Figure 22

Clone 2120.4.19 – Variable Heavy Chain (Nucleic Acid Sequence)

CAGGTGCAGCTGAAGGAGTCAGGACCTGGTCTGGTGCAGCCCTCACAGACCCTG
TCTCTCACCTGCACTGTCTCTGGATTCTCATTAACCAGCAATGGTGTAAGCTGGGT
TCGCCAGCCTCCAGGAAAGGGTCTGGAGTGGATTGCAGCAATATCATCTGGTGGA
ACCACATATTATAATTCAGCGTTCAAATCCCGACTGAGCATCAGCAGGAACACCTC
CAAGAGCCAAGTTCTCTTAAAAATGAACAGTCTGCAAACTGAAGACACAGCCATGT
ACTTCTGTGCCAGACGGTATGGGTACGGGTGGTACTTTGACTTCTGGGGCCCAGG
AACCATGGTCACAGTCTCCTCA (SEQ ID NO:76)

Clone 2120.4.19 – Variable Heavy Chain (Amino Acid Sequence)

QVQLKESGPGLVQPSQTLSLTCTVSGFSLTSNGVSWVRQPPGKGLEWIAAISSGGTT
YYNSAFKSRLSISRNTSKSQVLLKMNSLQTEDTAMYFCARRYGYGWYFDFWGPGTM
VTVSS (SEQ ID NO:77)

Clone 2120.4.19 – CDR-H1 (Amino Acid Sequence)

GFSLTSNGVS (SEQ ID NO:78)

Clone 2120.4.19 – CDR-H2 (Amino Acid Sequence)

AISSGGTTYYNSAFKS (SEQ ID NO:79)

Clone 2120.4.19 – CDR-H3 (Amino Acid Sequence)

RYGYGWYFDF (SEQ ID NO:80)

SEQUENCE LISTING

<110> FLANAGAN, Kenneth
BAKER, Jeanne
YEDNOCK, Theodore A.

<120> ANTI-MCAM ANTIBODIES AND ASSOCIATED METHODS OF USE

<130> 057450/436599

<150> 61/797,179
<151> 2012-11-30

<150> 61/797,356
<151> 2012-12-05

<150> 61/698,916
<151> 2012-09-10

<160> 155

<170> FastSEQ for Windows Version 4.0

<210> 1
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

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<222> (1)...(426)

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atg agg gtc cag att cag ttt ctg ggg ctc ctt ctg ctc tgg aca tca 48
Met Arg Val Gln Ile Gln Phe Leu Gly Leu Leu Leu Trp Thr Ser
1 5 10 15

gtt gtc cag tgt gat gtc cag atg acc cag tct cca tct tat ctt gct 96
Val Val Gln Cys Asp Val Gln Met Thr Gln Ser Pro Ser Tyr Leu Ala
20 25 30

acg tct cct gga gag agt gtt tcc atc agt tgc aag gca agt aaa aac 144
Thr Ser Pro Gly Glu Ser Val Ser Ile Ser Cys Lys Ala Ser Lys Asn
35 40 45

att gac aca tac tta gcc tgg tat cag gag aaa cct ggg aaa acg aat 192

```
Ile Asp Thr Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly Lys Thr Asn
     50                  55                  60
aag ctt ctt atc tac tct ggg tca act ttg caa tct gga act cca tcg   240
Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly Thr Pro Ser
 65                  70                  75                  80

aga ttc agt ggc agt gga tct ggt aca gat ttc acg ctc acc atc aga   288
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Arg
                 85                  90                  95

aac ctg gag tct gaa gat ttt gca gtc tac tac tgt caa cag cat aat   336
Asn Leu Glu Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Asn
            100                 105                 110

gaa tac ccg ctc acg ttc ggt tct ggg acc aag ctg gag atc aaa cgg   384
Glu Tyr Pro Leu Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
        115                 120                 125

gct gat gct gca cca act gta tcc atc ttc cca cca tcc tcg           426
Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser
    130                 135                 140

ga                                                    428
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<210> 2
<211> 142
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 2

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

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Peptide

<400> 3
Lys Ala Ser Lys Asn Ile Asp Thr Tyr Leu Ala
 1   5   10

<210> 4
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 4
Ser Gly Ser Thr Leu
 1   5

<210> 5
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 5
Gln Gln His Asn Glu Tyr Pro Leu Thr
 1   5

<210> 6
<211> 483
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<221> CDS
<222> (1)...(483)

<400> 6
atg gac acc agg ctc tgc ttg gtt ttc ctt gtc ctt ttc ata aaa ggt   48
Met Asp Thr Arg Leu Cys Leu Val Phe Leu Val Leu Phe Ile Lys Gly

```
 1               5                  10                  15

gtc cag tgt gag gtg cag ctg gtg gag tct ggt gga ggc tta gtg cag   96
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
            20                  25                  30

cct gga agg tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc act ttc   144
Pro Gly Arg Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
         35                  40                  45

agt aac tat tac atg gcc tgg gtc cgc cag gct cca acg aag ggt ctg   192
Ser Asn Tyr Tyr Met Ala Trp Val Arg Gln Ala Pro Thr Lys Gly Leu
     50                  55                  60

gag tgg gtc gca tcc att agt ttt gag ggt aat aga aat cac tat gga   240
Glu Trp Val Ala Ser Ile Ser Phe Glu Gly Asn Arg Asn His Tyr Gly
 65                  70                  75                  80

