SEQUENCE LISTING

<110> Astellas Pharma Inc.
NATIONAL CANCER CENTER

<120> anti-CLDN4-anti-CD137 bispecific antibody

<130> FA1535-21350

<150> JP2021-72429
<151> 2021-04-22

<160> 55

<170> PatentIn version 3.5

<210> 1
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<212> DNA
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<220>
<223> 3D11 VH

<220>
<221> CDS
<222> (1)..(375)

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cag gtt cag ttg gga cag tct ggc ccc gaa gtg aag aaa cct ggc gcc         48
Gln Val Gln Leu Gly Gln Ser Gly Pro Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

tct gtg aag gtg tcc tgc aag gct tcc ggc tac tcc ttt atc tcc tac         96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ile Ser Tyr
            20                  25                  30

ggc atc tcc tgg gtc cga cag gct cct gga caa ggc ttg gaa tgg atg        144
Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

ggc tgg tcc tcc gtg tac aac ggc aac acc aac tac gtg cag aaa ttc        192
Gly Trp Ser Ser Val Tyr Asn Gly Asn Thr Asn Tyr Val Gln Lys Phe
    50                  55                  60

cag ggc aga gtg acc atg acc acc gac acc tct gcc tcc acc gcc tac        240
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

atg gaa ctg cgg tcc ctg aga tct gat gac gcc gcc gtg tac tac tgc        288
Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Ala Ala Val Tyr Tyr Cys
                85                  90                  95
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gcc aga gac tct tac tcc tcc ggc tgg tct tac tac tac tcc ggc atg        336
Ala Arg Asp Ser Tyr Ser Ser Gly Trp Ser Tyr Tyr Tyr Ser Gly Met
            100                 105                 110

gat gtg tgg ggc cag ggc aca aca gtg acc gtg tcc tcc                    375
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
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<210> 2
<211> 125
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ile Ser Tyr
            20                  25                  30

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

Gly Trp Ser Ser Val Tyr Asn Gly Asn Thr Asn Tyr Val Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Asp Ser Tyr Ser Ser Gly Trp Ser Tyr Tyr Tyr Ser Gly Met
            100                 105                 110

Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
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<210> 3

<211> 327
<212> DNA
<213> Artificial Sequence

<220>
<223> 3D11 VL

<220>
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<222> (1)..(327)

<400> 3
gag att gtg ctg acc cag tct cct ggc aca ctg tct ttg agc cct ggc 48
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

gag aga gct acc ctg tcc tgt aga gcc tct cag tcc gtg tcc tcc tct 96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

tac ctg gcc tgg tat cag cag aag cct gga cag gct ccc cgg ctg ttg 144
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

atc tac ggc gct tct tct aga gcc aca ggc atc cct gac cgg ttc tcc 192
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

gga tct ggc tct ggc acc gat ttc acc ctg acc atc aac cgg ctg gaa 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Arg Leu Glu
65 70 75 80

ccc gag gat ttc gcc gtg tac tac tgc cag cag tac ggc tcc tct cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

tac tct ttt ggc cag ggc acc aag ctg gaa atc aag cgg 327
Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 4
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 4

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly

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1               5                   10                  15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
    50                  55                  60

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

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

Tyr Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105


<210>  5
<211>  369
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hKM3900 VH


<220>
<221>  CDS
<222>  (1)..(369)

<400>  5
gaa gtg cag ctg gtt cag tct ggc gcc gaa gtg aag aaa cct ggc gcc         48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

tcc gtg aag atc tcc tgc aag gct tct ggc tac acc ttc acc gac tac         96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

tac atg aac tgg gtc cga cag gct cct gga cag gga ctt gag tgg atg        144
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
gga gat gtg gtg ccc aac aac ggc gtg ccc acc tac aac cag aaa ttc        192
Gly Asp Val Val Pro Asn Asn Gly Val Pro Thr Tyr Asn Gln Lys Phe
    50                  55                  60

aag ggc aga gtg acc atc acc gcc gac aag tct acc tcc acc gcc tac        240
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

atg gaa ctg cgg agc ctg aga tct gag gac acc gcc gtg tac tac tgc        288
Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcc aga cct cac tac tac tac gcc ggc aga tct ggc gcc atg gat tat        336
Ala Arg Pro His Tyr Tyr Tyr Ala Gly Arg Ser Gly Ala Met Asp Tyr
            100                 105                 110

tgg gga cag ggc acc ctg gtc acc gtg tcc tct                            369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 6
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 6

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


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


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


Gly Asp Val Val Pro Asn Asn Gly Val Pro Thr Tyr Asn Gln Lys Phe
    50                  55                  60


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


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

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Ala Arg Pro His Tyr Tyr Tyr Ala Gly Arg Ser Gly Ala Met Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  7
<211>  327
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hKM3900 VL


<220>
<221>  CDS
<222>  (1)..(327)

<400>  7
gac atc cag ctg acc cag tct cca tcc tct ctg tct gcc tct gtg ggc         48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

gac aga gtg aca att acc tgc acc gcc tcc tcc acc gtg tcc tct acc         96
Asp Arg Val Thr Ile Thr Cys Thr Ala Ser Ser Thr Val Ser Ser Thr
            20                  25                  30

tac ctg cac tgg tat cag cag aag ccc ggc aag gct ccc aag ctg ctg        144
Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45

atc tac tcc acc tcc aat ctg gcc tct ggc gtg ccc tct aga ttc tcc        192
Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60

gga tct ggc tct gga acc gac tat acc ctg aca atc tcc agc ctg cag        240
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

cct gag gac ttc gcc acc tac tac tgc cac cag tac cac aga tcc cca        288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
                85                  90                  95

cct acc ttt ggc cag ggc acc aag ctg gaa atc aag cgt                    327
Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
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<210> 8
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 8

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

Asp Arg Val Thr Ile Thr Cys Thr Ala Ser Ser Thr Val Ser Ser Thr
20 25 30

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

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

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 9
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> 3-34 VH

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

<400> 9
cag gtc cag ctg cag cag tct gag gct gag ctg gtg agg cct ggg gcc 48

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

tca gtg aag att tcc tgc aag gct ttt ggc tac acc ttc aca aac cat         96
Ser Val Lys Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe Thr Asn His
            20                  25                  30

cat ata aac tgg gtg aag cag agg cct gga cag ggc ctg gac tgg att        144
His Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Asp Trp Ile
        35                  40                  45

gga tat att aat cct tat aat gat tat act acc ttc aac cgg aag ttc        192
Gly Tyr Ile Asn Pro Tyr Asn Asp Tyr Thr Thr Phe Asn Arg Lys Phe
    50                  55                  60

aag gac aag gcc aca ttg act gta cac aaa tcc tcc agc aca gcc tat        240
Lys Asp Lys Ala Thr Leu Thr Val His Lys Ser Ser Ser Thr Ala Tyr
65                  70                  75                  80

atg gag ctt agc ggc ctg aca tct gac gac tct gca gtc tat tac tgt        288
Met Glu Leu Ser Gly Leu Thr Ser Asp Asp Ser Ala Val Tyr Tyr Cys
                85                  90                  95

gca aga acc tgg ggt cac tgg tat ttc gat ctc tgg ggc cgt ggc acc        336
Ala Arg Thr Trp Gly His Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

gtg gtc act gtc tcc tca                                               354
Val Val Thr Val Ser Ser
        115


