Sequence listing with corrections to SEQ ID NOs 48 215 and 216 N402043WO

SEQUENCE LISTING

<110> Medical Research Council Technology

<120> Compounds

<130> MEDBX/P53198PC

<140> PCT/GB2013/051373
<141> 2013-05-24

<150> GB1209096.5
<151> 2012-05-24

<160> 296

<170> BiSSAP 1.2

<210> 1
<211> 2064
<212> DNA
<213> Homo sapiens

<220>
<221> source
<222> 1..2064
<223> /mol_type="unassigned DNA"
/note="Human TG2 nucleotide sequence"
/organism="Homo sapiens"

<400> 1
atggccgagg agctggtctt agagaggtgt gatctggagc tggagaccaa tggccgagac 60

caccacacgg ccgacctgtg ccgggagaag ctggtggtgc gacggggcca gcccttctgg 120

ctgaccctgc actttgaggg ccgcaactac gaggccagtg tagacagtct caccttcagt 180

gtcgtgaccg gcccagcccc tagccaggag gccgggacca aggcccgttt tccactaaga 240

gatgctgtgg aggagggtga ctggacagcc accgtggtgg accagcaaga ctgcaccctc 300

tcgctgcagc tcaccacccc ggccaacgcc cccatcggcc tgtatcgcct cagcctggag 360

gcctccactg gctaccaggg atccagcttt gtgctgggcc acttcatttt gctcttcaac 420

gcctggtgcc cagcggatgc tgtgtacctg gactcggaag aggagcggca ggagtatgtc 480

ctcacccagc agggctttat ctaccagggc tcggccaagt tcatcaagaa cataccttgg 540

aattttgggc agtttgaaga tgggatccta gacatctgcc tgatccttct agatgtcaac 600

cccaagttcc tgaagaacgc cggccgtgac tgctcccgcc gcagcagccc cgtctacgtg 660

ggccgggtgg tgagtggcat ggtcaactgc aacgatgacc agggtgtgct gctgggacgc 720

tgggacaaca actacgggga cggcgtcagc cccatgtcct ggatcggcag cgtggacatc 780

ctgcggcgct ggaagaacca cggctgccag cgcgtcaagt atggccagtg ctgggtcttc 840

gccgccgtgg cctgcacagt gctgaggtgc ctgggcatcc ctacccgcgt cgtgaccaac 900

tacaactcgg cccatgacca gaacagcaac cttctcatcg agtacttccg caatgagttt 960

ggggagatcc agggtgacaa gagcgagatg atctggaact tccactgctg ggtggagtcg 1020

tggatgacca ggccggacct gcagccgggg tacgagggct ggcaggccct ggacccaacg 1080

ccccaggaga agagcgaagg gacgtactgc tgtggcccag ttccagttcg tgccatcaag 1140

gagggcgacc tgagcaccaa gtacgatgcg ccctttgtct ttgcggaggt caatgccgac 1200

gtggtagact ggatccagca ggacgatggg tctgtgcaca aatccatcaa ccgttccctg 1260

atcgttgggc tgaagatcag cactaagagc gtgggccgag acgagcggga ggatatcacc 1320

cacacctaca aatacccaga ggggtcctca gaggagaggg aggccttcac aagggcgaac 1380

cacctgaaca aactggccga gaaggaggag acagggatgg ccatgcggat ccgtgtgggc 1440

cagagcatga acatgggcag tgactttgac gtctttgccc acatcaccaa caacaccgct 1500

gaggagtacg tctgccgcct cctgctctgt gcccgcaccg tcagctacaa tgggatcttg 1560

gggcccgagt gtggcaccaa gtacctgctc aacctcaacc tggagccttt ctctgagaag 1620

agcgttcctc tttgcatcct ctatgagaaa taccgtgact gccttacgga gtccaacctc 1680

atcaaggtgc gggccctcct cgtggagcca gttatcaaca gctacctgct ggctgagagg 1740

gacctctacc tggagaatcc agaaatcaag atccggatcc ttggggagcc caagcagaaa 1800

cgcaagctgg tggctgaggt gtccctgcag aacccgctcc ctgtggccct ggaaggctgc 1860

accttcactg tggaggggc cggcctgact gaggagcaga agacggtgga gatcccagac 1920

cccgtggagg caggggagga agttaaggtg agaatggacc tgctgccgct ccacatgggc 1980

ctccacaagc tggtggtgaa cttcgagagc gacaagctga aggctgtgaa gggcttccgg 2040

aatgtcatca ttggccccgc ctaa 2064

<210> 2
<211> 687
<212> PRT
<213> Homo sapiens

<220>
<223> Human TG2 Amino Acid sequence

<400> 2

```
Met Ala Glu Glu Leu Val Leu Glu Arg Cys Asp Leu Glu Leu Glu Thr
1               5                  10                  15
Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Arg Glu Lys Leu Val
            20                  25                  30
Val Arg Arg Gly Gln Pro Phe Trp Leu Thr Leu His Phe Glu Gly Arg
        35                  40                  45
Asn Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Ser Val Val Thr Gly
    50                  55                  60
Pro Ala Pro Ser Gln Glu Ala Gly Thr Lys Ala Arg Phe Pro Leu Arg
65                  70                  75                  80
Asp Ala Val Glu Glu Gly Asp Trp Thr Ala Thr Val Val Asp Gln Gln
                85                  90                  95
Asp Cys Thr Leu Ser Leu Gln Leu Thr Thr Pro Ala Asn Ala Pro Ile
            100                 105                 110
Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
        115                 120                 125
Ser Phe Val Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
    130                 135                 140
Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu Tyr Val
145                 150                 155                 160
Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe Ile Lys
                165                 170                 175
Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ile
            180                 185                 190
Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn Ala Gly
```

```
        195                 200                 205
Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg Val Val
    210                 215                 220
Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
225                 230                 235                 240
Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp Ile Gly
                245                 250                 255
Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln Arg Val
            260                 265                 270
Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
        275                 280                 285
Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
    290                 295                 300
His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
305                 310                 315                 320
Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe His Cys
                325                 330                 335
Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
            340                 345                 350
Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
        355                 360                 365
Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly Asp Leu
    370                 375                 380
Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
385                 390                 395                 400
Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys Ser Ile
                405                 410                 415
Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser Val Gly
            420                 425                 430
Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
        435                 440                 445
Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys
    450                 455                 460
Leu Ala Glu Lys Glu Glu Thr Gly Met Ala Met Arg Ile Arg Val Gly
465                 470                 475                 480
Gln Ser Met Asn Met Gly Ser Asp Phe Asp Val Phe Ala His Ile Thr
                485                 490                 495
Asn Asn Thr Ala Glu Glu Tyr Val Cys Arg Leu Leu Leu Cys Ala Arg
            500                 505                 510
Thr Val Ser Tyr Asn Gly Ile Leu Gly Pro Glu Cys Gly Thr Lys Tyr
        515                 520                 525
Leu Leu Asn Leu Asn Leu Glu Pro Phe Ser Glu Lys Ser Val Pro Leu
    530                 535                 540
Cys Ile Leu Tyr Glu Lys Tyr Arg Asp Cys Leu Thr Glu Ser Asn Leu
545                 550                 555                 560
Ile Lys Val Arg Ala Leu Leu Val Glu Pro Val Ile Asn Ser Tyr Leu
                565                 570                 575
Leu Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg
            580                 585                 590
Ile Leu Gly Glu Pro Lys Gln Lys Arg Lys Leu Val Ala Glu Val Ser
        595                 600                 605
Leu Gln Asn Pro Leu Pro Val Ala Leu Glu Gly Cys Thr Phe Thr Val
    610                 615                 620
Glu Gly Ala Gly Leu Thr Glu Glu Gln Lys Thr Val Glu Ile Pro Asp
625                 630                 635                 640
Pro Val Glu Ala Gly Glu Glu Val Lys Val Arg Met Asp Leu Leu Pro
                645                 650                 655
Leu His Met Gly Leu His Lys Leu Val Val Asn Phe Glu Ser Asp Lys
            660                 665                 670
Leu Lys Ala Val Lys Gly Phe Arg Asn Val Ile Ile Gly Pro Ala
        675                 680                 685
```

<210> 3
<211> 2062
<212> DNA
<213> Rattus

<220>

<221> source
<222> 1..2062
<223> /mol_type="unassigned DNA"
/note="Rat TG2 Nucleotide sequence"
/organism="Rattus"

