                 230                 235

ggc ccc agc gtg ttc ctg ttc ccc cca aag ccc aag gac acc ctg atg       2570
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
240                 245                 250                 255

atc agc cgg acc ccc gaa gtg acc tgc gtg gtg gtg gac gtg tcc cac       2618
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
                260                 265                 270

gag gac cct gaa gtg aag ttt aat tgg tac gtg gac ggc gtg gaa gtg       2666
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
            275                 280                 285

cac aac gcc aag acc aag ccc aga gag gaa cag tac aac agc acc tac       2714
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
        290                 295                 300

cgg gtg gtg tcc gtg ctg acc gtg ctg cac cag gac tgg ctg aac ggc       2762
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
    305                 310                 315

aaa gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gcc ccc atc       2810
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
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320                 325                 330                 335

gag aaa acc atc agc aag gcc aag ggc cag ccc cgc gag cct cag gtc       2858
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
                340                 345                 350

tac aca ctg ccc ccc agc cgg gaa gag atg acc aag aac cag gtg tcc       2906
Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
            355                 360                 365

ctg acc tgc ctg gtc aag ggc ttc tac ccc agc gac atc gcc gtg gaa       2954
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
        370                 375                 380

tgg gag agc aac ggc cag ccc gag aac aac tac aag acc acc ccc cct       3002
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
    385                 390                 395

gtg ctg gac agc gac ggc tca ttc ttc ctg tat agc aag ctg acc gtg       3050
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
400                 405                 410                 415

gac aag agc cgg tgg cag cag ggc aac gtg ttc agc tgc agc gtg atg       3098
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
                420                 425                 430

cac gag gcc ctg cac aac cac tac acc cag aag tcc ctg agc ctg agc       3146
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
            435                 440                 445

ccc ggc agaaagcgga gagcccccgt gaagcagacc ctgaacttcg acctgctgaa       3202
Pro Gly


gctggccggc gacgtggaaa gcaaccctgg ccctatgtac agaatgcagc tgctgagctg     3262

catcgccctg agcctggccc tggtgaccaa cagc cag gtg caa cta gtg gag agc     3317
                                      Gln Val Gln Leu Val Glu Ser
                                      450                 455

gga gga gga gtg gtg cag cca gga cgg agc ctg cgg ctg agc tgc gcc       3365
Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala
            460                 465                 470

gcc agc gga ttc acc ttc agc acc tac gcc atg cac tgg gtg cgg cag       3413
Ala Ser Gly Phe Thr Phe Ser Thr Tyr Ala Met His Trp Val Arg Gln
        475                 480                 485

gcc cca gga aag gga ctg gag tgg gtg gcc gtg atc agc tac gat gcc       3461
Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser Tyr Asp Ala
    490                 495                 500

aac tac aag tac tac gcc gat agc gtg aag gga cgg ttc acc atc agc       3509
Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
505                 510                 515                 520

cgg gat aac agc aag aac acc ctg tac ctg cag atg aac agc ctg cgg       3557
Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
                525                 530                 535
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gcc gag gat acc gcc gtg tac tac tgc gcc aag gat agc cag ctg cgg       3605
Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Ser Gln Leu Arg
            540                 545                 550

agc ctg ctg tac ttc gag tgg ctg agc cag gga tac ttc gat tac tgg       3653
Ser Leu Leu Tyr Phe Glu Trp Leu Ser Gln Gly Tyr Phe Asp Tyr Trp
        555                 560                 565

gga cag gga acc ctg gtg acc gtg agc agc gcc agc acc aag ggg ccc       3701
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
    570                 575                 580

agc gtg ttc cca ctg gcc cca agc agc aag agc acc agc gga gga acc       3749
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
585                 590                 595                 600

gcc gcc ctg gga tgc ctg gtg aag gat tac ttc cca gag cca gtg acc       3797
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
                605                 610                 615

gtg agc tgg aac agc gga gcc ctg acc agc gga gtg cac acc ttc cca       3845
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
            620                 625                 630

gcc gtg ctg cag agc agc gga ctg tat agc ctg agc agc gtg gtg acc       3893
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
        635                 640                 645

gtg cca agc agc agc ctg gga acc cag acc tac atc tgc aac gtg aac       3941
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
    650                 655                 660