<210>  10
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic Construct

<400>  10

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


Ser Val Lys Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe Thr Asn His
            20                  25                  30


His Ile Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Asp Trp Ile
        35                  40                  45
```

```
Gly Tyr Ile Asn Pro Tyr Asn Asp Tyr Thr Thr Phe Asn Arg Lys Phe
    50                  55                  60

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

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

Ala Arg Thr Trp Gly His Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr
            100                 105                 110

Val Val Thr Val Ser Ser
        115


<210>  11
<211>  327
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  3-34 VL


<220>
<221>  CDS
<222>  (1)..(327)

<400>  11
gaa ata gtg atg acg cag tct cca gcc acc ctg tct gtg tct cca ggg         48
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1               5                   10                  15

gaa aga gcc acc ctc tcc tgt agg gcc agt cag agt gtt agc agc aac         96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
            20                  25                  30

tta gcc tgg tac cag cag aaa cct ggc cag gct ccc agg ctc ctc atc        144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35                  40                  45

tat gat tca tcc acc agg gcc act ggt atc cca gcc agg ttc agt ggc        192
Tyr Asp Ser Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
    50                  55                  60

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc ctg cag tct        240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
```

65 70 75 80

gaa gat ttt gca gtt tat tac tgt cag cag tat aat aac tgg cct ccg 288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asn Asn Trp Pro Pro
85 90 95

tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa cgg 327
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 12
<211> 109
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 12

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

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

Tyr Asp Ser Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 13
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> A2-32 VH

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

<400> 13
cag gtg cag ctg cag gaa tcg ggc cca gga ctg gtg aag cct tcg gag 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1   5   10   15

acc ctg tcc ctc acc tgc act gtc tct ggc ggc tcc atc agt ggt tat 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Gly Tyr
            20   25   30

tac tgg agc tgg atc cgg cag ccc cca ggg aag ggc ctg gag tgg att 144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35   40   45

gga tat atc tat tac agt gga ttc acc aac tac aac ccc tcc ctc aag 192
Gly Tyr Ile Tyr Tyr Ser Gly Phe Thr Asn Tyr Asn Pro Ser Leu Lys
    50   55   60

agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttc tcc ctg 240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65   70   75   80

aaa ctg agc tct gtg acc gct gcg gac acg gcc gtg tat tat tgt acg 288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Thr
                85   90   95

aga gat cac tcc cac tac tac tac atg gac gtc tgg ggc caa ggg acc 336
Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr
            100   105   110

acg gtc acc gtc tcc tca   354
Thr Val Thr Val Ser Ser
        115

<210> 14
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 14

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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 Gly Ser Ile Ser Gly Tyr
            20                  25                  30

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

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

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

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Thr
                85                  90                  95

Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser
        115


<210>  15
<211>  333
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  A2-32 VL


<220>
<221>  CDS
<222>  (1)..(333)

<400>  15
cag tct gtg ctg act cag cca ccc tca gcg tct ggg acc ccc ggg cag         48
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15

agg gtc acc atc tct tgt tct gga agc agc tcc aac atc gga agt aat         96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30
```

```
act gta aac tgg tac cag cag ttc cca gga acg gcc ccc aaa ctc ctc        144
Thr Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

atc tat agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct        192
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

ggc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag        240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80

tct gag gat gag gct gat tat tac tgt gca gga tgg gat gac agc ctg        288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly Trp Asp Asp Ser Leu
                85                  90                  95

aat ggt ccg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt            333
Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 16
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 16

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly Trp Asp Asp Ser Leu
```

```
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  17
<211>  354
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  A2-48 VH


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

<400>  17
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag         48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agt agt tac         96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30

tac tgg agc tgg atc cgg cag ccc ccc ggg aag gga ctg gaa tgg att        144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

ggg tat atc tat tac agt ggg tac acc aac tac aac ccc tcc ctc aag        192
Gly Tyr Ile Tyr Tyr Ser Gly Tyr Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

agt cga gtt aac ata tca gta gac acg tcc cag aac cag ttc tcc ctg        240
Ser Arg Val Asn Ile Ser Val Asp Thr Ser Gln Asn Gln Phe Ser Leu
65                  70                  75                  80

aag ctg aat tct ctg acc gct gcg gac acg gcc gtt tat tac tgt gcg        288
Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga aca cac tcc tat tac tac ggt atg gac gtc tgg ggc caa ggg acc        336
Arg Thr His Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

acg gtc acc gtc tcc tca                                               354
Thr Val Thr Val Ser Ser
        115
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<210> 18
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

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 Gly Ser Ile Ser Ser Tyr
20 25 30

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

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

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

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr His Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 19
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> A2-48 VL

<220>

<221> CDS
<222> (1)..(333)

<400> 19
cag tct gtg ctg act cag cca ccc tca gcg tct ggg acc ccc ggg cag 48
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

agg gtc acc atc tct tgt tct gga agc agc tcc aac atc gga aat aat 96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

cct gta aac tgg tac cag cag ttc cca gga acg gcc ccc aaa ctc ctc 144
Pro Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

atc tat agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct 192
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

ggc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag 240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

tct gag gat gag gct gat tat tac tgt gaa gca tgg gat gac agc ctg 288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Ala Trp Asp Asp Ser Leu
85 90 95

aat ggt ccg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt 333
Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 20
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 20

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  21
<211>  363
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  A2-73 VH


<220>
<221>  CDS
<222>  (1)..(363)

<400>  21
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag         48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc agt agt tac         96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30

tac tgg acc tgg atc cgg cag ccc cca ggg aag gga ctg gaa ttg gtt        144
Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Leu Val
        35                  40                  45

gga tat atc tat tac agt ggt tac acc agc tac aac ccc tcc ctc aag        192
Gly Tyr Ile Tyr Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu Lys
    50                  55                  60

agt cga gtc acc ata tca att gac acg tcc aag aac cag ttc tcc ctg        240
Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

cag ctg aac tct gtg acc gct gcg gac acg gcc gtg tat ttc tgt gcg        288
```

```
Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
                85                  90                  95

cga gat gac tat ggt ggt aac ggc tac tac ggt gtg gac gtc tgg ggc        336
Arg Asp Asp Tyr Gly Gly Asn Gly Tyr Tyr Gly Val Asp Val Trp Gly
            100                 105                 110

caa ggg acc acg gtc acc gtc tcc tca                                    363
Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 22
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 22