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

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

tat tat tgt gca aga cat cgg ggg tat agt acg aat ttt tat cac gac   384
Tyr Tyr Cys Ala Arg His Arg Gly Tyr Ser Thr Asn Phe Tyr His Asp
        115                 120                 125

gtt ttg gat gcc tgg ggt caa gga gct tta gtc act gtc tcc tca gct   432
Val Leu Asp Ala Trp Gly Gln Gly Ala Leu Val Thr Val Ser Ser Ala
    130                 135                 140

gaa aca aca gcc cca tct gtc tat cca ctg gct cct gga act gct ctc   480
Glu Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Gly Thr Ala Leu
145                 150                 155                 160

aaa                                                   483
Lys
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<210> 7
<211> 161
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 7
Met Asp Thr Arg Leu Cys Leu Val Phe Leu Val Leu Phe Ile Lys Gly

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

<210> 8
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 8
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Gly Phe Thr Phe Ser Asn Tyr Tyr Met Ala
 1               5                  10
```

<210> 9
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 9
```
Ser Ile Ser Phe Glu Gly Asn Arg Asn His Tyr Gly Asp Ser Val Lys
 1               5                  10                  15
```

<210> 10
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 10
His Arg Gly Tyr Ser Thr Asn Phe Tyr His Asp Val Leu Asp Ala Trp
 1   5   10   15
Gly Gln Gly

<210> 11
<211> 646
<212> PRT
<213> Homo sapiens

<400> 11
Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys
 1   5   10   15
Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala
            20   25   30
Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys
        35   40   45
Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser
    50   55   60
Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln
65   70   75   80
Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp
                85   90   95
Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg
            100   105   110
Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile
        115   120   125
Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn
    130   135   140
Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr
145   150   155   160
Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys
                165   170   175
Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser
            180   185   190
Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
        195   200   205
Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
    210   215   220
Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
225   230   235   240
Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
                245   250   255
Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
            260   265   270
Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
        275   280   285
Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
    290   295   300

```
Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
305                 310                 315                 320
Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
                325                 330                 335
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
            340                 345                 350
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
        355                 360                 365
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
    370                 375                 380
Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
385                 390                 395                 400
Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly
                405                 410                 415
Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp
            420                 425                 430
Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu
        435                 440                 445
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp
    450                 455                 460
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val
465                 470                 475                 480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly
                485                 490                 495
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu
            500                 505                 510
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr
        515                 520                 525
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn
    530                 535                 540
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val
545                 550                 555                 560
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly
                565                 570                 575
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg
            580                 585                 590
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu
        595                 600                 605
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu
    610                 615                 620
Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys
625                 630                 635                 640
Tyr Ile Asp Leu Arg His
                645
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<210> 12
<211> 474
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<221> CDS
<222> (1)...(474)

<400> 12
atg gaa tca cag acc cag gtc ctc atg tcc ctg ctg ctc tgg att tct 48
Met Glu Ser Gln Thr Gln Val Leu Met Ser Leu Leu Leu Trp Ile Ser
 1   5   10   15

ggt acc tgt ggg gac att gtg atg acc cag tct cca tcc tct ctg gct 96
Gly Thr Cys Gly Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala
            20   25   30

gtg tca gct ggg gag acg gtc tct ata cac tgc aag tcc agt cag agt 144
Val Ser Ala Gly Glu Thr Val Ser Ile His Cys Lys Ser Ser Gln Ser
        35   40   45

ctt tta tac agt gga acc caa aag aac tac ttg gcc tgg ttc cag cag 192
Leu Leu Tyr Ser Gly Thr Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln
    50   55   60

aaa cca gga cag tct cct aaa ctg ctg atc ttc tgg gca tct act agg 240
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg
65   70   75   80

cag tct ggt gtc cct gat cgc ttc ata ggc cgt gga tct ggg aca gac 288
Gln Ser Gly Val Pro Asp Arg Phe Ile Gly Arg Gly Ser Gly Thr Asp
                85   90   95

ttc act ctg acc atc agc ggt gtg cag gca gaa gat ctg gca att tat 336
Phe Thr Leu Thr Ile Ser Gly Val Gln Ala Glu Asp Leu Ala Ile Tyr
            100   105   110

tac tgt caa caa tat tat gat act ctc acg gac acg ttt gga gcg ggg 384
Tyr Cys Gln Gln Tyr Tyr Asp Thr Leu Thr Asp Thr Phe Gly Ala Gly
        115   120   125

acc aag ctg gaa ctg aaa cgg gct gat gct gca cca act gta tct atc 432
Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile
    130   135   140

ttc cca cca tcc acg gaa cag tta gca act gga ggt gcc tca 474
Phe Pro Pro Ser Thr Glu Gln Leu Ala Thr Gly Gly Ala Ser
145   150   155

<210> 13
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 13
Met Glu Ser Gln Thr Gln Val Leu Met Ser Leu Leu Leu Trp Ile Ser
 1   5   10   15
Gly Thr Cys Gly Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala
            20   25   30
Val Ser Ala Gly Glu Thr Val Ser Ile His Cys Lys Ser Ser Gln Ser
        35   40   45
Leu Leu Tyr Ser Gly Thr Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln
    50   55   60
Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Phe Trp Ala Ser Thr Arg
65   70   75   80
Gln Ser Gly Val Pro Asp Arg Phe Ile Gly Arg Gly Ser Gly Thr Asp
                85   90   95
Phe Thr Leu Thr Ile Ser Gly Val Gln Ala Glu Asp Leu Ala Ile Tyr
            100   105   110
Tyr Cys Gln Gln Tyr Tyr Asp Thr Leu Thr Asp Thr Phe Gly Ala Gly
        115   120   125
Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile
    130   135   140
Phe Pro Pro Ser Thr Glu Gln Leu Ala Thr Gly Gly Ala Ser
145   150   155