cac aag cca agc aac acc aag gtg gat aag aag gtg gag cca aag agc       3989
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
665                 670                 675                 680

tgc gat aag acc cac acg tgc cct cca tgt cca gcc ccc gaa ctg ctg       4037
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
                685                 690                 695

ggc ggg cct agc gtg ttc ctg ttt ccc cct aag cct aaa gat aca ctg       4085
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            700                 705                 710

atg att agt aga acc cca gag gtc aca tgc gtg gtc gtg gac gtg tcc       4133
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        715                 720                 725

cac gaa gag cct gac gtg aag ttc aac tgg tac gtg gat ggc gtg gag       4181
His Glu Glu Pro Asp Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    730                 735                 740

gtg cac aat gct aag act aaa cca cgc gaa gag cag tat aat agt aca       4229
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
745                 750                 755                 760

tac cga gtc gtg tca gtc ctg aca gtg ctg cac cag gat tgg ctg aac       4277
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
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                765                 770                 775

ggc aag gag tat aag tgc aag gtg tct aac aag gcc ctg ccc gcc cct       4325
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            780                 785                 790

atc gag aaa aca att agc aag gcc aaa ggg cag cca cgg gaa ccc cag       4373
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        795                 800                 805

gtc tac act ctg cca ccc tca aga gat gaa ctg act aag aac cag gtc       4421
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    810                 815                 820

agc ctg acc tgt ctg gtg aaa ggc ttc tac ccc agc gac atc gcc gtg       4469
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
825                 830                 835                 840

gag tgg gaa agt aac ggc cag cct gag aat aac tac aag act acc cct       4517
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                845                 850                 855

cca gtg ctg gat agc gac ggg tcc ttc ttc ctg tat agc aag ctg aca       4565
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            860                 865                 870

gtg gac aaa tcc cgc tgg cag cag gga aac gtc ttt tcc tgt tct gtg       4613
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        875                 880                 885

atg cat gag gcc ctg cac aat cat tac acc cag aag agt ctg tca ctg       4661
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    890                 895                 900

agc ccc ggc aaa tgataaaaag cttctcgaga aggaacccgc gctatgacgg           4713
Ser Pro Gly Lys
905

caataaaaag acagaataaa acccacgggt gttgggtcgt ttgttcataa acccgggaag     4773

cttatcgata aggatcttcc tagagcatgg ctacgtagat aagtagcatg gcgggttaat     4833

cattaactac aaggaacccc tagtgatgga gttggccact ccctctctgc gcgctcgctc     4893

gctcactgag gccgggcgac caaaggtcgc ccgacgcccg ggctttgccc gggcggcctc     4953

agtgagcgag cgagcgcgca gccttaatta acctaattca ctggccgtcg ttttacaacg     5013

tcgtgactgg gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt     5073

cgccagctgg cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag     5133

cctgaatggc gaatgggacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt     5193

tacgcgcagc gtgaccgcta cacttgccag cgccctagcg cccgctcctt tcgctttctt     5253

cccttccttt ctcgccacgt tcgccggctt tccccgtcaa gctctaaatc gggggctccc     5313

tttagggttc cgatttagtg ctttacggca cctcgacccc aaaaaacttg attagggtga     5373
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tggttcacgt agtgggccat cgccctgata gacggttttt cgccctttga cgttggagtc     5433

cacgttcttt aatagtggac tcttgttcca aactggaaca acactcaacc ctatctcggt     5493

ctattctttt gatttataag ggattttgcc gatttcggcc tattggttaa aaaatgagct     5553

gatttaacaa aaatttaacg cgaattttaa caaaatatta acgcttacaa tttaggtggc     5613

acttttcggg gaaatgtgcg cggaacccct atttgtttat ttttctaaat acattcaaat     5673

atgtatccgc tcatgagaca ataaccctga taaatgcttc aataatattg aaaaaggaag     5733

agt atg agt att caa cat ttc cgt gtc gcc ctt att ccc ttt ttt gcg       5781
    Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala
        910                 915                 920

gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg ctg gtg aaa gta       5829
Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val
    925                 930                 935

aaa gat gct gaa gat cag ttg ggt gca cga gtg ggt tac atc gaa ctg       5877
Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu
940                 945                 950                 955