```
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 Gly Ser Ile Ser Ser Tyr
            20                  25                  30

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

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

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

Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
                85                  90                  95

Arg Asp Asp Tyr Gly Gly Asn Gly Tyr Tyr Gly Val Asp Val Trp Gly
            100                 105                 110

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

<210> 23
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> A2-73 VL

<220>
<221> CDS
<222> (1)..(333)

<400> 23
cag tct gtg ctg act cag cca ccc tca gcg tct ggg acc ccc ggg cag 48
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15

agg gtc acc atc tct tgt tct ggc agc agc tcc aac atc gga aat aat 96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

cct gta aac tgg tac cgg cag ctc cca gga acg gcc ccc aaa ctc ctc 144
Pro Val Asn Trp Tyr Arg Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

atc tat agt aat aat cag cgg ccc tca ggg gtc cct gac cga ttc tct 192
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

ggc tcc aag tct ggc acc tca gcc tcc ctg gcc atc agt ggg ctc cag 240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

tct gag gat gag gct gat tat tac tgt gca gca tgg gat gac agc ctg 288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
85 90 95

aat ggt tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta ggt 333
Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 24
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 24

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


Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
            20                  25                  30


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


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


Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80


Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu
                85                  90                  95


Asn Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


<210>  25
<211>  726
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  3-34-j6 scFv


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

<400>  25
gaa gtt cag ctg ttg gaa agt ggt ggc gga ctg gtc cag cct ggc gaa         48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu
1               5                   10                  15

tct ctg aga ctg agc tgc aag gcc ttc ggg tat acc ttt acc aac cac         96
Ser Leu Arg Leu Ser Cys Lys Ala Phe Gly Tyr Thr Phe Thr Asn His
            20                  25                  30

cac atc aat tgg gtt cga caa gcc cct ggc aag tgc ctg gaa tgg gtc        144
His Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
```

```
        35                  40                  45

gga tat atc aac ccc tac aac gac tac acc acc ttc aac gac aag ttc        192
Gly Tyr Ile Asn Pro Tyr Asn Asp Tyr Thr Thr Phe Asn Asp Lys Phe
    50                  55                  60

aag gac cgg ttc acc ctg tcc gtg gat aag tcc aag agc acc gct tac        240
Lys Asp Arg Phe Thr Leu Ser Val Asp Lys Ser Lys Ser Thr Ala Tyr
65                  70                  75                  80

ctg cag atg aac tcc ctg aga gcc gag gat aca gct gtg tat tac tgt        288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcc cgg acc tgg ggc cac tgg tac ttt gat ttg tgg ggc cag gga acc        336
Ala Arg Thr Trp Gly His Trp Tyr Phe Asp Leu Trp Gly Gln Gly Thr
            100                 105                 110

ctc gtg aca gtc tct tct ggc ggc gga gga agc gga ggc gga ggt tca        384
Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

ggc ggc ggt gga tct aac atc cag atg acc cag tct cca tcc agc ctg        432
Gly Gly Gly Gly Ser Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

tct gcc tct gtg ggc gac aga gtg aca att acc tgt cgg gcc tct cag        480
Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

tcc gtg tcc agc aat ctg gct tgg tat cag cag aag ccc ggc aag gct        528
Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

ccc aag ctg ctg atc tac gac tcc tcc acc aga gct acc ggc gtg cca        576
Pro Lys Leu Leu Ile Tyr Asp Ser Ser Thr Arg Ala Thr Gly Val Pro
            180                 185                 190

tct aga ttc tcc ggc tct ggc tct ggc acc gac ttt acc ctg aca att        624
Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

tcc agc ctg cag cct gag gac ttc gcc acc tac tac tgc cag cag tac        672
Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
    210                 215                 220

aac aac tgg cct cct tgg acc ttc ggc tgc ggc acc aaa ctg gaa atc        720
Asn Asn Trp Pro Pro Trp Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile
225                 230                 235                 240

aag cgc                                                                726
Lys Arg
```

<210> 26
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 26

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


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


His Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val
        35                  40                  45


Gly Tyr Ile Asn Pro Tyr Asn Asp Tyr Thr Thr Phe Asn Asp Lys Phe
    50                  55                  60


Lys Asp Arg Phe Thr Leu Ser Val Asp Lys Ser Lys Ser Thr Ala 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 Arg Thr Trp Gly His Trp Tyr Phe Asp Leu Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160


Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
```

```
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ser Ser Thr Arg Ala Thr Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr
    210                 215                 220

Asn Asn Trp Pro Pro Trp Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile
225                 230                 235                 240

Lys Arg
```

<210> 27
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> tA2-32 scFv

<220>
<221> CDS
<222> (1)..(732)

<400> 27

```
cag gtt cag ttg caa gaa tct ggc cca ggc ctc gtg aag ccc tcc gaa         48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

aca ctg tct ctg acc tgc aca gtg tcc ggc ggc tct atc tct ggc tac         96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Gly Tyr
            20                  25                  30

tac tgg tcc tgg atc aga cag cct cct ggc aag tgc ctg gaa tgg atc        144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
        35                  40                  45

ggc tac atc tac tac tct ggc ttc acc aac tac aac ccc agc ctg aag        192
Gly Tyr Ile Tyr Tyr Ser Gly Phe Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60
```

```
tcc aga gtg acc atc agc gtg gac acc tct aag aac cag ttc tct ctg        240
Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65                  70                  75                  80

aag ctg tcc tcc gtg acc gcc gct gat acc gct gtg tat tac tgc acc        288
Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Thr
                85                  90                  95

cgg gac cac agc cac tac tac tac atg gac gtg tgg gga cag gga aca        336
Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

acc gtg aca gtc tct tca ggc ggt ggt gga tca ggc ggc gga gga agt        384
Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

ggt ggc gga ggt tct cag tct gtg ctg acc caa cct cct tcc gct tct        432
Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser
    130                 135                 140

ggc aca cct ggc cag aga gtg aca atc tct tgc tcc ggc tcc tcc tcc        480
Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145                 150                 155                 160

aac atc ggc tct aac acc gtg aac tgg tat cag cag ttc ccc ggc acc        528
Asn Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr
                165                 170                 175

gct cct aag ctg ctg atc tac tcc aac aac cag cgg cct tcc ggc gtg        576
Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val
            180                 185                 190

ccc gat aga ttc tct ggc tct aag tcc ggc acc tct gcc agc ctg gct        624
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
        195                 200                 205

att tct gga ctg cag agc gag gac gag gcc gac tat tat tgt gcc ggc        672
Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly
    210                 215                 220

tgg gac gac tct ctg aac ggc cct gtt ttt ggc tgc ggc acc aaa ctg        720
Trp Asp Asp Ser Leu Asn Gly Pro Val Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

act gtg ctg ggc                                                       732
Thr Val Leu Gly
```