<210> 14
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 14
Lys Ser Ser Gln Ser Leu Leu Tyr Ser Gly Thr Gln Lys Asn Tyr Leu
 1   5   10   15
Ala

<210> 15
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 15
Trp Ala Ser Thr Arg Gln Ser
 1   5

<210> 16
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
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<400> 16
Gln Gln Tyr Tyr Asp Thr Leu Thr Asp Thr
 1   5   10

<210> 17
<211> 469
<212> DNA
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<220>
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<222> (1)...(468)

<400> 17
atg gac atc agg ctc agc ttg gct ttc ctg gtc ctt ttc ata aaa ggt   48
Met Asp Ile Arg Leu Ser Leu Ala Phe Leu Val Leu Phe Ile Lys Gly
 1   5   10   15

gtc cag tgt gag gtg cgg ctg gtg gag tct ggg gga ggc tta gtg cag   96
Val Gln Cys Glu Val Arg Leu Val Glu Ser Gly Gly Gly Leu Val Gln
             20   25   30

cct gga aag tcc atg aaa ctc tcc tgt gta gcc tcg gga ttc aaa ttc   144
Pro Gly Lys Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Lys Phe
         35   40   45

agt aac tat tac atg tcc tgg gtc cgc cag gct cca gcg aag ggt ctg   192
Ser Asn Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Ala Lys Gly Leu
     50   55   60

gag tgg gtc gca tcc att agt gat ggt ggt ggt gac act ttc tgt cga   240
Glu Trp Val Ala Ser Ile Ser Asp Gly Gly Gly Asp Thr Phe Cys Arg
 65   70   75   80

gac ttg gtg aag ggc cga ttc act atc tcc aga gat aat gca aaa agt   288
Asp Leu Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser
                 85   90   95

acc ctt tac ctg caa atg gac agt ctg agg cct gag gac acg gcc act   336
Thr Leu Tyr Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Ala Thr
            100   105   110

tat tac tgt gca aga cgg gga gca gct atg ggg ggt gtt atg gat gcc   384
Tyr Tyr Cys Ala Arg Arg Gly Ala Ala Met Gly Gly Val Met Asp Ala
        115   120   125

```
tgg ggt caa gga act tca gtc act gtc tcc tca gct gaa aca aca gcc   432
Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Ala Glu Thr Thr Ala
    130                 135                 140

cca tct gtc tat cca ctg gct cct gga act gct ctc a               469
Pro Ser Val Tyr Pro Leu Ala Pro Gly Thr Ala Leu
145                 150                 155
```