<400> 3
atggccgagg agctgaacct ggagaggtgc gatttggaga tacaggccaa tggccgtgat 60

caccacacgg ccgacctgtg ccaagagaaa ctggtgctgc ggcgaggcca gcgcttccgg 120

ctgacactgt acttcgaggg ccgtggctat gaggccagcg tggacagact tacatttggt 180

gccgtgaccg gcccagatcc cagtgaagag gcagggacca aggcccgctt ctcactgtct 240

gacgatgtgg aggagggatc ctggtcagcc tctgtgctgg accaacagga caatgtcctc 300

tcgctgcagc tctgcacccc agccaatgct cctgttggcc agtaccgcct cagcctggag 360

acttctactg gctaccaagg ctccagcttc atgctgggtc acttcatcct gctcttcaat 420

gcctggtgcc cagcggatga cgtgtaccta gattcagagg cggagcgccg ggaatacgtc 480

ctcacacagc agggcttcat ctaccagggc tctgtcaagt tcatcaagag tgtgccttgg 540

aactttgggc agtttgagga tgggatcctg gatgcctgcc tgatgctttt ggatgtgaac 600

cccaagttcc tgaaggaccg tagccgggac tgctcacgac gcagcagtcc catctatgtg 660

ggccgcgtgg tgagcggcat ggtcaactgc aatgatgacc agggtgtgct tctgggtcgc 720

tgggacaaca attatgggga cggtatcagt cccatggcct ggattggcag cgtggacatt 780

ctgcggcgct ggaaggaaca cggctgtcag caagtgaagt atggccagtg ctgggtgttt 840

gcggcggtag cctgcacagt gctgcggtgc cttggcatcc ctaccagagt ggtgaccaac 900

tacaactccg cccacgacca gaacagcaac ctgctcatcg agtacttccg aaacgagtac 960

ggggagctgg agagcaacaa gagcgagatg atctggaatt tccactgctg ggtggagtcc 1020

tggatgacca ggccagacct acagccaggc tatgaggggt ggcaggccat tgaccccaca 1080

ccgcaggaga agagcgaagg aacatactgt tgtggcccag tctcagtgcg ggccatcaag 1140

gagggtgacc tgagcaccaa gtatgatgcg tccttcgtgt ttgccgaggt caacgctgat 1200

gtggtggact ggatccggca gtcagatggg tctgtgctca aatccatcaa caattccctg 1260

gtcgtggggc agaagatcag cactaagagc gtgggccgtg atgaccggga ggacatcacc 1320

tatacctaca agtacccaga ggggtcccca gaggagaggg aagtcttcac cagagccaac 1380

cacctgaaca aactggcaga gaaagaggag acaggggtgg ccatgcggat ccgagtgggg 1440

gatggtatga gcttgggcaa tgactttgac gtgtttgccc acatcggcaa cgacacctcg 1500

gagagccgtg agtgccgcct cctgctctgt gcccgcactg tcagctacaa cggcgtgctg 1560

gggcccgagt gtggcactga ggacatcaac ctgaccctgg atccctactc tgagaacagc 1620

atccccttc gcatcctcta cgagaagtac agcggttgcc tgaccgagtc aaacctcatc 1680

aaggtgcggg gtctcctcgt cgagccagcc gctaacagct acctgctggc tgagagagat 1740

ctctacctgg agaatcctga aatcaagatc cggatcctgg gggagcccaa gcagaaccgc 1800

aaactggtgg ctgaggtgtc cctgaagaac ccactttctg attccctgta tgactgtgtc 1860

ttcactgtgg agggggctgg cctgaccaag gaacagaagt ctgtggaggt ctcagaccct 1920

gtgccagcag gagatgcggt caaggtgcgg gttgacctgt tcccgactga tattggcctc 1980

cacaagttgg tggtgaactt ccagtgtgac aagctgaagt cggtcaaggg ttaccggaat 2040

atcatcatcg gcccggccta ag 2062

<210> 4
<211> 686
<212> PRT
<213> Rattus

<220>
<223> Rat TG2 Amino Acid sequence

<400> 4

```
Met Ala Glu Glu Leu Asn Leu Glu Arg Cys Asp Leu Glu Ile Gln Ala
1               5                  10                  15
Asn Gly Arg Asp His His Thr Ala Asp Leu Cys Gln Glu Lys Leu Val
            20                  25                  30
Leu Arg Arg Gly Gln Arg Phe Arg Leu Thr Leu Tyr Phe Glu Gly Arg
        35                  40                  45
Gly Tyr Glu Ala Ser Val Asp Arg Leu Thr Phe Gly Ala Val Thr Gly
    50                  55                  60
Pro Asp Pro Ser Glu Glu Ala Gly Thr Lys Ala Arg Phe Ser Leu Ser
65                  70                  75                  80
Asp Asp Val Glu Glu Gly Ser Trp Ser Ala Ser Val Leu Asp Gln Gln
                85                  90                  95
Asp Asn Val Leu Ser Leu Gln Leu Cys Thr Pro Ala Asn Ala Pro Val
            100                 105                 110
Gly Gln Tyr Arg Leu Ser Leu Glu Thr Ser Thr Gly Tyr Gln Gly Ser
        115                 120                 125
Ser Phe Met Leu Gly His Phe Ile Leu Leu Phe Asn Ala Trp Cys Pro
    130                 135                 140
Ala Asp Asp Val Tyr Leu Asp Ser Glu Ala Glu Arg Arg Glu Tyr Val
145                 150                 155                 160
Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Val Lys Phe Ile Lys
                165                 170                 175
Ser Val Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Ala
            180                 185                 190
Cys Leu Met Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asp Arg Ser
        195                 200                 205
Arg Asp Cys Ser Arg Arg Ser Ser Pro Ile Tyr Val Gly Arg Val Val
    210                 215                 220
Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
225                 230                 235                 240
Trp Asp Asn Asn Tyr Gly Asp Gly Ile Ser Pro Met Ala Trp Ile Gly
                245                 250                 255
Ser Val Asp Ile Leu Arg Arg Trp Lys Glu His Gly Cys Gln Gln Val
            260                 265                 270
Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
        275                 280                 285
Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
    290                 295                 300
His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Tyr
305                 310                 315                 320
Gly Glu Leu Glu Ser Asn Lys Ser Glu Met Ile Trp Asn Phe His Cys
                325                 330                 335
Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
            340                 345                 350
Gly Trp Gln Ala Ile Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
        355                 360                 365
Tyr Cys Cys Gly Pro Val Ser Val Arg Ala Ile Lys Glu Gly Asp Leu
    370                 375                 380
Ser Thr Lys Tyr Asp Ala Ser Phe Val Phe Ala Glu Val Asn Ala Asp
```

```
385                 390                 395                 400
Val Val Asp Trp Ile Arg Gln Ser Asp Gly Ser Val Leu Lys Ser Ile
                405                 410                 415
Asn Asn Ser Leu Val Val Gly Gln Lys Ile Ser Thr Lys Ser Val Gly
            420                 425                 430
Arg Asp Asp Arg Glu Asp Ile Thr Tyr Thr Tyr Lys Tyr Pro Glu Gly
        435                 440                 445
Ser Pro Glu Glu Arg Glu Val Phe Thr Arg Ala Asn His Leu Asn Lys
    450                 455                 460
Leu Ala Glu Lys Glu Glu Thr Gly Val Ala Met Arg Ile Arg Val Gly
465                 470                 475                 480
Asp Gly Met Ser Leu Gly Asn Asp Phe Asp Val Phe Ala His Ile Gly
                485                 490                 495
Asn Asp Thr Ser Glu Ser Arg Glu Cys Arg Leu Leu Leu Cys Ala Arg
            500                 505                 510
Thr Val Ser Tyr Asn Gly Val Leu Gly Pro Glu Cys Gly Thr Glu Asp
        515                 520                 525
Ile Asn Leu Thr Leu Asp Pro Tyr Ser Glu Asn Ser Ile Pro Leu Arg
    530                 535                 540
Ile Leu Tyr Glu Lys Tyr Ser Gly Cys Leu Thr Glu Ser Asn Leu Ile
545                 550                 555                 560
Lys Val Arg Gly Leu Leu Val Glu Pro Ala Ala Asn Ser Tyr Leu Leu
                565                 570                 575
Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg Ile
            580                 585                 590
Leu Gly Glu Pro Lys Gln Asn Arg Lys Leu Val Ala Glu Val Ser Leu
        595                 600                 605
Lys Asn Pro Leu Ser Asp Ser Leu Tyr Asp Cys Val Phe Thr Val Glu
    610                 615                 620
Gly Ala Gly Leu Thr Lys Glu Gln Lys Ser Val Glu Val Ser Asp Pro
625                 630                 635                 640
Val Pro Ala Gly Asp Ala Val Lys Val Arg Val Asp Leu Phe Pro Thr
                645                 650                 655
Asp Ile Gly Leu His Lys Leu Val Val Asn Phe Gln Cys Asp Lys Leu
            660                 665                 670
Lys Ser Val Lys Gly Tyr Arg Asn Ile Ile Ile Gly Pro Ala
        675                 680                 685
```

<210> 5
<211> 2061
<212> DNA
<213> Mus musculus

<220>
<221> source
<222> 1..2061
<223> /mol_type="unassigned DNA"
/note="Mouse TG2 Nucleotide sequence"
/organism="Mus musculus"

<400> 5

```
atggcagagg agctgctcct ggagaggtgt gatttggaga ttcaggccaa tggccgtgac      60

caccacacgg ccgacctatg ccaagagaaa ctggtgctgc gtcgtggtca gcgcttccgg     120

ctgactctgt acttcgaggg ccgtggctac gaggccagcg tggacagcct cacgttcggt     180

gctgtgaccg gcccagatcc cagtgaagag gcagggacca aggcccgctt ctcactgtct     240

gacaatgtgg aggagggatc ttggtcagcc tcagtgctgg accaacagga caatgtcctc     300

tcgctacagc tctgcacccc agccaatgct cctattggcc tgtaccgtct cagcctagag     360

gcttctactg gctaccaggg ctccagcttt gtgctgggcc acttcatcct gctctacaat     420

gcctggtgcc cagccgatga tgtgtaccta gactcagagg aggagcgacg ggaatatgtc     480

cttacgcaac agggcttcat ctaccaaggc tctgtcaagt tcatcaagag tgtgccttgg     540
```