<210> 28
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 28

```
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 Gly Ser Ile Ser Gly Tyr
            20                  25                  30


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


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


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


Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Thr
                85                  90                  95


Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


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


Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145                 150                 155                 160


Asn Ile Gly Ser Asn Thr Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr
                165                 170                 175


Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val
            180                 185                 190
```

```
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
        195                 200                 205


Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly
    210                 215                 220


Trp Asp Asp Ser Leu Asn Gly Pro Val Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240


Thr Val Leu Gly
```

<210> 29
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> tA2-32LH scFv

<220>
<221> CDS
<222> (1)..(747)

<400> 29

```
caa tct gtt ctg acc caa cct cct tcc gcc tct ggc aca cct ggc cag         48
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1               5                   10                  15

aga gtg acc atc tct tgc tcc ggc tcc tcc tcc aac atc ggc tct aac         96
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

acc gtg aac tgg tat cag cag ttc ccc ggc acc gct cct aag ctg ctg        144
Thr Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu
        35                  40                  45

atc tac tcc aac aac cag cgg cct tcc ggc gtg ccc gat aga ttc tct        192
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
    50                  55                  60

ggc tct aag tcc ggc acc tct gcc agc ctg gct att tct gga ctg cag        240
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80

agc gag gac gag gcc gac tat tat tgt gcc ggc tgg gac gac tct ctg        288
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly Trp Asp Asp Ser Leu
```

```
                85                  90                  95

aac ggc cct gtt ttt ggc ggt ggc acc aaa ctg aca gtg ctt gga ggc        336
Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
            100                 105                 110

ggt ggt gga tca ggc ggc ggt gga agt ggt ggt ggt ggt agc gga ggt        384
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

ggt gga tct cag gtg cag ctc caa gag tct gga cct ggc ctc gtg aag        432
Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
    130                 135                 140

cct tcc gag aca ctg tct ctg acc tgc aca gtg tcc ggc ggc tct atc        480
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
145                 150                 155                 160

tct ggc tac tac tgg tcc tgg atc aga cag cct cct ggc aag gga ctc        528
Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
                165                 170                 175

gag tgg atc ggc tac atc tac tac tct ggc ttc acc aac tac aac ccc        576
Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Phe Thr Asn Tyr Asn Pro
            180                 185                 190

agc ctg aag tcc cgc gtg acc atc agc gtg gac acc tct aag aac cag        624
Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
        195                 200                 205

ttc tct ctg aag ctg tcc tcc gtg acc gcc gct gat acc gct gtg tat        672
Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
    210                 215                 220

tac tgc acc cgg gac cac agc cac tac tac tac atg gac gtg tgg gga        720
Tyr Cys Thr Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly
225                 230                 235                 240

cag gga aca acc gtg aca gtg tcc tcc                                    747
Gln Gly Thr Thr Val Thr Val Ser Ser
                245
```

<210> 30
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
            20                  25                  30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln
65                  70                  75                  80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly Trp Asp Asp Ser Leu
                85                  90                  95

Asn Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly
            100                 105                 110

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
    130                 135                 140

Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
145                 150                 155                 160

Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
                165                 170                 175

Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Phe Thr Asn Tyr Asn Pro
            180                 185                 190

Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
        195                 200                 205

Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
```

```
    210                 215                 220

Tyr Cys Thr Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly
225                 230                 235                 240

Gln Gly Thr Thr Val Thr Val Ser Ser
                245
```

<210> 31
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> tA2-48 scFv

<220>
<221> CDS
<222> (1)..(732)

<400> 31

```
cag gtt cag ttg caa gaa tct ggc cca ggc ctc gtg aag ccc tcc gaa         48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

aca ctg tct ctg acc tgc aca gtg tcc ggc ggc tcc atc tct tcc tac         96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
            20                  25                  30

tac tgg tcc tgg atc aga cag cct cct ggc aag tgc ctg gaa tgg atc        144
Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Trp Ile
        35                  40                  45

ggc tac atc tac tac tcc ggc tac acc aac tac aac ccc agc ctg aag        192
Gly Tyr Ile Tyr Tyr Ser Gly Tyr Thr Asn Tyr Asn Pro Ser Leu Lys
    50                  55                  60

tcc aga gtg aac atc tcc gtg gac acc agc cag aac cag ttc tct ctg        240
Ser Arg Val Asn Ile Ser Val Asp Thr Ser Gln Asn Gln Phe Ser Leu
65                  70                  75                  80

aag ctg aac tcc ctg acc gcc gct gat acc gct gtg tat tac tgc gct        288
Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

cgg acc cac agc tac tac tat ggc atg gac gtg tgg gga caa ggg aca        336
Arg Thr His Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110
```

```
acc gtg aca gtc tct tca ggc ggt ggt gga tca ggc ggc gga gga agt        384
Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

ggt ggc gga ggt tct cag tct gtg ctg acc caa cct cct tcc gct tct        432
Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser
    130                 135                 140

ggc aca cct ggc cag aga gtg acc atc agc tgt agc ggc tcc tcc tcc        480
Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145                 150                 155                 160

aac atc ggc aac aac ccc gtg aac tgg tat cag cag ttc ccc ggc aca        528
Asn Ile Gly Asn Asn Pro Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr
                165                 170                 175

gcc cct aag ctg ctg atc tac tcc aac aac cag cgg cct tcc ggc gtg        576
Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val
            180                 185                 190

ccc gat aga ttc tct ggc tct aag tcc ggc acc tct gcc agc ctg gct        624
Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
        195                 200                 205

att tct gga ctg cag agc gag gac gag gcc gac tac tat tgc gag gct        672
Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Ala
    210                 215                 220

tgg gac gac tct ctg aac ggc cct gtg ttt ggc tgt ggc acc aaa ctg        720
Trp Asp Asp Ser Leu Asn Gly Pro Val Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240

act gtg ctg ggc                                                       732
Thr Val Leu Gly
```

<210> 32
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 32

```
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 Gly Ser Ile Ser Ser Tyr
            20                  25                  30
```

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

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

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

Lys Leu Asn Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

Arg Thr His Ser Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

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

Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser
145                 150                 155                 160

Asn Ile Gly Asn Asn Pro Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val
            180                 185                 190

Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala
        195                 200                 205

Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Ala
    210                 215                 220

Trp Asp Asp Ser Leu Asn Gly Pro Val Phe Gly Cys Gly Thr Lys Leu
225                 230                 235                 240
```

Thr Val Leu Gly

<210> 33
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<223> tA2-73 scFv

<220>
<221> CDS
<222> (1)..(741)