<210> 18
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 18

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

<210> 19
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 19

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Gly Phe Lys Phe Ser Asn Tyr Tyr Met Ser
 1               5                  10
```

<210> 20
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 20
Ser Ile Ser Asp Gly Gly Gly Asp Thr Phe Cys Arg Asp Leu Val Lys
 1   5   10   15
Gly

<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 21
Arg Gly Ala Ala Met Gly Gly Val Met Asp Ala Trp Gly Gln Gly
 1   5   10   15

<210> 22
<211> 111
<212> PRT
<213> Homo sapiens

<400> 22
Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala Pro Glu
 1   5   10   15
Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys Gly Leu
            20   25   30
Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser Val His
        35   40   45
Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln Gly Gln
    50   55   60
Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp Arg Gly
65   70   75   80
Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg Ile Phe
                85   90   95
Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile Gln
            100   105   110

<210> 23
<211> 104
<212> PRT

<213> Homo sapiens

<400> 23
Pro Asn Ile Gln Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu
 1   5   10   15
Pro Glu Glu Val Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro
            20   25   30
Gln Val Ile Trp Tyr Lys Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn
        35   40   45
Arg Val His Ile Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr
    50   55   60
Thr Leu Gln Ser Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp
65   70   75   80
Ala Gln Phe Tyr Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His
                85   90   95
Met Lys Glu Ser Arg Glu Val Thr
            100

<210> 24
<211> 78
<212> PRT
<213> Homo sapiens

<400> 24
Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val Glu Pro Val
 1   5   10   15
Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys Leu Ala Asp
            20   25   30
Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn Pro Ser Thr
        35   40   45
Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val Leu Val Leu
    50   55   60
Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys Gln
65   70   75

<210> 25
<211> 90
<212> PRT
<213> Homo sapiens

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

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Pro Gly Leu Asn Arg Thr Gln Leu Val Lys
                85                  90


<210> 26
<211> 81
<212> PRT
<213> Homo sapiens

<400> 26
Pro Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn
 1               5                  10                  15
Met Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr
            20                  25                  30
Ile Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro
        35                  40                  45
Gln Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu
    50                  55                  60
Glu Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr
65                  70                  75                  80
Ser
<210> 27
<211> 1823
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<213> Homo sapiens

<400> 27
Met Ala Leu Ser Ser Ala Trp Arg Ser Val Leu Pro Leu Trp Leu Leu
 1               5                  10                  15
Trp Ser Ala Ala Cys Ser Arg Ala Ala Ser Gly Asp Asp Asn Ala Phe
            20                  25                  30
Pro Phe Asp Ile Glu Gly Ser Ser Ala Val Gly Arg Gln Asp Pro Pro
        35                  40                  45
Glu Thr Ser Glu Pro Arg Val Ala Leu Gly Arg Leu Pro Pro Ala Ala
    50                  55                  60
Glu Lys Cys Asn Ala Gly Phe Phe His Thr Leu Ser Gly Glu Cys Val
65                  70                  75                  80
Pro Cys Asp Cys Asn Gly Asn Ser Asn Glu Cys Leu Asp Gly Ser Gly
                85                  90                  95
Tyr Cys Val His Cys Gln Arg Asn Thr Thr Gly Glu His Cys Glu Lys
            100                 105                 110
Cys Leu Asp Gly Tyr Ile Gly Asp Ser Ile Arg Gly Ala Pro Gln Phe
        115                 120                 125
Cys Gln Pro Cys Pro Cys Pro Leu Pro His Leu Ala Asn Phe Ala Glu
    130                 135                 140
Ser Cys Tyr Arg Lys Asn Gly Ala Val Arg Cys Ile Cys Asn Glu Asn
145                 150                 155                 160
Tyr Ala Gly Pro Asn Cys Glu Arg Cys Ala Pro Gly Tyr Tyr Gly Asn
                165                 170                 175
Pro Leu Leu Ile Gly Ser Thr Cys Lys Lys Cys Asp Cys Ser Gly Asn
            180                 185                 190
Ser Asp Pro Asn Leu Ile Phe Glu Asp Cys Asp Glu Val Thr Gly Gln
        195                 200                 205
```

```
Cys Arg Asn Cys Leu Arg Asn Thr Thr Gly Phe Lys Cys Glu Arg Cys
    210                 215                 220
Ala Pro Gly Tyr Tyr Gly Asp Ala Arg Ile Ala Lys Asn Cys Ala Val
225                 230                 235                 240
Cys Asn Cys Gly Gly Gly Pro Cys Asp Ser Val Thr Gly Glu Cys Leu
                245                 250                 255
Glu Glu Gly Phe Glu Pro Pro Thr Gly Met Asp Cys Pro Thr Ile Ser