aactttgggc agttcgagga tggaatcctg gatacctgcc tgatgctctt ggatatgaac 600

cccaagttcc tgaagaaccg tagtcgggac tgctcacgcc gcagcagtcc catctatgtg 660

ggccgcgtgg tgagcgccat ggtcaactgc aatgatgacc agggtgtgct tctgggccgc 720

tgggacaaca actatgggga tggtatcagt cccatggcct ggattggcag tgtggacatt 780

ctgcggcgct ggaaggaaca cggctgtcag caagtgaagt acgggcagtg ctgggtgttt 840

gcagcggtgg cctgcacagt gctgcggtgc ctcggcatcc ctaccagagt ggtgaccaac 900

tacaactccg cccacgacca gaacagcaac ctgctcatcg agtacttccg aaatgagttc 960

ggggagctgg agagcaacaa gagcgagatg atctggaact tccactgctg ggtggagtcc 1020

tggatgacca ggccagacct acagccgggc tatgaggggt ggcaggccat tgaccccaca 1080

ccacaggaga agagcgaagg gacatactgt tgtggcccag tctcagtgcg agccatcaag 1140

gagggagacc tgagtaccaa gtatgatgca cccttcgtgt ttgccgaggt caacgctgat 1200

gtggtggact ggatccggca ggaagatggg tctgtgctca aatccatcaa ccgttccttg 1260

gtcgtggggc agaagatcag cactaagagt gtgggccgtg atgaccggga ggacatcacc 1320

catacctaca agtacccaga ggggtcaccc gaggagaggg aagtcttcac caaggccaac 1380

cacctgaaca aactggcaga gaaagaggag acaggggtgg ccatgcgcat ccgagtgggg 1440

gacagtatga gcatgggcaa cgacttcgac gtgtttgccc acatcggcaa cgacacctcg 1500

gagactcgag agtgtcgtct cctgctctgt gcccgcactg tcagctacaa cggggtgctg 1560

gggcccgagt gtggcactga ggacatcaac ctgaccctgg atccctactc tgagaacagc 1620

atcccacttc gaatcctcta cgagaagtac agcgggtgcc tgacagagtc aaacctcatc 1680

aaggtgcggg gccttctcat cgaaccagct gccaacagct acctgctggc tgagagagat 1740

ctctacctgg agaatcccga aatcaagatc cgggtcctgg gagaacccaa gcaaaaccgc 1800

aaactggtgg ctgaggtgtc cctgaagaac ccactttccg atcccctgta tgactgcatc 1860

ttcactgtgg agggggctgg cctgaccaag gagcagaagt ctgtggaagt ctcagacccg 1920

gtgccagcgg gcgatttggt caaggcacgg gtcgacctgt tcccgactga tattggcctc 1980

cacaagctgg tggtgaactt ccagtgtgac aagctgaagt cggtgaaggg ttaccggaat 2040

gttatcatcg gcccggccta a 2061

<210> 6
<211> 686
<212> PRT
<213> Mus musculus

<220>
<223> Mouse TG2 Amino Acid sequence

<400> 6

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

```
        35                  40                  45
Gly Tyr Glu Ala Ser Val Asp Ser Leu Thr Phe Gly Ala Val Thr Gly
    50                  55                  60
Pro Asp Pro Ser Glu Glu Ala Gly Thr Lys Ala Arg Phe Ser Leu Ser
65                  70                  75                  80
Asp Asn Val Glu Glu Gly Ser Trp Ser Ala Ser Val Leu Asp Gln Gln
                85                  90                  95
Asp Asn Val Leu Ser Leu Gln Leu Cys Thr Pro Ala Asn Ala Pro Ile
            100                 105                 110
Gly Leu Tyr Arg Leu Ser Leu Glu Ala Ser Thr Gly Tyr Gln Gly Ser
        115                 120                 125
Ser Phe Val Leu Gly His Phe Ile Leu Leu Tyr Asn Ala Trp Cys Pro
    130                 135                 140
Ala Asp Asp Val Tyr Leu Asp Ser Glu Glu Glu Arg Arg Glu Tyr Val
145                 150                 155                 160
Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Val Lys Phe Ile Lys
                165                 170                 175
Ser Val Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu Asp Thr
            180                 185                 190
Cys Leu Met Leu Leu Asp Met Asn Pro Lys Phe Leu Lys Asn Arg Ser
        195                 200                 205
Arg Asp Cys Ser Arg Arg Ser Ser Pro Ile Tyr Val Gly Arg Val Val
    210                 215                 220
Ser Ala Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu Gly Arg
225                 230                 235                 240
Trp Asp Asn Asn Tyr Gly Asp Gly Ile Ser Pro Met Ala Trp Ile Gly
                245                 250                 255
Ser Val Asp Ile Leu Arg Arg Trp Lys Glu His Gly Cys Gln Gln Val
            260                 265                 270
Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr Val Leu
        275                 280                 285
Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn Ser Ala
    290                 295                 300
His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu Phe
305                 310                 315                 320
Gly Glu Leu Glu Ser Asn Lys Ser Glu Met Ile Trp Asn Phe His Cys
                325                 330                 335
Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly Tyr Glu
            340                 345                 350
Gly Trp Gln Ala Ile Asp Pro Thr Pro Gln Glu Lys Ser Glu Gly Thr
        355                 360                 365
Tyr Cys Cys Gly Pro Val Ser Val Arg Ala Ile Lys Glu Gly Asp Leu
    370                 375                 380
Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ala Asp
385                 390                 395                 400
Val Val Asp Trp Ile Arg Gln Glu Asp Gly Ser Val Leu Lys Ser Ile
                405                 410                 415
Asn Arg Ser Leu Val Val Gly Gln Lys Ile Ser Thr Lys Ser Val Gly
            420                 425                 430
Arg Asp Asp Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro Glu Gly
        435                 440                 445
Ser Pro Glu Glu Arg Glu Val Phe Thr Lys Ala Asn His Leu Asn Lys
    450                 455                 460
Leu Ala Glu Lys Glu Glu Thr Gly Val Ala Met Arg Ile Arg Val Gly
465                 470                 475                 480
Asp Ser Met Ser Met Gly Asn Asp Phe Asp Val Phe Ala His Ile Gly
                485                 490                 495
Asn Asp Thr Ser Glu Thr Arg Glu Cys Arg Leu Leu Leu Cys Ala Arg
            500                 505                 510
Thr Val Ser Tyr Asn Gly Val Leu Gly Pro Glu Cys Gly Thr Glu Asp
        515                 520                 525
Ile Asn Leu Thr Leu Asp Pro Tyr Ser Glu Asn Ser Ile Pro Leu Arg
    530                 535                 540
Ile Leu Tyr Glu Lys Tyr Ser Gly Cys Leu Thr Glu Ser Asn Leu Ile
545                 550                 555                 560
Lys Val Arg Gly Leu Leu Ile Glu Pro Ala Ala Asn Ser Tyr Leu Leu
                565                 570                 575
Ala Glu Arg Asp Leu Tyr Leu Glu Asn Pro Glu Ile Lys Ile Arg Val
```

```
            580                 585                 590
Leu Gly Glu Pro Lys Gln Asn Arg Lys Leu Val Ala Glu Val Ser Leu
        595                 600                 605
Lys Asn Pro Leu Ser Asp Pro Leu Tyr Asp Cys Ile Phe Thr Val Glu
    610                 615                 620
Gly Ala Gly Leu Thr Lys Glu Gln Lys Ser Val Glu Val Ser Asp Pro
625                 630                 635                 640
Val Pro Ala Gly Asp Leu Val Lys Ala Arg Val Asp Leu Phe Pro Thr
                645                 650                 655
Asp Ile Gly Leu His Lys Leu Val Val Asn Phe Gln Cys Asp Lys Leu
            660                 665                 670
Lys Ser Val Lys Gly Tyr Arg Asn Val Ile Ile Gly Pro Ala
        675                 680                 685

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1, BB-7 and DC-1 CDR

<400> 7
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr
1               5                   10

<210> 8
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 CDR

<400> 8
Arg Thr Asn Arg Leu Phe Asp
1               5

<210> 9
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 and DC-1 CDR

<400> 9
Leu Gln Tyr Asp Asp Phe Pro Tyr Thr
1               5

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 and BB-7 CDR

<400> 10
Ser Ser Ala Met Ser
1               5

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
```

<223> AB-1 CDR

<400> 11
Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15
Gly

<210> 12
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 CDR

<400> 12
Leu Ile Ser Leu Tyr
1 5

<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 CDR - 1

<400> 13
Leu Thr Asn Arg Leu Met Asp
1 5

<210> 14
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 CDR - 1

<400> 14
Leu Gln Tyr Val Asp Phe Pro Tyr Thr
1 5

<210> 15
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 CDR

<400> 15
Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15
Gly

<210> 16
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 CDR

<400> 16
Leu Ile Ser Pro Tyr

1 5

<210> 17
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 CDR

<400> 17
Leu Val Asn Arg Leu Val Asp
1 5

<210> 18
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 CDR

<400> 18
Thr His Ala Met Ser
1 5

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 CDR

<400> 19
Leu Ile Ser Thr Tyr
1 5

<210> 20
<211> 331
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acids 143 to 473 of human TG2

<400> 20
Cys Pro Ala Asp Ala Val Tyr Leu Asp Ser Glu Glu Glu Arg Gln Glu
1 5 10 15
Tyr Val Leu Thr Gln Gln Gly Phe Ile Tyr Gln Gly Ser Ala Lys Phe
20 25 30
Ile Lys Asn Ile Pro Trp Asn Phe Gly Gln Phe Glu Asp Gly Ile Leu
35 40 45
Asp Ile Cys Leu Ile Leu Leu Asp Val Asn Pro Lys Phe Leu Lys Asn
50 55 60
Ala Gly Arg Asp Cys Ser Arg Arg Ser Ser Pro Val Tyr Val Gly Arg
65 70 75 80
Val Val Ser Gly Met Val Asn Cys Asn Asp Asp Gln Gly Val Leu Leu
85 90 95
Gly Arg Trp Asp Asn Asn Tyr Gly Asp Gly Val Ser Pro Met Ser Trp
100 105 110
Ile Gly Ser Val Asp Ile Leu Arg Arg Trp Lys Asn His Gly Cys Gln
115 120 125
Arg Val Lys Tyr Gly Gln Cys Trp Val Phe Ala Ala Val Ala Cys Thr
130 135 140
Val Leu Arg Cys Leu Gly Ile Pro Thr Arg Val Val Thr Asn Tyr Asn
145 150 155 160
Ser Ala His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn

```
                165                 170                 175
Glu Phe Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile Trp Asn Phe
            180                 185                 190
His Cys Trp Val Glu Ser Trp Met Thr Arg Pro Asp Leu Gln Pro Gly
        195                 200                 205
Tyr Glu Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser Glu
    210                 215                 220
Gly Thr Tyr Cys Cys Gly Pro Val Pro Val Arg Ala Ile Lys Glu Gly
225                 230                 235                 240
Asp Leu Ser Thr Lys Tyr Asp Ala Pro Phe Val Phe Ala Glu Val Asn
                245                 250                 255
Ala Asp Val Val Asp Trp Ile Gln Gln Asp Asp Gly Ser Val His Lys
            260                 265                 270
Ser Ile Asn Arg Ser Leu Ile Val Gly Leu Lys Ile Ser Thr Lys Ser
        275                 280                 285
Val Gly Arg Asp Glu Arg Glu Asp Ile Thr His Thr Tyr Lys Tyr Pro
    290                 295                 300
Glu Gly Ser Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu
305                 310                 315                 320
Asn Lys Leu Ala Glu Lys Glu Glu Thr Gly Met
                325                 330
```

<210> 21
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acids 304 to 326 of human TG2

<400> 21
```
Ala His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe Arg Asn Glu
1               5                   10                  15
Phe Gly Glu Ile Gln Gly Asp
            20
```

<210> 22
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acids 351 to 365 of human TG2

<400> 22
```
Tyr Glu Gly Trp Gln Ala Leu Asp Pro Thr Pro Gln Glu Lys Ser
1               5                   10                  15
```

<210> 23
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acids 450 to 467 of human TG2

<400> 23
```
Ser Glu Glu Arg Glu Ala Phe Thr Arg Ala Asn His Leu Asn Lys Leu
1               5                   10                  15
Ala Glu
```

<210> 24
<211> 15
<212> PRT
<213> Artificial Sequence

<220>

<223> Antibody or antigen-binding fragment

<400> 24
Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Trp Phe
1 5 10 15

<210> 25
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 25
Thr Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro
1 5 10

<210> 26
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 15,16
<223> Can be any amino acid.

<400> 26
Thr Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Xaa Xaa
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe
20 25

<210> 27
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 27
Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr Thr Phe Gly
1 5 10

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 28
Phe Thr Leu Ser Ser Ser Ala Met Ser Trp Val Arg
1 5 10

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 2,4,5
<223> Can be any amino acid.

<400> 29
Cys Xaa Ala Xaa Xaa Phe Thr Leu Ser Ser Ser Ala Met Ser Trp Val
1 5 10 15
Arg

<210> 30
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 30
Trp Val Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
20 25

<210> 31
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 27,29,30,31,32
<223> Can be any amino acid.

<400> 31
Trp Val Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Xaa Asn Xaa Xaa Xaa Xaa
20 25 30
Leu

<210> 32
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 32
Tyr Cys Ala Lys Leu Ile Ser Leu Tyr Trp Gly
1 5 10

<210> 33
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>

Sequence listing with corrections to SEQ ID NOs 48 215 and 216 N402043WO

<221> VARIANT
<222>
12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,34,35,36,37,38,39,40,41,42,43,44,45
,46,47,48,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
<223> Can be any amino acid.

<400> 33
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Thr Asn Arg Leu Phe
20 25 30
Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Leu Gln Tyr Asp Asp Phe Pro Tyr Thr
65 70

<210> 34
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222>
12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
,39,40,41,42,43,44,45,46,47,48
<223> Can be any amino acid.

<400> 34
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Phe

<210> 35
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222> 8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
<223> Can be any amino acid.

<400> 35
Arg Thr Asn Arg Leu Phe Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Phe
20

<210> 36
<211> 26
<212> PRT
<213> Artificial Sequence

<220>

<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222> 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
<223> Can be any amino acid.

<400> 36
Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Leu Gln Tyr Asp Asp Phe Pro Tyr Thr
20 25

<210> 37
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 37
Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Trp Tyr
1 5 10 15

<210> 38
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 38
Leu Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro
1 5 10

<210> 39
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 39
Ser Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro
1 5 10

<210> 40
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 15,16
<223> Can be any amino acid.

<400> 40
Leu Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Xaa Xaa
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe
20 25

<210> 41
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 15,16
<223> Can be any amino acid.

<400> 41
Ser Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Xaa Xaa
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe
20 25

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 42
Phe Thr Phe Ser Ser Ser Ala Met Ser Trp Val Arg
1 5 10

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 2,4,5
<223> Can be any amino acid.

<400> 43
Cys Xaa Ala Xaa Xaa Phe Thr Phe Ser Ser Ser Ala Met Ser Trp Val
1 5 10 15
Arg

<210> 44
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<400> 44
Trp Val Ser Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
20 25

<210> 45
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 27,29,30,31,32
<223> Can be any amino acid.