<400> 33
cag gtt cag ttg caa gaa tct ggc cca ggc ctc gtg aag ccc tcc gaa 48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

aca ctg tct ctg acc tgc aca gtg tcc ggc ggc tcc atc tct tcc tac 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

tac tgg acc tgg atc aga cag cct cct ggc aag tgc ttg gaa ctc gtg 144
Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Leu Val
35 40 45

ggc tac atc tac tac tcc ggc tac acc agc tac aac ccc agc ctg aag 192
Gly Tyr Ile Tyr Tyr Ser Gly Tyr Thr Ser Tyr Asn Pro Ser Leu Lys
50 55 60

tcc aga gtg acc atc agc atc gac acc tct aag aac cag ttc agc ctg 240
Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

cag ctc aac tcc gtg acc gct gct gat acc gct gtg tac ttc tgc gcc 288
Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
85 90 95

aga gat gac tac ggc ggc aac ggc tat tat ggc gtg gac gtt tgg gga 336
Arg Asp Asp Tyr Gly Gly Asn Gly Tyr Tyr Gly Val Asp Val Trp Gly
100 105 110

caa ggg aca acc gtg aca gtg tct agc gga ggt ggt gga tca ggc ggc 384
Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

ggt gga agt ggt ggt ggt ggc tct cag tct gtg ctg acc caa cct cct 432
Gly Gly Ser Gly Gly Gly Gly Ser Gln Ser Val Leu Thr Gln Pro Pro

```
    130                 135                 140

tct gcc tct ggc aca cct ggc cag aga gtg aca atc tct tgc tcc ggc        480
Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly
145                 150                 155                 160

tcc tcc tcc aac atc ggc aac aac ccc gtg aac tgg tac aga cag ctg        528
Ser Ser Ser Asn Ile Gly Asn Asn Pro Val Asn Trp Tyr Arg Gln Leu
                165                 170                 175

cca ggc aca gcc cct aag ctg ctg atc tac tcc aac aac cag cgg cct        576
Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro
            180                 185                 190

tcc ggc gtg ccc gat aga ttc tct gga tct aag tcc ggc acc agc gcc        624
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala
        195                 200                 205

agc ctg gct att tct gga ctg cag agc gag gac gag gcc gac tac tac        672
Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
    210                 215                 220

tgt gcc gct tgg gac gat tct ctg aac gga tgg gtg ttc ggc tgc ggc        720
Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp Val Phe Gly Cys Gly
225                 230                 235                 240

acc aaa ctg act gtg ctg gga                                           741
Thr Lys Leu Thr Val Leu Gly
                245
```

<210> 34
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 34

```
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 Gly Ser Ile Ser Ser Tyr
            20                  25                  30

Tyr Trp Thr Trp Ile Arg Gln Pro Pro Gly Lys Cys Leu Glu Leu Val
        35                  40                  45
```

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

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

Gln Leu Asn Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala
                85                  90                  95

Arg Asp Asp Tyr Gly Gly Asn Gly Tyr Tyr Gly Val Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

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

Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser Cys Ser Gly
145                 150                 155                 160

Ser Ser Ser Asn Ile Gly Asn Asn Pro Val Asn Trp Tyr Arg Gln Leu
                165                 170                 175

Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Ser Asn Asn Gln Arg Pro
            180                 185                 190

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala
        195                 200                 205

Ser Leu Ala Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr
    210                 215                 220

Cys Ala Ala Trp Asp Asp Ser Leu Asn Gly Trp Val Phe Gly Cys Gly
225                 230                 235                 240

Thr Lys Leu Thr Val Leu Gly
                245
```

<210> 35

<211> 2115
<212> DNA
<213> Artificial Sequence

<220>
<223> hKM3900_3-34-j6 HC

<220>
<221> CDS
<222> (1)..(2115)

<400> 35
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gaa gtg cag ctg gtt cag tct ggc gcc gaa gtg aag aaa cct ggc gcc          48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

tcc gtg aag atc tcc tgc aag gct tct ggc tac acc ttc acc gac tac          96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

tac atg aac tgg gtc cga cag gct cct gga cag gga ctt gag tgg atg         144
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

gga gat gtg gtg ccc aac aac ggc gtg ccc acc tac aac cag aaa ttc         192
Gly Asp Val Val Pro Asn Asn Gly Val Pro Thr Tyr Asn Gln Lys Phe
    50                  55                  60

aag ggc aga gtg acc atc acc gcc gac aag tct acc tcc acc gcc tac         240
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

atg gaa ctg cgg agc ctg aga tct gag gac acc gcc gtg tac tac tgc         288
Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcc aga cct cac tac tac tac gcc ggc aga tct ggc gcc atg gat tat         336
Ala Arg Pro His Tyr Tyr Tyr Ala Gly Arg Ser Gly Ala Met Asp Tyr
            100                 105                 110

tgg gga cag ggc acc ctg gtc acc gtg tcc tct gct agc aca aag ggc         384
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

ccc tct gtg ttc cct ctg gct cct agc tct aag tcc acc tct ggc gga         432
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

aca gct gct ctg ggc tgt ctg gtc aag gac tac ttc cct gag cct gtg         480
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160
```

```
acc gtg tct tgg aac tct ggc gct ctg aca tcc ggc gtg cac aca ttt        528
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

cca gct gtg ctg cag tcc tcc ggc ctg tac tct ctg tcc tct gtc gtg        576
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

acc gtg cct tcc agc tct ctg gga acc cag acc tac atc tgc aat gtg        624
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

aac cac aag cct tcc aac acc aag gtg gac aag aag gtg gaa ccc aag        672
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

tcc tgc gac aag acc cac acc tgt cct cca tgt cct gct cca gaa gct        720
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

gct ggc gga cct tcc gtg ttc ctg ttt cct cca aag cct aag gac acc        768
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

ctg atg atc tct cgg acc cct gaa gtg acc tgc gtg gtg gtg gat gtg        816
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

tct cac gag gac cca gaa gtg aag ttc aat tgg tac gtg gac ggc gtg        864
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

gaa gtg cac aac gcc aag acc aag cct aga gag gaa cag tac aac tcc        912
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

acc tac aga gtg gtg tcc gtg ctg acc gtg ctg cac cag gat tgg ctg        960
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

aac ggc aaa gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gcc       1008
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

ggc atc gaa aag acc atc tcc aag gcc aag ggc cag cct agg gaa ccc       1056
Gly Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

cag gtt tac acc ttg cca cct tct cgg gac gag ctg acc aag aac cag       1104
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

gtg tcc ctg acc tgt ctc gtg aag ggc ttc tac ccc tcc gat atc gcc       1152
```