            260                 265                 270
Cys Asp Lys Cys Val Trp Asp Leu Thr Asp Asp Leu Arg Leu Ala Ala
        275                 280                 285
Leu Ser Ile Glu Glu Gly Lys Ser Gly Val Leu Ser Val Ser Ser Gly
    290                 295                 300
Ala Ala Ala His Arg His Val Asn Glu Ile Asn Ala Thr Ile Tyr Leu
305                 310                 315                 320
Leu Lys Thr Lys Leu Ser Glu Arg Glu Asn Gln Tyr Ala Leu Arg Lys
                325                 330                 335
Ile Gln Ile Asn Asn Ala Glu Asn Thr Met Lys Ser Leu Leu Ser Asp
            340                 345                 350
Val Glu Glu Leu Val Glu Lys Glu Asn Gln Ala Ser Arg Lys Gly Gln
        355                 360                 365
Leu Val Gln Lys Glu Ser Met Asp Thr Ile Asn His Ala Ser Gln Leu
    370                 375                 380
Val Glu Gln Ala His Asp Met Arg Asp Lys Ile Gln Glu Ile Asn Asn
385                 390                 395                 400
Lys Met Leu Tyr Tyr Gly Glu Glu His Glu Leu Ser Pro Lys Glu Ile
                405                 410                 415
Ser Glu Lys Leu Val Leu Ala Gln Lys Met Leu Glu Glu Ile Arg Ser
            420                 425                 430
Arg Gln Pro Phe Phe Thr Gln Arg Glu Leu Val Asp Glu Glu Ala Asp
        435                 440                 445
Glu Ala Tyr Glu Leu Leu Ser Gln Ala Glu Ser Trp Gln Arg Leu His
    450                 455                 460
Asn Glu Thr Arg Thr Leu Phe Pro Val Val Leu Glu Gln Leu Asp Asp
465                 470                 475                 480
Tyr Asn Ala Lys Leu Ser Asp Leu Gln Glu Ala Leu Asp Gln Ala Leu
                485                 490                 495
Asn Tyr Val Arg Asp Ala Glu Asp Met Asn Arg Ala Thr Ala Ala Arg
            500                 505                 510
Gln Arg Asp His Glu Lys Gln Gln Glu Arg Val Arg Glu Gln Met Glu
        515                 520                 525
Val Val Asn Met Ser Leu Ser Thr Ser Ala Asp Ser Leu Thr Thr Pro
    530                 535                 540
Arg Leu Thr Leu Ser Glu Leu Asp Asp Ile Ile Lys Asn Ala Ser Gly
545                 550                 555                 560
Ile Tyr Ala Glu Ile Asp Gly Ala Lys Ser Glu Leu Gln Val Lys Leu
                565                 570                 575
Ser Asn Leu Ser Asn Leu Ser His Asp Leu Val Gln Glu Ala Ile Asp
            580                 585                 590
His Ala Gln Asp Leu Gln Gln Glu Ala Asn Glu Leu Ser Arg Lys Leu
        595                 600                 605
His Ser Ser Asp Met Asn Gly Leu Val Gln Lys Ala Leu Asp Ala Ser
    610                 615                 620
Asn Val Tyr Glu Asn Ile Val Asn Tyr Val Ser Glu Ala Asn Glu Thr
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625 630 635 640
Ala Glu Phe Ala Leu Asn Thr Thr Asp Arg Ile Tyr Asp Ala Val Ser
645 650 655
Gly Ile Asp Thr Gln Ile Ile Tyr His Lys Asp Glu Ser Glu Asn Leu
660 665 670
Leu Asn Gln Ala Arg Glu Leu Gln Ala Lys Ala Glu Ser Ser Ser Asp
675 680 685
Glu Ala Val Ala Asp Thr Ser Arg Arg Val Gly Gly Ala Leu Ala Arg
690 695 700
Lys Ser Ala Leu Lys Thr Arg Leu Ser Asp Ala Val Lys Gln Leu Gln
705 710 715 720
Ala Ala Glu Arg Gly Asp Ala Gln Gln Arg Leu Gly Gln Ser Arg Leu
725 730 735
Ile Thr Glu Glu Ala Asn Arg Thr Thr Met Glu Val Gln Gln Ala Thr
740 745 750
Ala Pro Met Ala Asn Asn Leu Thr Asn Trp Ser Gln Asn Leu Gln His
755 760 765
Phe Asp Ser Ser Ala Tyr Asn Thr Ala Val Asn Ser Ala Arg Asp Ala
770 775 780
Val Arg Asn Leu Thr Glu Val Val Pro Gln Leu Leu Asp Gln Leu Arg
785 790 795 800
Thr Val Glu Gln Lys Arg Pro Ala Ser Asn Val Ser Ala Ser Ile Gln
805 810 815
Arg Ile Arg Glu Leu Ile Ala Gln Thr Arg Ser Val Ala Ser Lys Ile
820 825 830
Gln Val Ser Met Met Phe Asp Gly Gln Ser Ala Val Glu Val His Ser
835 840 845
Arg Thr Ser Met Asp Asp Leu Lys Ala Phe Thr Ser Leu Ser Leu Tyr
850 855 860
Met Lys Pro Pro Val Lys Arg Pro Glu Leu Thr Glu Thr Ala Asp Gln
865 870 875 880
Phe Ile Leu Tyr Leu Gly Ser Lys Asn Ala Lys Lys Glu Tyr Met Gly
885 890 895
Leu Ala Ile Lys Asn Asp Asn Leu Val Tyr Val Tyr Asn Leu Gly Thr
900 905 910
Lys Asp Val Glu Ile Pro Leu Asp Ser Lys Pro Val Ser Ser Trp Pro
915 920 925
Ala Tyr Phe Ser Ile Val Lys Ile Glu Arg Val Gly Lys His Gly Lys
930 935 940
Val Phe Leu Thr Val Pro Ser Leu Ser Ser Thr Ala Glu Glu Lys Phe
945 950 955 960
Ile Lys Lys Gly Glu Phe Ser Gly Asp Asp Ser Leu Leu Asp Leu Asp
965 970 975
Pro Glu Asp Thr Val Phe Tyr Val Gly Gly Val Pro Ser Asn Phe Lys
980 985 990
Leu Pro Thr Ser Leu Asn Leu Pro Gly Phe Val Gly Cys Leu Glu Leu
995 1000 1005
Ala Thr Leu Asn Asn Asp Val Ile Ser Leu Tyr Asn Phe Lys His Ile
1010 1015 1020
Tyr Asn Met Asp Pro Ser Thr Ser Val Pro Cys Ala Arg Asp Lys Leu
1025 1030 1035 1040
Ala Phe Thr Gln Ser Arg Ala Ala Ser Tyr Phe Phe Asp Gly Ser Gly
1045 1050 1055

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Tyr Ala Val Val Arg Asp Ile Thr Arg Arg Gly Lys Phe Gly Gln Val
            1060                1065                1070
Thr Arg Phe Asp Ile Glu Val Arg Thr Pro Ala Asp Asn Gly Leu Ile
        1075                1080                1085
Leu Leu Met Val Asn Gly Ser Met Phe Phe Arg Leu Glu Met Arg Asn
    1090                1095                1100
Gly Tyr Leu His Val Phe Tyr Asp Phe Gly Phe Ser Gly Gly Pro Val
1105                1110                1115                1120
His Leu Glu Asp Thr Leu Lys Lys Ala Gln Ile Asn Asp Ala Lys Tyr