<400> 45
Trp Val Ser Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Xaa Asn Xaa Xaa Xaa Xaa
20 25 30
Leu

<210> 46
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 light chain variable region

<400> 46
Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 47
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 light chain variable region

<400> 47
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 48
<211> 107
<212> PRT

Sequence listing with corrections to SEQ ID NOs 48 215 and 216 N402043WO

<213> Artificial Sequence

<220>
<223> AB-1_VK

<400> 48

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

<210> 49
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1_VK1

<400> 49

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

<210> 50
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> hAB-1_RKE

<400> 50

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

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> hAB-1_RKJ

<400> 51
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Phe Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 52
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 heavy chain variable region

<400> 52
Glu Val Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 53
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1 heavy chain variable region

<400> 53
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 54
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB-1_VH

<400> 54
Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 55
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> hAB-1_RHA

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

<210> 56
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222>
12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,34,35,36,37,38,39,40,41,42,43,44,45
,46,47,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
<223> Can be any amino acid.

<400> 56
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Thr Asn Arg Leu Met
20 25 30
Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe
35 40 45
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Leu Gln Tyr Val Asp Phe Pro Tyr Thr
65 70

<210> 57
<211> 48
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222>
12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
,39,40,41,42,43,44,45,46,47
<223> Can be any amino acid.

<400> 57
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe
35 40 45

<210> 58
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222> 8,9,10,11,12,13,14,15,16,17,18,19,20,21
<223> Can be any amino acid.

<400> 58
Leu Thr Asn Arg Leu Met Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Phe
20

<210> 59
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222> 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18
<223> Can be any amino acid.

<400> 59
Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Leu Gln Tyr Val Asp Phe Pro Tyr Thr
20 25

<210> 60
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 light chain variable region

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

<210> 61
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 heavy chain variable region

<400> 61
Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ile Ile Phe Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Ser Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 62
<211> 107
<212> PRT

<213> Artificial Sequence

<220>
<223> BB-7 light chain variable region (humanised)

<400> 62
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Phe Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Val Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 63
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 light chain variable region (humanised)

<400> 63
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Thr Leu Ile
35 40 45
Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Glu Phe Leu Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Val Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 64
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 heavy chain variable region (humanised)

<400> 64
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Pro Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser

<210> 65
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> BB-7 heavy chain variable region (humanised)

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

<210> 66
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222>
12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,34,35,36,37,38,39,40,41,42,43,44,45
,46,47,48,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65
<223> Can be any amino acid.

<400> 66
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Val Asn Arg Leu Val
20 25 30
Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
50 55 60
Xaa Leu Gln Tyr Asp Asp Phe Pro Tyr Thr
65 70

<210> 67
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222>
12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38

,39,40,41,42,43,44,45,46,47,48
<223> Can be any amino acid.

<400> 67
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
35 40 45
Ala

<210> 68
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222> 8,9,10,11,12,13,14,15,16,17,18,19,20,21,22
<223> Can be any amino acid.

<400> 68
Leu Val Asn Arg Leu Val Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Ala
20

<210> 69
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody amino acid sequence

<220>
<221> VARIANT
<222> 2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17
<223> Can be any amino acid.

<400> 69
Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15
Xaa Leu Gln Tyr Asp Asp Phe Pro Tyr Thr
20 25

<210> 70
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 light chain variable region

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

```
Ser Gly Ser Gly Gln Asp Tyr Ala Leu Thr Ile Ser Ser Leu Glu Tyr
65                  70                  75                  80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 71
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 heavy chain variable region

<400> 71

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

<210> 72
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 light chain variable region (humanised)

<400> 72

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

<210> 73
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 light chain variable region (humanised)

<400> 73

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

```
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
            20                  25                  30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ile Leu Ile
        35                  40                  45
Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Gln Asp Tyr Ala Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 74
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 heavy chain variable region (humanised)

<400> 74

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

<210> 75
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> DC-1 heavy chain variable region (humanised)

<400> 75

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

<210> 76
<211> 7
<212> PRT

<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1,2,6
<223> Can be any amino acid.

<400> 76
Xaa Xaa Asn Arg Leu Xaa Asp
1 5

<210> 77
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 4
<223> Can be any amino acid.

<400> 77
Leu Gln Tyr Xaa Asp Phe Pro Tyr Thr
1 5

<210> 78
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1,2
<223> Can be any amino acid.

<400> 78
Xaa Xaa Ala Met Ser
1 5

<210> 79
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 4,7,8
<223> Can be any amino acid.

<400> 79
Thr Ile Ser Xaa Gly Gly Xaa Xaa Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15
Gly

<210> 80

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

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 4
<223> Can be any amino acid.

<400> 80
Leu Ile Ser Xaa Tyr
1 5

<210> 81
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1
<223> May also be Gln or Arg.

<220>
<221> VARIANT
<222> 5
<223> May also be Gly.

<220>
<221> VARIANT
<222> 7
<223> May also be Ser or Arg.

<220>
<221> VARIANT
<222> 8
<223> May also be Asn.

<220>
<221> VARIANT
<222> 11
<223> May also be Asn or Ala.

<400> 81
Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Thr
1 5 10

<210> 82
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1
<223> May also be Leu or Val or Asp or Ala.

<220>
<221> VARIANT

<222> 2
<223> May also be Val or Ala.

<220>
<221> VARIANT
<222> 3
<223> May also be Ser.

<220>
<221> VARIANT
<222> 4
<223> May also be Asn.

<220>
<221> VARIANT
<222> 6
<223> May also be Met or, Val, or Glu or Gln.

<220>
<221> VARIANT
<222> 7
<223> May also be Thr or Ser.

<400> 82
Arg Thr Asn Arg Leu Phe Asp
1 5

<210> 83
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1
<223> May also be Gln.

<220>
<221> VARIANT
<222> 3
<223> May also be His.

<220>
<221> VARIANT
<222> 4
<223> May also be Val or Asn.

<220>
<221> VARIANT
<222> 5
<223> May also be Thr.

<220>
<221> VARIANT
<222> 6
<223> May also be Tyr.

<220>
<221> VARIANT
<222> 8
<223> May also be Leu or Trp.

<400> 83
Leu Gln Tyr Asp Asp Phe Pro Tyr Thr
1 5

<210> 84
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1
<223> May also be Thr.

<220>
<221> VARIANT
<222> 2
<223> May also be His or Tyr.

<400> 84
Ser Ser Ala Met Ser
1 5

<210> 85
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1
<223> May also be Ala.

<220>
<221> VARIANT
<222> 4
<223> May also be Ser or Gly.

<220>
<221> VARIANT
<222> 5
<223> May also be Ser.

<220>
<221> VARIANT
<222> 7
<223> May also be Arg.

<220>
<221> VARIANT
<222> 8
<223> May also be Ser.

<220>
<221> VARIANT
<222> 12
<223> May also be Ala.

<400> 85
Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val Lys
1 5 10 15
Gly

<210> 86

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

<220>
<223> Antibody or antigen-binding fragment

<220>
<221> VARIANT
<222> 1
<223> May also be Asp.

<220>
<221> VARIANT
<222> 2
<223> May also be Gly.

<220>
<221> VARIANT
<222> 3
<223> May also be Gly.

<220>
<221> VARIANT
<222> 4
<223> May also be Pro or Thr or Val.

<400> 86
Leu Ile Ser Leu Tyr
1 5

<210> 87
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> DD-9 light chain variable region

<400> 87
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Asp Tyr Met
20 25 30
Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Tyr
35 40 45
Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Gly Ala Glu
65 70 75 80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Asn Ser Ser Pro Leu Thr
85 90 95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 88
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> DD-9 heavy chain variable region

<400> 88
Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15
Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

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

<210> 89
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> DH-2 light chain variable region

<400> 89
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15
Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30
Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Tyr
35 40 45
Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60
Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80
Asp Ala Ala Thr Phe Tyr Cys Gln Gln Trp Ser Ser Ser Pro Leu Thr
85 90 95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 90
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> DH-2 heavy chain variable region

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

<210> 91
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="Isolated polynucleotide "
/organism="Artificial Sequence"

<400> 91
gacatccaga tgacacagac tccatcttcc atgtatgcat ctctaggaga gagagtcact 60

atcacttgca aggcgagtca ggacattaat agctatttaa cctggttcca gcagaaacca 120

gggaaatctc ctaagaccct gatctatcgt acaaatagat tgtttgatgg ggtcccatcc 180

aggttcagtg gcagtggatc tgggcaagat ttttttctca ccatcagcag cctggaatat 240

gaagatatgg gaatttatta ttgtctacag tatgatgact ttccgtacac gttcggaggg 300

gggaccaaac tggaaataaa a 321

<210> 92
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="Isolated polynucleotide "
/organism="Artificial Sequence"

<400> 92
gaagtacagc tggaggagtc agggggggggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactctcagt tcctctgcca tgtcttgggt tcgccagact 120

ccggacagga ggctggagtg ggtcgcaacc attagtgttg gtggtggtaa aacctactat 180

ccagacagtg tgaagggtcg cttcaccatc tccagagaca atgccaagaa caccctctat 240

ctgcaaatga acagtctgag gtctgaggac acggccatgt attactgtgc aaaactaatc 300

agtctctact ggggccaagg caccactctc acagtctcct ca 342

<210> 93
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="Isolated polynucleotide "
/organism="Artificial Sequence"

<400> 93
gccatcaaga tgacccagtc tccatcttcc atgtatgcat ctctaggaga gagagtcatc 60

atcacttgca aggcgagtca ggacataaat agttatttaa cctggttcca acagaaacca 120

ggaaagtctc ctaagaccct gatctatctt acaaatagat tgatggatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggcaagaa tttttactca ccatcagcgg cctggaacat 240

gaagatatgg gcatttatta ttgtctccag tatgttgact ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 94
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="Isolated polynucleotide "
/organism="Artificial Sequence"

<400> 94
gcagtgcaac tggtagagtc tgggggaggc ttggtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggaat cattttcagt tcctctgcca tgtcttgggt tcgccagact 120

ccggaaaaga gactggagtg ggtcgcaact attagtagtg gtggtcgttc cacctactat 180

ccagacagtg tgaagggtcg attcaccgtc tccagagaca gtgccaagaa caccctatac 240

ctgcaaatgg acagtctgag gtctgaggac acggccattt attactgtgc aaaactaatc 300

agtccctact ggggccaagg caccactctc acagtctcct ca 342

<210> 95
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="Isolated polynucleotide "
/organism="Artificial Sequence"

<400> 95
gacatcacga tgacccagtc tccatcttcc atatatgcat ctctgggaga gagagtcact 60

atcacttgca aggcgagtca ggacattaat agctatttaa cctggttcca gcagaaacca 120

gggaaatctc ctaagatcct gatctatctt gtaaatagat tggtagatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggcaagat tatgctctca ccatcagcag tctggaatat 240

gaagatatgg gaatttatta ttgtctacaa tatgatgact ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 96
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="Isolated polynucleotide "
/organism="Artificial Sequence"

<400> 96
gaagtgcagt tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactctcagt acccatgcca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtcgttc cacctactat 180

ccagacagtg tgaagggtcg attcactatc tccagagaca atgtcaagaa caccctatat 240

ctgcaactga gcagtctgag gtctgaggac acggccgtgt atttctgtgc aagactaatc 300

agtacctact ggggccaagg caccactctc acagtctcct ca 342

<210> 97
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..39
<223> /mol_type="unassigned DNA"
/note="Sense primer"
/organism="Artificial Sequence"

<400> 97
gcgcgcgcta gctgcccagc ggatgctgtg tacctggac 39

<210> 98
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..39
<223> /mol_type="unassigned DNA"
/note="Anti-sense primer"
/organism="Artificial Sequence"

<400> 98
gcgcgcaagc ttcatccctg tctcctcctt ctcggccag 39

<210> 99
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..25
<223> /mol_type="unassigned DNA"
/note="TG2-FL-1 primer"
/organism="Artificial Sequence"

<400> 99
atggccgagg agctggtctt agaga 25

<210> 100
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="TG2-FL-2 primer"
/organism="Artificial Sequence"

<400> 100
ggcggggcca atgatgacat tccgga 26

<210> 101
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..29
<223> /mol_type="unassigned DNA"
/note="MH1 primer"
/organism="Artificial Sequence"

<220>
<221> misc_difference
<222> 18
<223> /note="Can be any nucleotide."