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

gtg gaa tgg gag tct aat ggc cag cct gag aac aac tac aag aca acc       1200
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

cct cct gtg ctg gac tcc gac ggc tca ttc ttc ctg tac tcc aag ctg       1248
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

aca gtg gac aag tcc aga tgg cag cag ggc aac gtg ttc tcc tgc agc       1296
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

gtg atg cac gag gcc ctg cac aat cac tac aca cag aag tct ctg tct       1344
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

ctg agc ccc ggc aaa ggt ggc gga gga tct ggc gga ggc gga tcc gaa       1392
Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    450                 455                 460

gtt cag ctg ttg gaa agt ggt ggc gga ctg gtc cag cct ggc gaa tct       1440
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu Ser
465                 470                 475                 480

ctg aga ctg agc tgc aag gcc ttc ggg tat acc ttt acc aac cac cac       1488
Leu Arg Leu Ser Cys Lys Ala Phe Gly Tyr Thr Phe Thr Asn His His
                485                 490                 495

atc aat tgg gtt cga caa gcc cct ggc aag tgc ctg gaa tgg gtc gga       1536
Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Gly
            500                 505                 510

tat atc aac ccc tac aac gac tac acc acc ttc aac gac aag ttc aag       1584
Tyr Ile Asn Pro Tyr Asn Asp Tyr Thr Thr Phe Asn Asp Lys Phe Lys
        515                 520                 525

gac cgg ttc acc ctg tcc gtg gat aag tcc aag agc acc gct tac ctg       1632
Asp Arg Phe Thr Leu Ser Val Asp Lys Ser Lys Ser Thr Ala Tyr Leu
    530                 535                 540

cag atg aac tcc ctg aga gcc gag gat aca gct gtg tat tac tgt gcc       1680
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
545                 550                 555                 560

cgg acc tgg ggc cac tgg tac ttt gat ttg tgg ggc cag gga acc ctc       1728
Arg Thr Trp Gly His Trp Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu
                565                 570                 575

gtg aca gtc tct tct ggc ggc gga gga agc gga ggc gga ggt tca ggc       1776
Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
```

```
            580                 585                 590

ggc ggt gga tct aac atc cag atg acc cag tct cca tcc agc ctg tct       1824
Gly Gly Gly Ser Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
        595                 600                 605

gcc tct gtg ggc gac aga gtg aca att acc tgt cgg gcc tct cag tcc       1872
Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
    610                 615                 620

gtg tcc agc aat ctg gct tgg tat cag cag aag ccc ggc aag gct ccc       1920
Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
625                 630                 635                 640

aag ctg ctg atc tac gac tcc tcc acc aga gct acc ggc gtg cca tct       1968
Lys Leu Leu Ile Tyr Asp Ser Ser Thr Arg Ala Thr Gly Val Pro Ser
                645                 650                 655

aga ttc tcc ggc tct ggc tct ggc acc gac ttt acc ctg aca att tcc       2016
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            660                 665                 670

agc ctg cag cct gag gac ttc gcc acc tac tac tgc cag cag tac aac       2064
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
        675                 680                 685

aac tgg cct cct tgg acc ttc ggc tgc ggc acc aaa ctg gaa atc aag       2112
Asn Trp Pro Pro Trp Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
    690                 695                 700

cgc                                                                   2115
Arg
705
```

<210> 36
<211> 705
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 36

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

Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30
```

```
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Asp Val Val Pro Asn Asn Gly Val Pro Thr Tyr Asn Gln Lys Phe
    50                  55                  60

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

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

Ala Arg Pro His Tyr Tyr Tyr Ala Gly Arg Ser Gly Ala Met Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

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

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

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

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

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

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

```
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

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

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

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

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

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

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

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
    450                 455                 460
```

```
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Glu Ser
465                 470                 475                 480

Leu Arg Leu Ser Cys Lys Ala Phe Gly Tyr Thr Phe Thr Asn His His
                485                 490                 495

Ile Asn Trp Val Arg Gln Ala Pro Gly Lys Cys Leu Glu Trp Val Gly
            500                 505                 510

Tyr Ile Asn Pro Tyr Asn Asp Tyr Thr Thr Phe Asn Asp Lys Phe Lys
        515                 520                 525

Asp Arg Phe Thr Leu Ser Val Asp Lys Ser Lys Ser Thr Ala Tyr Leu
    530                 535                 540

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
545                 550                 555                 560

Arg Thr Trp Gly His Trp Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu
                565                 570                 575

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
            580                 585                 590

Gly Gly Gly Ser Asn Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
        595                 600                 605

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
    610                 615                 620

Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
625                 630                 635                 640

Lys Leu Leu Ile Tyr Asp Ser Ser Thr Arg Ala Thr Gly Val Pro Ser
                645                 650                 655

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            660                 665                 670
```

```
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn
        675                 680                 685


Asn Trp Pro Pro Trp Thr Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
    690                 695                 700


Arg
705


<210>  37
<211>  2136
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hKM3900_tA2-32LH HC


<220>
<221>  CDS
<222>  (1)..(2136)

<400>  37
gaa gtg cag ctg gtt cag tct ggc gcc gaa gtg aag aaa cct ggc gcc         48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

tcc gtg aag atc tcc tgc aag gct tct ggc tac acc ttc acc gac tac         96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

tac atg aac tgg gtc cga cag gct cct gga cag gga ctt gag tgg atg        144
Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

gga gat gtg gtg ccc aac aac ggc gtg ccc acc tac aac cag aaa ttc        192
Gly Asp Val Val Pro Asn Asn Gly Val Pro Thr Tyr Asn Gln Lys Phe
    50                  55                  60

aag ggc aga gtg acc atc acc gcc gac aag tct acc tcc acc gcc tac        240
Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

atg gaa ctg cgg agc ctg aga tct gag gac acc gcc gtg tac tac tgc        288
Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcc aga cct cac tac tac tac gcc ggc aga tct ggc gcc atg gat tat        336
Ala Arg Pro His Tyr Tyr Tyr Ala Gly Arg Ser Gly Ala Met Asp Tyr
```

```
            100                 105                 110

tgg gga cag ggc acc ctg gtc acc gtg tcc tct gct agc aca aag ggc        384
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125

ccc tct gtg ttc cct ctg gct cct agc tct aag tcc acc tct ggc gga        432
Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
    130                 135                 140

aca gct gct ctg ggc tgt ctg gtc aag gac tac ttc cct gag cct gtg        480
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145                 150                 155                 160

acc gtg tct tgg aac tct ggc gct ctg aca tcc ggc gtg cac aca ttt        528
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
                165                 170                 175

cca gct gtg ctg cag tcc tcc ggc ctg tac tct ctg tcc tct gtc gtg        576
Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
            180                 185                 190

acc gtg cct tcc agc tct ctg gga acc cag acc tac atc tgc aat gtg        624
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
        195                 200                 205

aac cac aag cct tcc aac acc aag gtg gac aag aag gtg gaa ccc aag        672
Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

tcc tgc gac aag acc cac acc tgt cct cca tgt cct gct cca gaa gct        720
Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

gct ggc gga cct tcc gtg ttc ctg ttt cct cca aag cct aag gac acc        768
Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

ctg atg atc tct cgg acc cct gaa gtg acc tgc gtg gtg gtg gat gtg        816
Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

tct cac gag gac cca gaa gtg aag ttc aat tgg tac gtg gac ggc gtg        864
Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val
        275                 280                 285

gaa gtg cac aac gcc aag acc aag cct aga gag gaa cag tac aac tcc        912
Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser
    290                 295                 300

acc tac aga gtg gtg tcc gtg ctg acc gtg ctg cac cag gat tgg ctg        960
Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320
```