                1125                1130                1135
His Glu Ile Ser Ile Ile Tyr His Asn Asp Lys Lys Met Ile Leu Val
            1140                1145                1150
Val Asp Arg Arg His Val Lys Ser Met Asp Asn Glu Lys Met Lys Ile
        1155                1160                1165
Pro Phe Thr Asp Ile Tyr Ile Gly Gly Ala Pro Pro Glu Ile Leu Gln
    1170                1175                1180
Ser Arg Ala Leu Arg Ala His Leu Pro Leu Asp Ile Asn Phe Arg Gly
1185                1190                1195                1200
Cys Met Lys Gly Phe Gln Phe Gln Lys Lys Asp Phe Asn Leu Leu Glu
                1205                1210                1215
Gln Thr Glu Thr Leu Gly Val Gly Tyr Gly Cys Pro Glu Asp Ser Leu
            1220                1225                1230
Ile Ser Arg Arg Ala Tyr Phe Asn Gly Gln Ser Phe Ile Ala Ser Ile
        1235                1240                1245
Gln Lys Ile Ser Phe Phe Asp Gly Phe Glu Gly Gly Phe Asn Phe Arg
    1250                1255                1260
Thr Leu Gln Pro Asn Gly Leu Leu Phe Tyr Tyr Ala Ser Gly Ser Asp
1265                1270                1275                1280
Val Phe Ser Ile Ser Leu Asp Asn Gly Thr Val Ile Met Asp Val Lys
                1285                1290                1295
Gly Ile Lys Val Gln Ser Val Asp Lys Gln Tyr Asn Asp Gly Leu Ser
            1300                1305                1310
His Phe Val Ile Ser Ser Val Ser Pro Thr Arg Tyr Glu Leu Ile Val
        1315                1320                1325
Asp Lys Ser Arg Val Gly Ser Lys Asn Pro Thr Lys Gly Lys Ile Glu
    1330                1335                1340
Gln Thr Gln Ala Ser Glu Lys Lys Phe Tyr Phe Gly Gly Ser Pro Ile
1345                1350                1355                1360
Ser Ala Gln Tyr Ala Asn Phe Thr Gly Cys Ile Ser Asn Ala Tyr Phe
                1365                1370                1375
Thr Arg Val Asp Arg Asp Val Glu Val Glu Asp Phe Gln Arg Tyr Thr
            1380                1385                1390
Glu Lys Val His Thr Ser Leu Tyr Glu Cys Pro Ile Glu Ser Ser Pro
        1395                1400                1405
Leu Phe Leu Leu His Lys Lys Gly Lys Asn Leu Ser Lys Pro Lys Ala
    1410                1415                1420
Ser Gln Asn Lys Lys Gly Gly Lys Ser Lys Asp Ala Pro Ser Trp Asp
1425                1430                1435                1440
Pro Val Ala Leu Lys Leu Pro Glu Arg Asn Thr Pro Arg Asn Ser His
                1445                1450                1455
Cys His Leu Ser Asn Ser Pro Arg Ala Ile Glu His Ala Tyr Gln Tyr
            1460                1465                1470
Gly Gly Thr Ala Asn Ser Arg Gln Glu Phe Glu His Leu Lys Gly Asp
```

```
        1475                1480                1485
Phe Gly Ala Lys Ser Gln Phe Ser Ile Arg Leu Arg Thr Arg Ser Ser
    1490                1495                1500
His Gly Met Ile Phe Tyr Val Ser Asp Gln Glu Glu Asn Asp Phe Met
1505                1510                1515                1520
Thr Leu Phe Leu Ala His Gly Arg Leu Val Tyr Met Phe Asn Val Gly
                1525                1530                1535
His Lys Lys Leu Lys Ile Arg Ser Gln Glu Lys Tyr Asn Asp Gly Leu
            1540                1545                1550
Trp His Asp Val Ile Phe Ile Arg Glu Arg Ser Ser Gly Arg Leu Val
        1555                1560                1565
Ile Asp Gly Leu Arg Val Leu Glu Glu Ser Leu Pro Pro Thr Glu Ala
    1570                1575                1580
Thr Trp Lys Ile Lys Gly Pro Ile Tyr Leu Gly Gly Val Ala Pro Gly
1585                1590                1595                1600
Lys Ala Val Lys Asn Val Gln Ile Asn Ser Ile Tyr Ser Phe Ser Gly
                1605                1610                1615
Cys Leu Ser Asn Leu Gln Leu Asn Gly Ala Ser Ile Thr Ser Ala Ser
            1620                1625                1630
Gln Thr Phe Ser Val Thr Pro Cys Phe Glu Gly Pro Met Glu Thr Gly
        1635                1640                1645
Thr Tyr Phe Ser Thr Glu Gly Gly Tyr Val Val Leu Asp Glu Ser Phe
    1650                1655                1660
Asn Ile Gly Leu Lys Phe Glu Ile Ala Phe Glu Val Arg Pro Arg Ser
1665                1670                1675                1680
Ser Ser Gly Thr Leu Val His Gly His Ser Val Asn Gly Glu Tyr Leu
                1685                1690                1695
Asn Val His Met Lys Asn Gly Gln Val Ile Val Lys Val Asn Asn Gly
            1700                1705                1710
Ile Arg Asp Phe Ser Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp
        1715                1720                1725
Gly Arg Trp His Arg Ile Thr Val Ile Arg Asp Ser Asn Val Val Gln
    1730                1735                1740
Leu Asp Val Asp Ser Glu Val Asn His Val Val Gly Pro Leu Asn Pro
1745                1750                1755                1760
Lys Pro Ile Asp His Arg Glu Pro Val Phe Val Gly Gly Val Pro Glu
                1765                1770                1775
Ser Leu Leu Thr Pro Arg Leu Ala Pro Ser Lys Pro Phe Thr Gly Cys
            1780                1785                1790
Ile Arg His Phe Val Ile Asp Gly His Pro Val Ser Phe Ser Lys Ala
        1795                1800                1805
Ala Leu Val Ser Gly Ala Val Ser Ile Asn Ser Cys Pro Ala Ala
    1810                1815                1820


<210> 28
<211> 1816
<212> PRT
<213> Homo sapiens

<400> 28
Met Ala Leu Ser Ser Ala Trp Arg Ser Val Leu Pro Leu Trp Leu Leu