<400> 101
cgcgcgctcg agsargtnma gctgsagtc 29

<210> 102
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="MH2 primer"
/organism="Artificial Sequence"

<220>
<221> misc_difference
<222> 18
<223> /note="Can be any nucleotide."

<400> 102
cgcgcgctcg agsargtnma gctgsagsag tc 32

<210> 103
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..43
<223> /mol_type="unassigned DNA"
/note="Mouse-G1 primer"
/organism="Artificial Sequence"

<400> 103
aggcgcagta ctacaatccc tgggcacaat tttcttgtcc acc 43

<210> 104
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..39
<223> /mol_type="unassigned DNA"
/note="Mouse-G2a primer"
/organism="Artificial Sequence"

<400> 104
aggcgcagta ctacagggct tgattgtggg ccctctggg 39

<210> 105
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..40
<223> /mol_type="unassigned DNA"
/note="Mouse-G2b primer"
/organism="Artificial Sequence"

<400> 105
aggcgcagta ctacaggggt tgattgttga aatgggcccg 40

<210> 106
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK1 primer"
/organism="Artificial Sequence"

<400> 106
cgctgcgagc tcgatattgt gatgacbcag dc 32

<210> 107
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK2 primer"
/organism="Artificial Sequence"

<400> 107
cgctgcgagc tcgagrttkt gatgacccar ac 32

<210> 108
<211> 32
<212> DNA

<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK3 primer"
/organism="Artificial Sequence"

<400> 108
cgctgcgagc tcgaaaatgt gctcacccag tc 32

<210> 109
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK4 primer"
/organism="Artificial Sequence"

<400> 109
cgctgcgagc tcgayattgt gatgacacag tc 32

<210> 110
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK5 primer"
/organism="Artificial Sequence"

<400> 110
cgctgcgagc tcgacatcca gatgacacag ac 32

<210> 111
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK6 primer"
/organism="Artificial Sequence"

<400> 111
cgctgcgagc tcgayattgt gctsacycar tc 32

<210> 112
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source

<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK7 primer"
/organism="Artificial Sequence"

<400> 112
cgctgcgagc tcgacatcca gatgacycar tc 32

<210> 113
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..32
<223> /mol_type="unassigned DNA"
/note="VK8 primer"
/organism="Artificial Sequence"

<400> 113
cgctgcgagc tccaaattgt tctcacccag tc 32

<210> 114
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..34
<223> /mol_type="unassigned DNA"
/note="K-CONST primer"
/organism="Artificial Sequence"

<400> 114
gcgccgtcta gaattaacac tcattcctgt tgaa 34

<210> 115
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VHc

<220>
<221> VARIANT
<222> 5
<223> Can be any amino acid.

<400> 115

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

100 105 110
Ser Ser

<210> 116
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260

<400> 116
Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
20 25 30
Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Lys Asp Gly Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 117
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VHC 5 Angstrom Proximity Residues

<400> 117
Glu Val Gln Leu Cys Ala Phe Thr Leu Ser Trp Val Arg Trp Val Ala
1 5 10 15
Arg Phe Thr Ile Ser Arg Asn Leu Tyr Cys Ala Lys Trp Gly
20 25 30

<210> 118
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260 5 Angstrom Proximity Residues

<400> 118
Glu Val Gln Leu Cys Ala Phe Thr Phe Ser Trp Val Arg Trp Val Ser
1 5 10 15
Arg Phe Thr Ile Ser Arg Asn Leu Tyr Cys Ala Lys Trp Gly
20 25 30

<210> 119
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> Z12347.seq

<400> 119
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

<210> 120
<211> 98
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260.seq

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

<210> 121
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc

<400> 121
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 122
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> AY247656

<400> 122
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 123
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc 5 Angstrom Proximity Residues

<400> 123
Glu Ile Val Leu Thr Gln Thr Cys Trp Phe Thr Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe Tyr Cys Phe Gly
20 25 30

<210> 124
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AY247656 5 Angstrom Proximity Residues

<400> 124
Glu Ile Val Leu Thr Gln Thr Cys Trp Tyr Leu Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Tyr Cys Phe Gly
20 25 30

<210> 125
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> X93620.seq

<400> 125
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro

65 70 75 80
Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro Pro
85 90 95

<210> 126
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> AY247656.seq

<400> 126
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Leu
85 90 95

<210> 127
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc

<400> 127
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 128
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 128
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile

```
        35                  40                  45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn Thr Tyr Pro Trp
                85                  90                  95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105

<210> 129
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc 5 Angstrom Proximity Residues

<400> 129
Asp Ile Gln Met Thr Gln Thr Cys Trp Phe Thr Leu Ile Tyr Gly Val
1               5                   10                  15
Pro Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe Tyr Cys Phe Gly
            20                  25                  30



<210> 130
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851 5 Angstrom Proximity Residues

<400> 130
Asp Ile Gln Met Thr Gln Thr Cys Trp Phe Ser Leu Ile Tyr Gly Val
1               5                   10                  15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Tyr Cys Phe Gly
            20                  25                  30



<210> 131
<211> 96
<212> PRT
<213> Artificial Sequence

<220>
<223> J00248.seq

<400> 131
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
            20                  25                  30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Pro
                85                  90                  95



<210> 132
<211> 96
```

<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851.seq

<400> 132
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn Thr Tyr Pro Trp
85 90 95

<210> 133
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VHc

<220>
<221> VARIANT
<222> 5
<223> Can be any amino acid.

<400> 133
Glu Val Gln Leu Xaa Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 134
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_RHA

<400> 134
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

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

<210> 135
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKC

<400> 135

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

<210> 136
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_RKE

<400> 136

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

<210> 137
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_RKJ

<400> 137

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

<210> 138
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..36
<223> /mol_type="unassigned DNA"
/note="RACE Anchor Primer"
/organism="Artificial Sequence"

<220>
<221> misc_difference
<222> 24,25,29,30,34,35
<223> /note="Wherein nucleotide is deoxyinosine."

<400> 138
ggccacgcgt cgactagtac gggnngggnn gggnng 36

<210> 139
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MHV1 primer"
/organism="Artificial Sequence"

<400> 139
atgaaatgca gctggggcat cttcttc 27

<210> 140
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="MHV2 primer"
/organism="Artificial Sequence"

<400> 140
atgggatgga gctrtatcat sytctt 26

<210> 141
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MHV3 primer"
/organism="Artificial Sequence"

<400> 141
atgaagwtgt ggttaaactg ggttttt 27

<210> 142
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..25
<223> /mol_type="unassigned DNA"
/note="MHV4 primer"
/organism="Artificial Sequence"

<400> 142
atgractttg ggytcagctt grttt 25

<210> 143
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..30
<223> /mol_type="unassigned DNA"
/note="MHV5 primer"
/organism="Artificial Sequence"

<400> 143
atggactcca ggctcaattt agttttcctt 30

<210> 144
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MHV6 primer"
/organism="Artificial Sequence"

<400> 144
atggctgtcy trgsgctrct cttctgc 27

<210> 145
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="MHV7 primer"
/organism="Artificial Sequence"

<400> 145
atggratgga gckggrtctt tmtctt 26

<210> 146
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..23
<223> /mol_type="unassigned DNA"
/note="MHV8 primer"
/organism="Artificial Sequence"

<400> 146
atgagagtgc tgattctttt gtg 23

<210> 147
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..30
<223> /mol_type="unassigned DNA"
/note="MHV9 primer"
/organism="Artificial Sequence"

<400> 147
atggmttggg tgtggamctt gctattcctg 30

<210> 148
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MHV10 primer"
/organism="Artificial Sequence"

<400> 148
atgggcagac ttacattctc attcctg 27

<210> 149
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..28

<223> /mol_type="unassigned DNA"
/note="MHV11 primer"
/organism="Artificial Sequence"

<400> 149
atggattttg ggctgatttt ttttattg 28

<210> 150
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MHV12 primer"
/organism="Artificial Sequence"

<400> 150
atgatggtgt taagtcttct gtacctg 27

<210> 151
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..21
<223> /mol_type="unassigned DNA"
/note="MHCG1 primer"
/organism="Artificial Sequence"

<400> 151
cagtggatag acagatgggg g 21

<210> 152
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..21
<223> /mol_type="unassigned DNA"
/note="MHCG2A primer"
/organism="Artificial Sequence"

<400> 152
cagtggatag accgatgggg c 21

<210> 153
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..21
<223> /mol_type="unassigned DNA"
/note="MHCG2b primer"
/organism="Artificial Sequence"

<400> 153
cagtggatag actgatgggg g 21

<210> 154
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..21
<223> /mol_type="unassigned DNA"
/note="MHCG3 primer"
/organism="Artificial Sequence"

<400> 154
caagggatag acagatgggg c 21

<210> 155
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..30
<223> /mol_type="unassigned DNA"
/note="MKV1 30-mer"
/organism="Artificial Sequence"

<400> 155
atgaagttgv vtgttaggct gttggtgctg 30

<210> 156
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..30
<223> /mol_type="unassigned DNA"
/note="MKV2 29-mer"
/organism="Artificial Sequence"

<400> 156
atggagwcag acacactcct gytatgggtg 30

<210> 157
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..30
<223> /mol_type="unassigned DNA"
/note="MKV3 30-mer"
/organism="Artificial Sequence"

<400> 157
atgagtgtgc tcactcaggt cctggsgttg 30

<210> 158
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..33
<223> /mol_type="unassigned DNA"
/note="MKV4 33-mer"
/organism="Artificial Sequence"

<400> 158
atgaggrccc ctgctcagwt tyttggmwtc ttg 33

<210> 159
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..29
<223> /mol_type="unassigned DNA"
/note="MKV5 30-mer"
/organism="Artificial Sequence"

<400> 159
atggatttwa ggtgcagatt wtcagcttc 29

<210> 160
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MKV6 27-mer"
/organism="Artificial Sequence"

<400> 160
atgaggtkck ktgktsagst sctgrgg 27

<210> 161
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..31
<223> /mol_type="unassigned DNA"
/note="MKV7 31-mer"
/organism="Artificial Sequence"

<400> 161
atgggcwtca agatggagtc acakwyycwg g 31

<210> 162
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..31
<223> /mol_type="unassigned DNA"
/note="MKV8 31-mer"
/organism="Artificial Sequence"

<400> 162
atgtggggay ctktttycmm tttttcaatt g 31

<210> 163
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..25
<223> /mol_type="unassigned DNA"
/note="MKV9 25-mer"
/organism="Artificial Sequence"

<400> 163
atggtrtccw casctcagtt ccttg 25

<210> 164
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..27
<223> /mol_type="unassigned DNA"
/note="MKV10 27-mer"
/organism="Artificial Sequence"