```
aac ggc aaa gag tac aag tgc aag gtg tcc aac aag gcc ctg cct gcc       1008
Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala
                325                 330                 335

ggc atc gaa aag acc atc tcc aag gcc aag ggc cag cct agg gaa ccc       1056
Gly Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            340                 345                 350

cag gtt tac acc ttg cca cct tct cgg gac gag ctg acc aag aac cag       1104
Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln
        355                 360                 365

gtg tcc ctg acc tgt ctc gtg aag ggc ttc tac ccc tcc gat atc gcc       1152
Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
    370                 375                 380

gtg gaa tgg gag tct aat ggc cag cct gag aac aac tac aag aca acc       1200
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
385                 390                 395                 400

cct cct gtg ctg gac tcc gac ggc tca ttc ttc ctg tac tcc aag ctg       1248
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

aca gtg gac aag tcc aga tgg cag cag ggc aac gtg ttc tcc tgc agc       1296
Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

gtg atg cac gag gcc ctg cac aat cac tac aca cag aag tct ctg tct       1344
Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

ctg agc ccc ggc aaa ggt ggc gga gga tct ggc gga ggc gga tcc caa       1392
Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    450                 455                 460

tct gtt ctg acc caa cct cct tcc gcc tct ggc aca cct ggc cag aga       1440
Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg
465                 470                 475                 480

gtg acc atc tct tgc tcc ggc tcc tcc tcc aac atc ggc tct aac acc       1488
Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr
                485                 490                 495

gtg aac tgg tat cag cag ttc ccc ggc acc gct cct aag ctg ctg atc       1536
Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu Ile
            500                 505                 510

tac tcc aac aac cag cgg cct tcc ggc gtg ccc gat aga ttc tct ggc       1584
Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly
        515                 520                 525
```

```
tct aag tcc ggc acc tct gcc agc ctg gct att tct gga ctg cag agc       1632
Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser
    530                 535                 540

gag gac gag gcc gac tat tat tgt gcc ggc tgg gac gac tct ctg aac       1680
Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly Trp Asp Asp Ser Leu Asn
545                 550                 555                 560

ggc cct gtt ttt ggc ggt ggc acc aaa ctg aca gtg ctt gga ggc ggt       1728
Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
                565                 570                 575

ggt gga tca ggc ggc ggt gga agt ggt ggt ggt ggt agc gga ggt ggt       1776
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            580                 585                 590

gga tct cag gtg cag ctc caa gag tct gga cct ggc ctc gtg aag cct       1824
Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
        595                 600                 605

tcc gag aca ctg tct ctg acc tgc aca gtg tcc ggc ggc tct atc tct       1872
Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser
    610                 615                 620

ggc tac tac tgg tcc tgg atc aga cag cct cct ggc aag gga ctc gag       1920
Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
625                 630                 635                 640

tgg atc ggc tac atc tac tac tct ggc ttc acc aac tac aac ccc agc       1968
Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Phe Thr Asn Tyr Asn Pro Ser
                645                 650                 655

ctg aag tcc cgc gtg acc atc agc gtg gac acc tct aag aac cag ttc       2016
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
            660                 665                 670

tct ctg aag ctg tcc tcc gtg acc gcc gct gat acc gct gtg tat tac       2064
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
        675                 680                 685

tgc acc cgg gac cac agc cac tac tac tac atg gac gtg tgg gga cag       2112
Cys Thr Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly Gln
    690                 695                 700

gga aca acc gtg aca gtg tcc tcc                                      2136
Gly Thr Thr Val Thr Val Ser Ser
705                 710
```

<210> 38
<211> 712
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 38

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


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


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


Gly Asp Val Val Pro Asn Asn Gly Val Pro Thr Tyr Asn Gln Lys Phe
    50                  55                  60


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


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


Ala Arg Pro His Tyr Tyr Tyr Ala Gly Arg Ser Gly Ala Met Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
        115                 120                 125


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


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


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


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

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

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
    210                 215                 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
225                 230                 235                 240

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
                245                 250                 255

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
            260                 265                 270

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

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

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
305                 310                 315                 320

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

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

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

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

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

```
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
                405                 410                 415

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
            420                 425                 430

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
        435                 440                 445

Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    450                 455                 460

Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg
465                 470                 475                 480

Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Thr
                485                 490                 495

Val Asn Trp Tyr Gln Gln Phe Pro Gly Thr Ala Pro Lys Leu Leu Ile
            500                 505                 510

Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly
        515                 520                 525

Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Gln Ser
    530                 535                 540

Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Gly Trp Asp Asp Ser Leu Asn
545                 550                 555                 560

Gly Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly
                565                 570                 575

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            580                 585                 590

Gly Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro
        595                 600                 605

Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser
```

```
    610                 615                 620

Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
625                 630                 635                 640

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Phe Thr Asn Tyr Asn Pro Ser
                645                 650                 655

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
            660                 665                 670

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
        675                 680                 685

Cys Thr Arg Asp His Ser His Tyr Tyr Tyr Met Asp Val Trp Gly Gln
    690                 695                 700

Gly Thr Thr Val Thr Val Ser Ser
705                 710


<210>  39
<211>  645
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  hKM3900 LC


<220>
<221>  CDS
<222>  (1)..(645)

<400>  39
gac atc cag ctg acc cag tct cca tcc tct ctg tct gcc tct gtg ggc         48
Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

gac aga gtg aca att acc tgc acc gcc tcc tcc acc gtg tcc tct acc         96
Asp Arg Val Thr Ile Thr Cys Thr Ala Ser Ser Thr Val Ser Ser Thr
            20                  25                  30

tac ctg cac tgg tat cag cag aag ccc ggc aag gct ccc aag ctg ctg        144
Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
```

```
atc tac tcc acc tcc aat ctg gcc tct ggc gtg ccc tct aga ttc tcc        192
Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60

gga tct ggc tct gga acc gac tat acc ctg aca atc tcc agc ctg cag        240
Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

cct gag gac ttc gcc acc tac tac tgc cac cag tac cac aga tcc cca        288
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
                85                  90                  95

cct acc ttt ggc cag ggc acc aag ctg gaa atc aag cgt acg gtg gcc        336
Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala
            100                 105                 110

gct cct tcc gtg ttc atc ttc cca cct tcc gac gag cag ctg aag tcc        384
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

ggc aca gct tct gtc gtg tgc ctg ctg aac aac ttc tac cct cgg gaa        432
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

gcc aag gtg cag tgg aag gtg gac aat gcc ctg cag tcc ggc aac tcc        480
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

caa gag tct gtg acc gag cag gac tcc aag gac agc acc tac agc ctg        528
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
                165                 170                 175

tcc tcc aca ctg acc ctg tcc aag gcc gac tac gag aag cac aag gtg        576
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
            180                 185                 190

tac gcc tgc gaa gtg acc cat cag ggc ctg tct agc cct gtg acc aag        624
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
        195                 200                 205

tct ttc aac cgg ggc gag tgc                                            645
Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 40
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 40