 1               5                  10                  15
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Trp Ser Ala Ala Cys Ser Arg Ala Ala Ser Gly Asp Asp Asn Ala Phe
            20                  25                  30
Pro Phe Asp Ile Glu Gly Ser Ser Ala Val Gly Arg Gln Asp Pro Pro
        35                  40                  45
Glu Thr Ser Glu Pro Arg Val Ala Leu Gly Arg Leu Pro Pro Ala Ala
    50                  55                  60
Glu Lys Cys Asn Ala Gly Phe Phe His Thr Leu Ser Gly Glu Cys Val
65                  70                  75                  80
Pro Cys Asp Cys Asn Gly Asn Ser Asn Glu Cys Leu Asp Gly Ser Gly
                85                  90                  95
Tyr Cys Val His Cys Gln Arg Asn Thr Thr Gly Glu His Cys Glu Lys
            100                 105                 110
Cys Leu Asp Gly Tyr Ile Gly Asp Ser Ile Arg Gly Ala Pro Gln Phe
        115                 120                 125
Cys Gln Pro Cys Pro Cys Pro Leu Pro His Leu Ala Asn Phe Ala Glu
    130                 135                 140
Ser Cys Tyr Arg Lys Asn Gly Ala Val Arg Cys Ile Cys Asn Glu Asn
145                 150                 155                 160
Tyr Ala Gly Pro Asn Cys Glu Arg Cys Ala Pro Gly Tyr Tyr Gly Asn
                165                 170                 175
Pro Leu Leu Ile Gly Ser Thr Cys Lys Lys Cys Asp Cys Ser Gly Asn
            180                 185                 190
Ser Asp Pro Asn Leu Ile Phe Glu Asp Cys Asp Glu Val Thr Gly Gln
        195                 200                 205
Cys Arg Asn Cys Leu Arg Asn Thr Thr Gly Phe Lys Cys Glu Arg Cys
    210                 215                 220
Ala Pro Gly Tyr Tyr Gly Asp Ala Arg Ile Ala Lys Asn Cys Ala Val
225                 230                 235                 240
Cys Asn Cys Gly Gly Gly Pro Cys Asp Ser Val Thr Gly Glu Cys Leu
                245                 250                 255
Glu Glu Gly Phe Glu Pro Pro Thr Gly Cys Asp Lys Cys Val Trp Asp
            260                 265                 270
Leu Thr Asp Asp Leu Arg Leu Ala Ala Leu Ser Ile Glu Glu Gly Lys
        275                 280                 285
Ser Gly Val Leu Ser Val Ser Ser Gly Ala Ala Ala His Arg His Val
    290                 295                 300
Asn Glu Ile Asn Ala Thr Ile Tyr Leu Leu Lys Thr Lys Leu Ser Glu
305                 310                 315                 320
Arg Glu Asn Gln Tyr Ala Leu Arg Lys Ile Gln Ile Asn Asn Ala Glu
                325                 330                 335
Asn Thr Met Lys Ser Leu Leu Ser Asp Val Glu Glu Leu Val Glu Lys
            340                 345                 350
Glu Asn Gln Ala Ser Arg Lys Gly Gln Leu Val Gln Lys Glu Ser Met
        355                 360                 365
Asp Thr Ile Asn His Ala Ser Gln Leu Val Glu Gln Ala His Asp Met
    370                 375                 380
Arg Asp Lys Ile Gln Glu Ile Asn Asn Lys Met Leu Tyr Tyr Gly Glu
385                 390                 395                 400
Glu His Glu Leu Ser Pro Lys Glu Ile Ser Glu Lys Leu Val Leu Ala
                405                 410                 415
Gln Lys Met Leu Glu Glu Ile Arg Ser Arg Gln Pro Phe Phe Thr Gln
            420                 425                 430
Arg Glu Leu Val Asp Glu Glu Ala Asp Glu Ala Tyr Glu Leu Leu Ser
```

```
        435                 440                 445
Gln Ala Glu Ser Trp Gln Arg Leu His Asn Glu Thr Arg Thr Leu Phe
    450                 455                 460
Pro Val Val Leu Glu Gln Leu Asp Asp Tyr Asn Ala Lys Leu Ser Asp
465                 470                 475                 480
Leu Gln Glu Ala Leu Asp Gln Ala Leu Asn Tyr Val Arg Asp Ala Glu
                485                 490                 495
Asp Met Asn Arg Ala Thr Ala Ala Arg Gln Arg Asp His Glu Lys Gln
            500                 505                 510
Gln Glu Arg Val Arg Glu Gln Met Glu Val Val Asn Met Ser Leu Ser
        515                 520                 525
Thr Ser Ala Asp Ser Leu Thr Thr Pro Arg Leu Thr Leu Ser Glu Leu
    530                 535                 540
Asp Asp Ile Ile Lys Asn Ala Ser Gly Ile Tyr Ala Glu Ile Asp Gly
545                 550                 555                 560
Ala Lys Ser Glu Leu Gln Val Lys Leu Ser Asn Leu Ser Asn Leu Ser
                565                 570                 575
His Asp Leu Val Gln Glu Ala Ile Asp His Ala Gln Asp Leu Gln Gln
            580                 585                 590
Glu Ala Asn Glu Leu Ser Arg Lys Leu His Ser Ser Asp Met Asn Gly
        595                 600                 605
Leu Val Gln Lys Ala Leu Asp Ala Ser Asn Val Tyr Glu Asn Ile Val
    610                 615                 620
Asn Tyr Val Ser Glu Ala Asn Glu Thr Ala Glu Phe Ala Leu Asn Thr
625                 630                 635                 640
Thr Asp Arg Ile Tyr Asp Ala Val Ser Gly Ile Asp Thr Gln Ile Ile
                645                 650                 655
Tyr His Lys Asp Glu Ser Glu Asn Leu Leu Asn Gln Ala Arg Glu Leu
            660                 665                 670
Gln Ala Lys Ala Glu Ser Ser Ser Asp Glu Ala Val Ala Asp Thr Ser
        675                 680                 685
Arg Arg Val Gly Gly Ala Leu Ala Arg Lys Ser Ala Leu Lys Thr Arg
    690                 695                 700
Leu Ser Asp Ala Val Lys Gln Leu Gln Ala Ala Glu Arg Gly Asp Ala
705                 710                 715                 720