<400> 164
atgtatatat gtttgttgtc tatttct 27

<210> 165
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..28
<223> /mol_type="unassigned DNA"
/note="MKV11 28-mer"
/organism="Artificial Sequence"

<400> 165
atggaagccc cagctcagct tctcttcc 28

<210> 166
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26

<223> /mol_type="unassigned DNA"
/note="CL12A primer"
/organism="Artificial Sequence"

<400> 166
atgragtywc agacccaggt cttyrt 26

<210> 167
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="CL12B primer"
/organism="Artificial Sequence"

<400> 167
atggagacac attctcaggt ctttgt 26

<210> 168
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="CL13 primer "
/organism="Artificial Sequence"

<400> 168
atggattcac aggcccaggt tcttat 26

<210> 169
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="CL14 primer "
/organism="Artificial Sequence"

<400> 169
atgatgagtc ctgcccagtt cctgtt 26

<210> 170
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..29
<223> /mol_type="unassigned DNA"
/note="CL15 primer "
/organism="Artificial Sequence"

<400> 170
atgaatttgc ctgttcatct cttggtgct 29

<210> 171
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..29
<223> /mol_type="unassigned DNA"
/note="CL16 primer "
/organism="Artificial Sequence"

<400> 171
atggattttc aattggtcct catctcctt 29

<210> 172
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="CL17A primer "
/organism="Artificial Sequence"

<400> 172
atgaggtgcc tarctsagtt cctgrg 26

<210> 173
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="CL17B primer"
/organism="Artificial Sequence"

<400> 173
atgaagtact ctgctcagtt tctagg 26

<210> 174
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..26
<223> /mol_type="unassigned DNA"
/note="CL17C primer "
/organism="Artificial Sequence"

<400> 174
atgaggcatt ctcttcaatt cttggg 26

<210> 175
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..20
<223> /mol_type="unassigned DNA"
/note="MKC 20-mer"
/organism="Artificial Sequence"

<400> 175
actggatggt gggaagatgg 20

<210> 176
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VHc (mAB001VH)

<400> 176
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 177
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7_VHc (mBB7001VH)

<400> 177
Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ile Ile Phe Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Ser Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 178
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1_VHc (mDC001VH)

<400> 178
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Thr His
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ala Arg Leu Ile Ser Thr Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 179
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260

<400> 179
Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
20 25 30
Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
50 55 60
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Lys Asp Gly Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 180
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260

<400> 180
Cys Ala Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ile Ile Phe Ser Ser
20 25 30
Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ser Ala Ile Ser Gly Ser Gly Arg Ser Thr Tyr Tyr Ala Asp Ser

50 55 60
Val Lys Gly Arg Phe Thr Val Ser Arg Asp Ser Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
85 90 95
Cys Ala Lys Asp Gly Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 181
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260

<400> 181
Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1 5 10 15
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr
20 25 30
Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45
Val Ser Ala Ile Ser Gly Ser Gly Arg Ser Thr Tyr Tyr Ala Asp Ser
50 55 60
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80
Tyr Leu Gln Leu Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
85 90 95
Cys Ala Arg Asp Gly Gly Val Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 182
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VHc (mAB001VH) 5 Angstrom Proximity Residues

<400> 182
Glu Val Gln Leu Cys Ala Phe Thr Leu Ser Trp Val Arg Trp Val Ala
1 5 10 15
Arg Phe Thr Ile Ser Arg Asn Leu Tyr Cys Ala Lys Trp Gly
20 25 30

<210> 183
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7_VHc (mBB7001VH) 5 Angstrom Proximity Residues

<400> 183
Ala Val Gln Leu Cys Ala Ile Ile Phe Ser Trp Val Arg Trp Val Ala
1 5 10 15
Arg Phe Thr Val Ser Arg Ser Leu Tyr Cys Ala Lys Trp Gly
20 25 30

<210> 184
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1_VHc (mDC001VH) 5 Angstrom Proximity Residues

<400> 184
Glu Val Gln Leu Cys Ala Phe Thr Leu Ser Trp Val Arg Trp Val Ala
1 5 10 15
Arg Phe Thr Ile Ser Arg Asn Leu Phe Cys Ala Arg Trp Gly
20 25 30

<210> 185
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260 5 Angstrom Proximity Residues

<400> 185
Glu Val Gln Leu Cys Ala Phe Thr Phe Ser Trp Val Arg Trp Val Ser
1 5 10 15
Arg Phe Thr Ile Ser Arg Asn Leu Tyr Cys Ala Lys Trp Gly
20 25 30

<210> 186
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260 5 Angstrom Proximity Residues

<400> 186
Ala Val Gln Leu Cys Ala Ile Ile Phe Ser Trp Val Arg Trp Val Ser
1 5 10 15
Arg Phe Thr Val Ser Arg Ser Leu Tyr Cys Ala Lys Trp Gly
20 25 30

<210> 187
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> AF062260 5 Angstrom Proximity Residues

<400> 187
Glu Val Gln Leu Cys Ala Phe Thr Phe Ser Trp Val Arg Trp Val Ser
1 5 10 15
Arg Phe Thr Ile Ser Arg Asn Leu Phe Cys Ala Arg Trp Gly
20 25 30

<210> 188
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc (mAB001VK)

<400> 188
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly

50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 189
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AY247656

<400> 189
Glu Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Gly Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Pro Leu
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 190
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc (mAB001VK)

<400> 190
Glu Ile Val Leu Thr Gln Thr Cys Trp Phe Thr Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe Tyr Cys Phe Gly
20 25 30

<210> 191
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AY247656 5 Angstrom Proximity Residues

<400> 191
Glu Ile Val Leu Thr Gln Thr Cys Trp Tyr Leu Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Tyr Cys Phe Gly
20 25 30

<210> 192
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB_VKc1 (mAB002VK)

<400> 192
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 193
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB1_VKc2 (mAB003VK)

<400> 193
Asp Ile Gln Lys Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 194
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7_VKc (mBB001VK)

<400> 194
Ala Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Ile Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Glu Phe Leu Leu Thr Ile Ser Gly Leu Glu His
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Val Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 195
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1_VKc (mDC001VK)

<400> 195
Asp Ile Thr Met Thr Gln Ser Pro Ser Ser Ile Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Ile Leu Ile
35 40 45
Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Tyr Ala Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 196
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 196
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn Thr Tyr Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 197
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 197
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn Thr Tyr Pro Trp

85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 198
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 198
Ala Ile Lys Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Ile Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Gly Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn Thr Tyr Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 199
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 199
Asp Ile Thr Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
20 25 30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45
Tyr Ala Ala Ser Asn Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Asn Thr Tyr Pro Trp
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 200
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AB1_VKc2 (mAB003VK) 5 Angstrom Proximity Residues

<400> 200
Asp Ile Gln Lys Thr Gln Thr Cys Trp Phe Thr Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Gln Asp Phe Phe Tyr Cys Phe Gly
20 25 30

<210> 201
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7_VKc (mBB001VK) 5 Angstrom Proximity Residues

<400> 201
Ala Ile Lys Met Thr Gln Thr Cys Trp Phe Thr Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Gln Glu Phe Leu Tyr Cys Phe Gly
20 25 30

<210> 202
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1_VKc (mDC001VK)

<400> 202
Asp Ile Thr Met Thr Gln Thr Cys Trp Phe Ile Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ala Tyr Cys Phe Gly
20 25 30

<210> 203
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 203
Asp Ile Gln Met Thr Gln Thr Cys Trp Phe Ser Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Tyr Cys Phe Gly
20 25 30

<210> 204
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 204
Asp Ile Gln Met Thr Gln Thr Cys Trp Phe Ser Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Tyr Cys Phe Gly
20 25 30

<210> 205
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 205
Ala Ile Lys Met Thr Gln Thr Cys Trp Phe Ser Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Tyr Cys Phe Gly
20 25 30

<210> 206
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AF193851

<400> 206
Asp Ile Thr Met Thr Gln Thr Cys Trp Phe Ser Leu Ile Tyr Gly Val
1 5 10 15
Pro Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Tyr Cys Phe Gly
20 25 30

<210> 207
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> AB Heavy Chain CDR1

<400> 207
Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser Ala Met Ser Trp Val
1 5 10 15
Arg

<210> 208
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHA Heavy Chain CDR 1

<400> 208
Cys Ala Ala Ser Gly Ile Ile Phe Ser Ser Ser Ala Met Ser Trp Val
1 5 10 15
Arg

<210> 209
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHA Heavy Chain CDR 1

<400> 209
Ile Ile Phe Ser Ser Ser Ala Met Ser Trp Val Arg
1 5 10

<210> 210
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHA Heavy Chain CDR1

<400> 210
Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr His Ala Met Ser Trp Val
1 5 10 15
Arg

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

<220>
<223> DC1 RHA Heavy Chain CDR1

<400> 211
Phe Thr Phe Ser Thr His Ala Met Ser Trp Val Arg
1 5 10

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

<220>
<223> DC1 RHA/DC1 RHB Heavy Chain CDR1

<400> 212
Thr His Ala Met Ser
1 5

<210> 213
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHB Heavy Chain CDR1

<400> 213
Cys Ala Ala Ser Gly Phe Thr Leu Ser Thr His Ala Met Ser Trp Val
1 5 10 15
Arg

<210> 214
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHB Heavy Chain CDR1

<400> 214
Phe Thr Leu Ser Thr His Ala Met Ser Trp Val Arg
1 5 10

<210> 215
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> AB Heavy Chain CDR2

<400> 215
Trp Val Ser Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
20 25 30
Leu

<210> 216
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> AB Heavy Chain CDR2

<400> 216
Trp Val Ser Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
20 25

<210> 217
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHB Heavy Chain CDR2

<400> 217
Trp Val Ser Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
20 25 30
Leu

<210> 218
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHB Heavy Chain CDR2

<400> 218
Trp Val Ser Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
20 25

<210> 219
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHB/DC1 RHA Heavy Chain CDR2

<400> 219
Trp Val Ser Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg

20 25

<210> 220
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHA Heavy Chain CDR2

<400> 220
Trp Val Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Val Ser Arg Asp Ser Ser Lys Asn Thr
20 25 30
Leu

<210> 221
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHA Heavy Chain CDR2

<400> 221
Trp Val Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Val Ser Arg Asp Ser
20 25

<210> 222
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHA Heavy Chain CDR2

<400> 222
Trp Val Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Val Ser Arg
20 25

<210> 223
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHB Heavy Chain CDR2

<400> 223
Trp Val Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr
20 25 30
Leu

<210> 224
<211> 28
<212> PRT
<213> Artificial Sequence

<220>

<223> DC1 RHB Heavy Chain CDR2

<400> 224
Trp Val Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
20 25

<210> 225
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHB Heavy Chain CDR2

<400> 225
Trp Val Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp
1 5 10 15
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
20 25

<210> 226
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RHB/BB7 RHA Heavy Chain CDR3

<400> 226
Tyr Cys Ala Lys Leu Ile Ser Pro Tyr Trp Gly
1 5 10

<210> 227
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHA Heavy Chain CDR3

<400> 227
Tyr Cys Ala Lys Leu Ile Ser Thr Tyr Trp Gly
1 5 10

<210> 228
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RHB Heavy Chain CDR3

<400> 228
Phe Cys Ala Arg Leu Ile Ser Thr Tyr Trp Gly
1 5 10

<210> 229
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> AB RKE Light Chain CDR2

<400> 229
Leu Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg

1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Phe
20 25

<210> 230
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> AB RJK Light Chain CDR2