gat ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt       5925
Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg
                960                 965                 970

ttt cca atg atg agc act ttt aaa gtt ctg cta tgt ggc gcg gta tta       5973
Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu
            975                 980                 985

tcc cgt att gac gcc ggg caa gag caa ctc ggt cgc cgc  ata cac tat      6021
Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg  Ile His Tyr
        990                 995                 1000

tct cag  aat gac ttg gtt gag  tac tca cca gtc aca  gaa aag cat        6066
Ser Gln  Asn Asp Leu Val Glu  Tyr Ser Pro Val Thr  Glu Lys His
    1005                1010                1015

ctt acg  gat ggc atg aca gta  aga gaa tta tgc agt  gct gcc ata        6111
Leu Thr  Asp Gly Met Thr Val  Arg Glu Leu Cys Ser  Ala Ala Ile
    1020                1025                1030

acc atg  agt gat aac act gcg  gcc aac tta ctt ctg  aca acg atc        6156
Thr Met  Ser Asp Asn Thr Ala  Ala Asn Leu Leu Leu  Thr Thr Ile
    1035                1040                1045

gga gga  ccg aag gag cta acc  gct ttt ttg cac aac  atg ggg gat        6201
Gly Gly  Pro Lys Glu Leu Thr  Ala Phe Leu His Asn  Met Gly Asp
    1050                1055                1060

cat gta  act cgc ctt gat cgt  tgg gaa ccg gag ctg  aat gaa gcc        6246
His Val  Thr Arg Leu Asp Arg  Trp Glu Pro Glu Leu  Asn Glu Ala
    1065                1070                1075

ata cca  aac gac gag cgt gac  acc acg atg cct gta  gca atg gca        6291
Ile Pro  Asn Asp Glu Arg Asp  Thr Thr Met Pro Val  Ala Met Ala
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    1080                1085                1090

aca acg  ttg cgc aaa cta tta  act ggc gaa cta ctt  act cta gct        6336
Thr Thr  Leu Arg Lys Leu Leu  Thr Gly Glu Leu Leu  Thr Leu Ala
    1095                1100                1105

tcc cgg  caa caa tta ata gac  tgg atg gag gcg gat  aaa gtt gca        6381
Ser Arg  Gln Gln Leu Ile Asp  Trp Met Glu Ala Asp  Lys Val Ala
    1110                1115                1120

gga cca  ctt ctg cgc tcg gcc  ctt ccg gct ggc tgg  ttt att gct        6426
Gly Pro  Leu Leu Arg Ser Ala  Leu Pro Ala Gly Trp  Phe Ile Ala
    1125                1130                1135

gat aaa  tct gga gcc ggt gag  cgt ggg tct cgc ggt  atc att gca        6471
Asp Lys  Ser Gly Ala Gly Glu  Arg Gly Ser Arg Gly  Ile Ile Ala
    1140                1145                1150

gca ctg  ggg cca gat ggt aag  ccc tcc cgt atc gta  gtt atc tac        6516
Ala Leu  Gly Pro Asp Gly Lys  Pro Ser Arg Ile Val  Val Ile Tyr
    1155                1160                1165

acg acg  ggg agt cag gca act  atg gat gaa cga aat  aga cag atc        6561
Thr Thr  Gly Ser Gln Ala Thr  Met Asp Glu Arg Asn  Arg Gln Ile
    1170                1175                1180

gct gag  ata ggt gcc tca ctg  att aag cat tgg taactgtcag             6604
Ala Glu  Ile Gly Ala Ser Leu  Ile Lys His Trp
    1185                1190