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

Asp Arg Val Thr Ile Thr Cys Thr Ala Ser Ser Thr Val Ser Ser Thr
            20                  25                  30

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

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

Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Tyr His Arg Ser Pro
                85                  90                  95

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

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
        115                 120                 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
    130                 135                 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145                 150                 155                 160

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

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

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

Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> 41
<211> 486
<212> PRT
<213> Artificial Sequence

<220>
<223> anti-CD3 scFv-human Fc fusion protein

<220>
<221> PEPTIDE
<222> (1)..(486)

<400> 41

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

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

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

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

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

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

Tyr Cys Val Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
            100   105   110

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

Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly Ser Gly Lys Pro Gly

```
    130                 135                 140

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

Gly Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr
                165                 170                 175

Ser Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg
            180                 185                 190

Gly Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg
        195                 200                 205

Phe Ser Gly Ser Leu Leu Gly Asp Lys Ala Ala Leu Thr Leu Ser Gly
    210                 215                 220

Ala Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser
225                 230                 235                 240

Asn Leu Trp Val Phe Gly Ser Gly Thr Lys Val Thr Val Leu Glu Pro
                245                 250                 255

Lys Ser Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
            260                 265                 270

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
        275                 280                 285

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    290                 295                 300

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
305                 310                 315                 320

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala
                325                 330                 335

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
            340                 345                 350
```

```
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
        355                 360                 365

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    370                 375                 380

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

Gln Val Ser Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                405                 410                 415

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
            420                 425                 430

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        435                 440                 445

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    450                 455                 460

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
465                 470                 475                 480

Ser Leu Ser Pro Gly Lys
                485
```

<210> 42
<211> 255
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(255)

<400> 42

```
Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1               5                   10                  15
```

```
Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Pro Cys Ser Asn Cys Pro
            20                  25                  30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Asn Gln Ile Cys Ser Pro Cys
        35                  40                  45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
    50                  55                  60

Cys Arg Gln Cys Lys Gly Val Phe Arg Thr Arg Lys Glu Cys Ser Ser
65                  70                  75                  80

Thr Ser Asn Ala Glu Cys Asp Cys Thr Pro Gly Phe His Cys Leu Gly
                85                  90                  95

Ala Gly Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
            100                 105                 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
        115                 120                 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys
    130                 135                 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145                 150                 155                 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Val Thr Pro Pro Ala
                165                 170                 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Ser Phe Phe Leu
            180                 185                 190

Ala Leu Thr Ser Thr Ala Leu Leu Phe Leu Leu Phe Phe Leu Thr Leu
        195                 200                 205

Arg Phe Ser Val Val Lys Arg Gly Arg Lys Lys Leu Leu Tyr Ile Phe
    210                 215                 220
```

Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly
225 230 235 240

Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
245 250 255

<210> 43
<211> 254
<212> PRT
<213> Macaca fascicularis

<220>
<221> PEPTIDE
<222> (1)..(254)

<400> 43

Met Gly Asn Ser Cys Tyr Asn Ile Val Ala Thr Leu Leu Leu Val Leu
1 5 10 15

Asn Phe Glu Arg Thr Arg Ser Leu Gln Asp Leu Cys Ser Asn Cys Pro
20 25 30

Ala Gly Thr Phe Cys Asp Asn Asn Arg Ser Gln Ile Cys Ser Pro Cys
35 40 45

Pro Pro Asn Ser Phe Ser Ser Ala Gly Gly Gln Arg Thr Cys Asp Ile
50 55 60

Cys Arg Gln Cys Lys Gly Val Phe Lys Thr Arg Lys Glu Cys Ser Ser
65 70 75 80

Thr Ser Asn Ala Glu Cys Asp Cys Ile Ser Gly Tyr His Cys Leu Gly
85 90 95

Ala Glu Cys Ser Met Cys Glu Gln Asp Cys Lys Gln Gly Gln Glu Leu
100 105 110

Thr Lys Lys Gly Cys Lys Asp Cys Cys Phe Gly Thr Phe Asn Asp Gln
115 120 125

Lys Arg Gly Ile Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Lys

```
    130                 135                 140

Ser Val Leu Val Asn Gly Thr Lys Glu Arg Asp Val Val Cys Gly Pro
145                 150                 155                 160

Ser Pro Ala Asp Leu Ser Pro Gly Ala Ser Ser Ala Thr Pro Pro Ala
                165                 170                 175

Pro Ala Arg Glu Pro Gly His Ser Pro Gln Ile Ile Phe Phe Leu Ala
            180                 185                 190

Leu Thr Ser Thr Val Val Leu Phe Leu Leu Phe Phe Leu Val Leu Arg
        195                 200                 205

Phe Ser Val Val Lys Arg Ser Arg Lys Lys Leu Leu Tyr Ile Phe Lys
    210                 215                 220

Gln Pro Phe Met Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys
225                 230                 235                 240

Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
                245                 250

<210>  44
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  His tag protein

<220>
<221>  PEPTIDE
<222>  (1)..(6)

<400>  44

His His His His His His
1               5

<210>  45
<211>  26
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> 3xFLAG tag proteinE

<220>
<221> PEPTIDE
<222> (1)..(26)

<400> 45

Asp Tyr Lys Asp Asp Asp Asp Lys Gly Asp Tyr Lys Asp Asp Asp Asp
1 5 10 15

Lys Ile Asp Tyr Lys Asp Asp Asp Asp Lys
20 25

<210> 46
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(4)

<400> 46

Gly Gly Gly Ser
1

<210> 47
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(4)

<400> 47

Ser Gly Gly Gly
1

<210> 48
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(5)

<400> 48

Gly Gly Gly Gly Ser
1 5

<210> 49
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(5)

<400> 49

Ser Gly Gly Gly Gly
1 5

<210> 50
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>

<221> PEPTIDE
<222> (1)..(6)

<400> 50

Gly Gly Gly Gly Gly Ser
1 5

<210> 51
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(6)

<400> 51

Ser Gly Gly Gly Gly Gly
1 5

<210> 52
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(7)

<400> 52

Gly Gly Gly Gly Gly Gly Ser
1 5

<210> 53
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(7)

<400> 53

Ser Gly Gly Gly Gly Gly Gly
1 5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> GS linker

<220>
<221> PEPTIDE
<222> (1)..(10)

<400> 54

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 55
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> GKPGS linker

<220>
<221> PEPTIDE
<222> (1)..(5)

<400> 55

Gly Lys Pro Gly Ser
1 5