<400> 230
Ser Leu Ile Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Phe
20 25

<210> 231
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RKB Light Chain CDR2

<400> 231
Ser Leu Ile Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro Ser Arg
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Phe
20 25

<210> 232
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RKB Light Chain CDR2

<400> 232
Ser Leu Ile Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro
1 5 10

<210> 233
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RKA Light Chain CDR2

<400> 233
Thr Leu Ile Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro Ser Arg
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Gln Glu Phe Leu
20 25

<210> 234
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RKA Light Chain CDR2

<400> 234
Thr Leu Ile Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro

1 5 10

<210> 235
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RKA Light Chain CDR2

<400> 235
Ser Leu Ile Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro Ser Arg
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Phe
20 25

<210> 236
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RKA Light Chain CDR2

<400> 236
Ser Leu Ile Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro
1 5 10

<210> 237
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RKB Light Chain CDR2

<400> 237
Ile Leu Ile Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro Ser Arg
1 5 10 15
Phe Ser Gly Ser Gly Ser Gly Gln Asp Tyr Ala
20 25

<210> 238
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 RKB Light Chain CDR2

<400> 238
Ile Leu Ile Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro
1 5 10

<210> 239
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 RKB Light Chain CDR3

<400> 239
Tyr Cys Leu Gln Tyr Val Asp Phe Pro Tyr Thr Phe Gly
1 5 10

<210> 240
<211> 31

<212> PRT
<213> Mus musculus

<220>
<223> Mouse substrate binding pocket

<400> 240
Tyr Asn Ser Ala His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe
1 5 10 15
Arg Asn Glu Phe Gly Glu Leu Glu Ser Asn Lys Ser Glu Met Ile
20 25 30

<210> 241
<211> 31
<212> PRT
<213> Rattus

<220>
<223> Rat substrate binding pocket

<400> 241
Tyr Asn Ser Ala His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe
1 5 10 15
Arg Asn Glu Tyr Gly Glu Leu Glu Ser Asn Lys Ser Glu Met Ile
20 25 30

<210> 242
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<223> Human substrate binding pocket

<400> 242
Tyr Asn Ser Ala His Asp Gln Asn Ser Asn Leu Leu Ile Glu Tyr Phe
1 5 10 15
Arg Asn Glu Phe Gly Glu Ile Gln Gly Asp Lys Ser Glu Met Ile
20 25 30

<210> 243
<211> 48
<212> PRT
<213> Mus musculus

<220>
<223> Mouse rear of core behind active site

<400> 243
Ser Glu Met Ile Trp Asn Phe His Cys Trp Val Glu Ser Trp Met Thr
1 5 10 15
Arg Pro Asp Leu Gln Pro Gly Tyr Glu Gly Trp Gln Ala Ile Asp Pro
20 25 30
Thr Pro Gln Glu Lys Ser Glu Gly Thr Tyr Cys Cys Gly Pro Val Ser
35 40 45

<210> 244
<211> 48
<212> PRT
<213> Rattus

<220>
<223> Rat rear of core behind active site

<400> 244
Ser Glu Met Ile Trp Asn Phe His Cys Trp Val Glu Ser Trp Met Thr

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

<210> 245
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<223> Human rear of core behind active site

<400> 245

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

<210> 246
<211> 39
<212> PRT
<213> Mus musculus

<220>
<223> Mouse rear of core junction with beta barrel-1

<400> 246

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

<210> 247
<211> 39
<212> PRT
<213> Rattus

<220>
<223> Rat rear of core junction with beta barrel-1

<400> 247

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

<210> 248
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<223> Human rear of core junction with beta barrel-1

<400> 248

```
Thr Tyr Lys Tyr Pro Glu Gly Ser Ser Glu Glu Arg Glu Ala Phe Thr
```

```
1               5                  10                  15
Arg Ala Asn His Leu Asn Lys Leu Ala Glu Lys Glu Glu Thr Gly Met
            20                  25                  30
Ala Met Arg Ile Arg Val Gly
        35
```

<210> 249
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="AB VH1"
/organism="Artificial Sequence"

<400> 249
gaagtacagc tggaggagtc agggggggggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactctcagt tcctctgcca tgtcttgggt tcgccagact 120

ccggacagga ggctggagtg ggtcgcaacc attagtgttg gtggtggtaa aacccactat 180

ccagacagtg tgaagggtcg cttcaccatc tccagagaca atgccaagaa caccctctat 240

ctgcaaatga acagtctgag gtctgaggac acggccatgt attactgtgc aaaactaatc 300

agtctctact ggggccaagg caccactctc acagtctcct ca 342

<210> 250
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AB VH1

<400> 250
```
Glu Val Gln Leu Glu Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1               5                  10                  15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
            20                  25                  30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
        35                  40                  45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr His Tyr Pro Asp Ser Val
    50                  55                  60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
            100                 105                 110
Ser Ser
```

<210> 251
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="AB1 VK"

/organism="Artificial Sequence"

<400> 251
gacatccaga tgacacagac tccatcttcc atgtatgcat ctctaggaga gagagtcact 60

atcacttgca aggcgagtca ggacattaat agctatttaa cctggttcca gcagaaacca 120

gggaaatctc ctaagaccct gatctatcgt acaaatagat tgtttgatgg ggtcccatcc 180

aggttcagtg gcagtggatc tgggcaagat ttttttctca ccatcagcag cctggaatat 240

gaagatatgg gaatttatta ttgtctacag tatgatgact ttccgtacac gttcggaggg 300

gggaccaaac tggaaataaa a 321

<210> 252
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB1 VK

<400> 252
Asp Ile Gln Met Thr Gln Thr Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 253
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="AB1 VH "
/organism="Artificial Sequence"

<400> 253
gaagtgcagc tggtggagtc tgggggggggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactctcagt tcctctgcca tgtcttgggt tcgccagact 120

ccggacagga ggctggagtg ggtcgcaacc attagtgttg gtggtggtaa aacctactat 180

ccagacagtg tgaagggtcg cttcaccatc tccagagaca atgccaagaa caccctctat 240

ctgcaaatga acagtctgag gtctgaggac acggccatgt attactgtgc aaaactaatc 300

agtctctact ggggccaagg caccactctc acagtctcct ca 342

<210> 254
<211> 114

<212> PRT
<213> Artificial Sequence

<220>
<223> AB1 VH

<400> 254
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Asp Arg Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Val Gly Gly Gly Lys Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Leu Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 255
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="AB1 VK "
/organism="Artificial Sequence"

<400> 255
gacatcaaga tgacccagtc tccatcttcc atgtatgcat ctctaggaga gagagtcact 60

atcacttgca aggcgagtca ggacattaat agctatttaa cctggttcca gcagaaacca 120

gggaaatctc ctaagaccct gatctatcgt acaaatagat tgtttgatgg ggtcccatcc 180

aggttcagtg gcagtggatc tgggcaagat ttttttctca ccatcagcag cctggaatat 240

gaagatatgg gaatttatta ttgtctacag tatgatgact ttccgtacac gttcggaggg 300

gggaccaaac tggaaataaa a 321

<210> 256
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> AB1 VK

<400> 256
Asp Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Arg Thr Asn Arg Leu Phe Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Phe Phe Leu Thr Ile Ser Ser Leu Glu Tyr

65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 257
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="BB7 VH "
/organism="Artificial Sequence"

<400> 257
gcagtgcaac tggtagagtc tgggggaggc ttggtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggaat cattttcagt tcctctgcca tgtcttgggt tcgccagact 120

ccggaaaaga gactggagtg ggtcgcaact attagtagtg gtggtcgttc cacctactat 180

ccagacagtg tgaagggtcg attcaccgtc tccagagaca gtgccaagaa caccctatac 240

ctgcaaatgg acagtctgag gtctgaggac acggccattt attactgtgc aaaactaatc 300

agtccctact ggggccaagg caccactctc acagtctcct ca 342

<210> 258
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 VH

<400> 258
Ala Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Ile Ile Phe Ser Ser Ser
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Val Ser Arg Asp Ser Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asp Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys
85 90 95
Ala Lys Leu Ile Ser Pro Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 259
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="BB7 VK "

/organism="Artificial Sequence"

<400> 259
gccatcaaga tgacccagtc tccatcttcc atgtatgcat ctctaggaga gagagtcatc 60

atcacttgca aggcgagtca ggacataaat agttatttaa cctggttcca acagaaacca 120

ggaaagtctc ctaagaccct gatctatctt acaaatagat tgatggatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggcaagaa tttttactca ccatcagcgg cctggaacat 240

gaagatatgg gcatttatta ttgtctccag tatgttgact ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 260
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> BB7 VK

<400> 260
Ala Ile Lys Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Ile Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Ile
35 40 45
Tyr Leu Thr Asn Arg Leu Met Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Glu Phe Leu Leu Thr Ile Ser Gly Leu Glu His
65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Val Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 261
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="DC1 VH"
/organism="Artificial Sequence"

<400> 261
gaagtgcagt tggtggagtc tgggggaggc ttagtgaagc ctggagggtc cctgaaactc 60

tcctgtgcag cctctggatt cactctcagt acccatgcca tgtcttgggt tcgccagact 120

ccggagaaga ggctggagtg ggtcgcaacc attagtagtg gtggtcgttc cacctactat 180

ccagacagtg tgaagggtcg attcactatc tccagagaca atgtcaagaa caccctatat 240

ctgcaactga gcagtctgag gtctgaggac acggccgtgt atttctgtgc aagactaatc 300

agtacctact ggggccaagg caccactctc acagtctcct ca 342

<210> 262
<211> 114

<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 VH

<400> 262
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Leu Ser Thr His
20 25 30
Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45
Ala Thr Ile Ser Ser Gly Gly Arg Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95
Ala Arg Leu Ile Ser Thr Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 263
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..321
<223> /mol_type="unassigned DNA"
/note="DC1 VK "
/organism="Artificial Sequence"

<400> 263
gacatcacga tgacccagtc tccatcttcc atatatgcat ctctgggaga gagagtcact 60

atcacttgca aggcgagtca ggacattaat agctatttaa cctggttcca gcagaaacca 120

gggaaatctc ctaagatcct gatctatctt gtaaatagat tggtagatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggcaagat tatgctctca ccatcagcag tctggaatat 240

gaagatatgg gaatttatta ttgtctacaa tatgatgact ttccgtacac gttcggaggg 300

gggaccaagc tggaaataaa a 321

<210> 264
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> DC1 VK

<400> 264
Asp Ile Thr Met Thr Gln Ser Pro Ser Ser Ile Tyr Ala Ser Leu Gly
1 5 10 15
Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30
Leu Thr Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Ile Leu Ile
35 40 45
Tyr Leu Val Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Gln Asp Tyr Ala Leu Thr Ile Ser Ser Leu Glu Tyr

65 70 75 80
Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Asp Phe Pro Tyr
85 90 95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 265
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="JE12 VH "
/organism="Artificial Sequence"

<400> 265
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata cagattcact agctatgtta tgcactgggt gaaacagaag 120

tctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg tgctaagtac 180

aatgagaagt tcaaaggcaa ggccacactg acttcagaca aatcctccag cacagcctac 240

atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagactatct 300

agtgactatt ggggccaagg caccactctc acagtctcct ca 342

<210> 266
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> JE12 VH

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

<210> 267
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..336
<223> /mol_type="unassigned DNA"
/note="JE12 VK "

/organism="Artificial Sequence"