accaagttta ctcatatata ctttagattg atttaaaact tcatttttaa tttaaaagga    6664

tctaggtgaa gatccttttt gataatctca tgaccaaaat cccttaacgt gagttttcgt    6724

tccactgagc gtcagacccc gtagaaaaga tcaaaggatc ttcttgagat cctttttttc    6784

tgcgcgtaat ctgctgcttg caaacaaaaa aaccaccgct accagcggtg gtttgtttgc    6844

cggatcaaga gctaccaact ctttttccga aggtaactgg cttcagcaga gcgcagatac    6904

caaatactgt tcttctagtg tagccgtagt taggccacca cttcaagaac tctgtagcac    6964

cgcctacata cctcgctctg ctaatcctgt taccagtggc tgctgccagt ggcgataagt    7024

cgtgtcttac cgggttggac tcaagacgat agttaccgga taaggcgcag cggtcgggct    7084

gaacgggggg ttcgtgcaca gcccagct tggagcgaac gacctacacc gaactgagat      7144

acctacagcg tgagctatga gaaagcgcca cgcttcccga agggagaaag gcggacaggt    7204

atccggtaag cggcagggtc ggaacaggag agcgcacgag ggagcttcca gggggaaacg    7264

cctggtatct ttatagtcct gtcgggtttc gccacctctg acttgagcgt cgatttttgt    7324

gatgctcgtc agggggggcgg agcctatgga aaaacgccag caacgcggcc tttttacggt    7384

tcctggcctt ttgctggcct tttgctcaca tgttctttcc tgcgttatcc cctgattctg    7444

tggataaccg tattaccgcc tttgagtgag ctgataccgc tcgccgcagc cgaacgaccg    7504
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agcgcagcga gtcagtgagc gaggaagcgg aagagcgccc aatacgcaaa ccgcctctcc 7564

ccgcgcgttg gccgattcat taatgcagct ggcacgacag gtttcccgac tggaaagcgg 7624

gcagtgagcg caacgcaatt aatgtgagtt agctcactca ttaggcaccc caggctttac 7684

actttatgct tccggctcgt atgttgtgtg gaattgtgag cggataacaa tttcacacag 7744

gaaacagcta tgaccatgat tacgccagat ttaattaa 7782

<210> 44
<211> 120
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 44

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Ser Ile Ser Asn Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Phe Ile Tyr Tyr Gly Gly Asn Thr Lys Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Gln Asp Thr Ser Lys Ser Gln Val Ser Leu
65 70 75 80

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

Arg Ala Ser Cys Ser Gly Gly Tyr Cys Ile Leu Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 45
<211> 98
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 45

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Lys Val

<210> 46
<211> 231
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 46

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

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Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65                  70                  75                  80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85                  90                  95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
            100                 105                 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
        115                 120                 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
    130                 135                 140

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

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165                 170                 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180                 185                 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
        195                 200                 205

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

Ser Leu Ser Leu Ser Pro Gly
225                 230
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<210> 47
<211> 129
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 47

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

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

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

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

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

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

Ala Lys Asp Ser Gln Leu Arg Ser Leu Leu Tyr Phe Glu Trp Leu Ser
            100                 105                 110

Gln Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

Ser
```

<210> 48
<211> 107
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 48

```
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1               5                   10                  15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
            20                  25                  30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
        35                  40                  45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
    50                  55                  60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65                  70                  75                  80
```

```
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
                85                  90                  95

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
            100                 105
```

<210> 49
<211> 223
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 49

```
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
1               5                  10                  15

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
            20                  25                  30

Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Glu Pro Asp
        35                  40                  45

Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
    50                  55                  60

Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
65                  70                  75                  80

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
                85                  90                  95

Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
            100                 105                 110

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
        115                 120                 125

Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
    130                 135                 140

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
145                 150                 155                 160
```

```
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
                165                 170                 175

Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
            180                 185                 190

Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
        195                 200                 205

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
    210                 215                 220
```

<210> 50
<211> 286
<212> PRT
<213> Artificial sequence

<220>
<223> Synthetic Construct

<400> 50

```
Met Ser Ile Gln His Phe Arg Val Ala Leu Ile Pro Phe Phe Ala Ala
1               5                   10                  15

Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr Leu Val Lys Val Lys
            20                  25                  30

Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
        35                  40                  45

Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
    50                  55                  60

Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
65                  70                  75                  80

Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
                85                  90                  95

Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
            100                 105                 110

Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
        115                 120                 125
```

```
Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
    130                 135                 140

Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
145                 150                 155                 160

Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg
                165                 170                 175

Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr Leu Arg Lys Leu Leu
            180                 185                 190

Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp
        195                 200                 205

Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro
    210                 215                 220

Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser
225                 230                 235                 240

Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile
                245                 250                 255

Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn
            260                 265                 270

Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile Lys His Trp
        275                 280                 285
```