<400> 267
gatgttttga tgacccaaaa tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagcattgaa catattaatg gaaacaccta tttagaatgg 120

tacctgcaga aaccaggcca gtctccaaag ttcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaggatc 240

agcagagtgg aggctgaaga tctgggaatt tattactgct ttcaaggttc acatgttccg 300

ttcacgttcg gaggggggac caagctggaa ataaaa 336

<210> 268
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> JE12 VK

<400> 268
Asp Val Leu Met Thr Gln Asn Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Glu His Ile
20 25 30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Phe Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80
Ser Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe Gln Gly
85 90 95
Ser His Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 269
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="EH6 VH "
/organism="Artificial Sequence"

<400> 269
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata cacattcact agttatgtta tgcactgggt gaagcagaag 120

cctgggcagg gccttgagtg gattggattt attaatcctt acaatgatgg tactaagtac 180

aatgagaagt tcaaaggcaa ggccacactg acctcagaca aagcctccac cacagcctac 240

atggagctca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagattctcc 300

tctgggtact ggggccaagg caccactctc acagtctcct ca 342

<210> 270
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> EH6 VH

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

<210> 271
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..336
<223> /mol_type="unassigned DNA"
/note="EH6 VK "
/organism="Artificial Sequence"

<400> 271
gatgttttga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60

atctcttgca gatctagtca gagtattgta catagtaatg gaaacaccta tttagaatgg 120

tacctgcaga aaccaggcca gtctccaaag ctcctgatct acaaagtttc caatcgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaagatc 240

agcagagtgg gggctgagga tctgggagtt tattactgcc ttcaagtttc acatgttcct 300

ttcacgttcg gctcggggac aaagttggaa ataaaa 336

<210> 272
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> EH6 VK

<400> 272
Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro

```
    50                  55                  60
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80
Ser Arg Val Gly Ala Glu Asp Leu Gly Val Tyr Tyr Cys Leu Gln Val
                85                  90                  95
Ser His Val Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110



<210> 273
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
      /note="AG9 VH "
      /organism="Artificial Sequence"

<400> 273
gaggtccagc tgcagcagtc tggacctgag ttggtaaagc ctggggcttc agtgaagatg      60

tcctgcaggg cttctggata cacattcact acctatgtta ttcactgggt gaagcagaag     120

cctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg tgctaggtac     180

aatgagaagt tcaaaggcaa ggccacactg acttcagaca aatcctccac cacagcctac     240

atggaactca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagactttct     300

agtgactact ggggccaagg caccactctc acagtctcct ca                       342


<210> 274
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AG9 VH

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


<210> 275
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
```

<221> source
<222> 1..336
<223> /mol_type="unassigned DNA"
/note="AG9 VK "
/organism="Artificial Sequence"

<400> 275
gatgttttga tgacccaaaa tccactctcc ctgcctgtca gtcttggcga tcaggcctcc 60

atctcttgca gatctagtcg gagcattgaa catagtaatg gaaacaccta tttggaatgg 120

tacctgcaga aaccaggcca gtctccaaag ttcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaggatc 240

agcagtgtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttccg 300

ttcacgttcg gaggggggac caagctggaa ataaaa 336

<210> 276
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> AG9 VK

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

<210> 277
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="AH3 VH"
/organism="Artificial Sequence"

<400> 277
gaggtccagc tgcagcagtc tggacctgag ctggtaaagc ctggggcttc agtgaagatg 60

tcctgcaggg cttctggata cacattcact acctatgtta ttcactgggt gaagcagaag 120

cctgggcagg gccttgagtg gattggatat attaatcctt acaatgatgg tgctaggtac 180

aatgagaagt tcaaaggcaa ggccacactg acttcagaca aatcctccac cacagcctac 240

atggaactca gcagcctgac ctctgaggac tctgcggtct attactgtgc aagactatct 300

agtgactact ggggccaagg caccactctc acagtctcct ca 342

<210> 278
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> AH3 VH

<400> 278
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30
Val Ile His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Ala Arg Tyr Asn Glu Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Ser Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80
Met Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Leu Ser Ser Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
100 105 110
Ser Ser

<210> 279
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..336
<223> /mol_type="unassigned DNA"
/note="AH3 VK "
/organism="Artificial Sequence"

<400> 279
gatgttttga tgacccaaaa tccactctcc ctgcctgtca gtcttggaga tcaggcctcc 60

atctcttgca gatctagtcg gagcattgaa catagtaatg gaaacaccta tttggaatgg 120

tacctgcaga aaccaggcca gtctccaaag ttcctgatct acaaagtttc caaccgattt 180

tctggggtcc cagacaggtt cagtggcagt ggatcaggga cagatttcac actcaggatc 240

agcagtgtgg aggctgagga tctgggagtt tattactgct ttcaaggttc acatgttccg 300

ttcacgttcg gaggggggac caagctggaa ataaaa 336

<210> 280
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> AH3 VK

<400> 280
Asp Val Leu Met Thr Gln Asn Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Arg Ser Ile Glu His Ser

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

<210> 281
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..357
<223> /mol_type="unassigned DNA"
/note="DD9 VH "
/organism="Artificial Sequence"

<400> 281
caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60

acttgttctt tttctgggtt ttcactgagc acttcgggta tgggtgtgag ttggattcgt 120

cagtcctcag gaaagggtct ggagtggctg gcacacattt actgggatga tgacaagcgc 180

tataacccat ccctgaagag ccggatcaca atctccaagg attcctcaag caaccaggta 240

ttcctcaaga tcaccagtgt ggacactgca gatactgcca catattactg tgctcgaagt 300

tggactacgg ccccgtttgc tttctggggc caagggactc tggtcactgt ctctgca 357

<210> 282
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> DD9 VH

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

<210> 283
<211> 318

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..318
<223> /mol_type="unassigned DNA"
/note="DD9 VK "
/organism="Artificial Sequence"

<400> 283
caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atgacctgca gtgccagctc aagtgtagat tacatgtact ggtaccagca gaagccagga 120

tcctccccca gactcctgat ttatgacaca tccaacctgg cttctggagt ccctgttcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagccgaat gggggctgaa 240

gatgctgcca cttattactg ccaacagtgg aatagttccc cgctcacgtt cggtgctggg 300

accaagctgg agctgaaa 318

<210> 284
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> DD9 VK

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

<210> 285
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..357
<223> /mol_type="unassigned DNA"
/note="DH2 VH "
/organism="Artificial Sequence"

<400> 285
caggttactc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60

acttgttctt tctctgggtt ttcactgagc acttctggta tgggtgtgag ctggattcgt 120

cagccttcag gaaagggtct ggagtggctg gcacacattt actgggatga tgacaagcgc 180

tataacccat ccctgaagag ccggctcaca atctccaagg atacctccag caaccaggta 240

ttcctcaaga tcaccagtgt ggacactgca gatactgcca catactactg tgctcgaagt 300

gggactacgg ccccgtttgc ttactggggc caagggactc tggtcactgt ctctgca 357

<210> 286
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> DH2 VH

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

<210> 287
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..318
<223> /mol_type="unassigned DNA"
/note="DH2 VK "
/organism="Artificial Sequence"

<400> 287
caaattgttc tcactcagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atgacctgca gtgccagctc aagtgtaagt tacatgtact ggtaccagca gaagccagga 120

tcctcccca gactcctgat ttatgacaca tccaacctgg cttctggagt ccctgttcgc 180

ttcagtggca gtgggtctgg gacctcttac tctctcacaa tcagccgaat ggaggctgaa 240

gatgctgcca ctttttactg ccagcagtgg agtagttccc cgctcacgtt cggtgctggg 300

accaagctgg agctgaaa 318

<210> 288
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> DH2 VK

<400> 288
Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly

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

<210> 289
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..339
<223> /mol_type="unassigned DNA"
/note="DD6 VH "
/organism="Artificial Sequence"

<400> 289
gaggtccagc tgcaacagtc tgggcctgaa ctggtgaagc ctggggcttc agtgaagatg 60

tcctgcaagg cttctggata cagattcact gactacaaca tgcactgggt gaagcagaac 120

cttggaaaga gccttgagtg gattggatat attaacccta aaaatggtgt tatttactac 180

aaccagaagt tcaagggcaa ggccacattg acagtgaaca ggtcctccaa cacagcctac 240

atggagatcc gcagcctgac atcggaagat tctgcagtct attactgtgc aacagctctg 300

acttactggg gacaagggac tctggtcact gtctctgca 339

<210> 290
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> DD6 VH

<400> 290
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
1 5 10 15
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Arg Phe Thr Asp Tyr
20 25 30
Asn Met His Trp Val Lys Gln Asn Leu Gly Lys Ser Leu Glu Trp Ile
35 40 45
Gly Tyr Ile Asn Pro Lys Asn Gly Val Ile Tyr Tyr Asn Gln Lys Phe
50 55 60
Lys Gly Lys Ala Thr Leu Thr Val Asn Arg Ser Ser Asn Thr Ala Tyr
65 70 75 80
Met Glu Ile Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95
Ala Thr Ala Leu Thr Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110
Ala

<210> 291
<211> 330

<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..330
<223> /mol_type="unassigned DNA"
/note="DD6 VL "
/organism="Artificial Sequence"

<400> 291
caggctgttg tgactcagga atctgcactc accacatcac ctggtgaaac agtcacactc 60

acttgtcgct caagtactgg ggctgttgca gctaataact atgccaactg gatccaagaa 120

aaaccagatc atttattcac tggtctgata gctggtacca acaagcgagc tccaggtgtt 180

cctgccagat tctcaggctc cctgatagga gacaaggctg ccctcaccat cacaggggca 240

cagactgagg atgaggcaat atatttctgt gctctatggt acagcaacta ttgggtgttc 300

ggtggaggaa ccaaagtgac tgtcctaggc 330

<210> 292
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> DD6 VL

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

<210> 293
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..342
<223> /mol_type="unassigned DNA"
/note="IA12 VH "
/organism="Artificial Sequence"

<400> 293
cagatccagt tggtacagtc tggacctgag ctgaagaagc ctggagagac agtcaagatc 60

tcctgcaagg cttctgggta taccttcaca acctatggaa tgacctgggt gaaacaggct 120

ccaggaaagg gtttaaagtg gatgggctgg ataaacacct cctctggagt gccaacatat 180

gctgatgact tcaagggacg gtttgccttc tctttggaaa cctctgccag cactgcctat 240

ttgcagatca acaacctcaa aagtgaggac acggctacat atttctgtgc aagaccggaa 300

gttgcttact ggggccaagg gactctggtc actgtctctg ca 342

<210> 294
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> IA12 VH

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

<210> 295
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<222> 1..336
<223> /mol_type="unassigned DNA"
/note="IA12 VK "
/organism="Artificial Sequence"

<400> 295
gatgttgtga tgacccagac tccactcact ttgtcggtta cctttggaca accagcctct 60

atctcttgca agtcaagtca gagcctctta tatgataatg gaaagactta tttgcattgg 120

ttatttcaga ggccaggcca gtctccaagg cgcctaatct atctggtgtc taaactggac 180

tctggagtcc ctgacaggtt cactggcagt ggatcaggaa cagattttac actgaaaatc 240

agcagagtgg aggctgagga tttgggagtt tattactgcg tgcaaggtac acattttccg 300

tacacgttcg gaggggggac caaactggaa ataaaa 336

<210> 296
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> IA12 VK

<400> 296
Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Phe Gly

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