Gln Gln Arg Leu Gly Gln Ser Arg Leu Ile Thr Glu Glu Ala Asn Arg
                725                 730                 735
Thr Thr Met Glu Val Gln Gln Ala Thr Ala Pro Met Ala Asn Asn Leu
            740                 745                 750
Thr Asn Trp Ser Gln Asn Leu Gln His Phe Asp Ser Ser Ala Tyr Asn
        755                 760                 765
Thr Ala Val Asn Ser Ala Arg Asp Ala Val Arg Asn Leu Thr Glu Val
    770                 775                 780
Val Pro Gln Leu Leu Asp Gln Leu Arg Thr Val Glu Gln Lys Arg Pro
785                 790                 795                 800
Ala Ser Asn Val Ser Ala Ser Ile Gln Arg Ile Arg Glu Leu Ile Ala
                805                 810                 815
Gln Thr Arg Ser Val Ala Ser Lys Ile Gln Val Ser Met Met Phe Asp
            820                 825                 830
Gly Gln Ser Ala Val Glu Val His Ser Arg Thr Ser Met Asp Asp Leu
        835                 840                 845
Lys Ala Phe Thr Ser Leu Ser Leu Tyr Met Lys Pro Pro Val Lys Arg
    850                 855                 860
```

```
Pro Glu Leu Thr Glu Thr Ala Asp Gln Phe Ile Leu Tyr Leu Gly Ser
865                 870                 875                 880
Lys Asn Ala Lys Lys Glu Tyr Met Gly Leu Ala Ile Lys Asn Asp Asn
                885                 890                 895
Leu Val Tyr Val Tyr Asn Leu Gly Thr Lys Asp Val Glu Ile Pro Leu
            900                 905                 910
Asp Ser Lys Pro Val Ser Ser Trp Pro Ala Tyr Phe Ser Ile Val Lys
        915                 920                 925
Ile Glu Arg Val Gly Lys His Gly Lys Val Phe Leu Thr Val Pro Ser
    930                 935                 940
Leu Ser Ser Thr Ala Glu Glu Lys Phe Ile Lys Lys Gly Glu Phe Ser
945                 950                 955                 960
Gly Asp Asp Ser Leu Leu Asp Leu Asp Pro Glu Asp Thr Val Phe Tyr
                965                 970                 975
Val Gly Gly Val Pro Ser Asn Phe Lys Leu Pro Thr Ser Leu Asn Leu
            980                 985                 990
Pro Gly Phe Val Gly Cys Leu Glu Leu Ala Thr Leu Asn Asn Asp Val
        995                 1000                1005
Ile Ser Leu Tyr Asn Phe Lys His Ile Tyr Asn Met Asp Pro Ser Thr
    1010                1015                1020
Ser Val Pro Cys Ala Arg Asp Lys Leu Ala Phe Thr Gln Ser Arg Ala
1025                1030                1035                1040
Ala Ser Tyr Phe Phe Asp Gly Ser Gly Tyr Ala Val Val Arg Asp Ile
                1045                1050                1055
Thr Arg Arg Gly Lys Phe Gly Gln Val Thr Arg Phe Asp Ile Glu Val
            1060                1065                1070
Arg Thr Pro Ala Asp Asn Gly Leu Ile Leu Leu Met Val Asn Gly Ser
        1075                1080                1085
Met Phe Phe Arg Leu Glu Met Arg Asn Gly Tyr Leu His Val Phe Tyr
    1090                1095                1100
Asp Phe Gly Phe Ser Gly Gly Pro Val His Leu Glu Asp Thr Leu Lys
1105                1110                1115                1120
Lys Ala Gln Ile Asn Asp Ala Lys Tyr His Glu Ile Ser Ile Ile Tyr
                1125                1130                1135
His Asn Asp Lys Lys Met Ile Leu Val Val Asp Arg Arg His Val Lys
            1140                1145                1150
Ser Met Asp Asn Glu Lys Met Lys Ile Pro Phe Thr Asp Ile Tyr Ile
        1155                1160                1165
Gly Gly Ala Pro Pro Glu Ile Leu Gln Ser Arg Ala Leu Arg Ala His
    1170                1175                1180
Leu Pro Leu Asp Ile Asn Phe Arg Gly Cys Met Lys Gly Phe Gln Phe
1185                1190                1195                1200
Gln Lys Lys Asp Phe Asn Leu Leu Glu Gln Thr Glu Thr Leu Gly Val
                1205                1210                1215
Gly Tyr Gly Cys Pro Glu Asp Ser Leu Ile Ser Arg Arg Ala Tyr Phe
            1220                1225                1230
Asn Gly Gln Ser Phe Ile Ala Ser Ile Gln Lys Ile Ser Phe Phe Asp
        1235                1240                1245
Gly Phe Glu Gly Gly Phe Asn Phe Arg Thr Leu Gln Pro Asn Gly Leu
    1250                1255                1260
Leu Phe Tyr Tyr Ala Ser Gly Ser Asp Val Phe Ser Ile Ser Leu Asp
1265                1270                1275                1280
Asn Gly Thr Val Ile Met Asp Val Lys Gly Ile Lys Val Gln Ser Val
```

```
                1285                1290                1295
Asp Lys Gln Tyr Asn Asp Gly Leu Ser His Phe Val Ile Ser Ser Val
            1300                1305                1310
Ser Pro Thr Arg Tyr Glu Leu Ile Val Asp Lys Ser Arg Val Gly Ser
        1315                1320                1325
Lys Asn Pro Thr Lys Gly Lys Ile Glu Gln Thr Gln Ala Ser Glu Lys
    1330                1335                1340
Lys Phe Tyr Phe Gly Gly Ser Pro Ile Ser Ala Gln Tyr Ala Asn Phe
1345                1350                1355                1360
Thr Gly Cys Ile Ser Asn Ala Tyr Phe Thr Arg Val Asp Arg Asp Val
                1365                1370                1375
Glu Val Glu Asp Phe Gln Arg Tyr Thr Glu Lys Val His Thr Ser Leu
            1380                1385                1390
Tyr Glu Cys Pro Ile Glu Ser Ser Pro Leu Phe Leu Leu His Lys Lys
        1395                1400                1405
Gly Lys Asn Leu Ser Lys Pro Lys Ala Ser Gln Asn Lys Lys Gly Gly
    1410                1415                1420
Lys Ser Lys Asp Ala Pro Ser Trp Asp Pro Val Ala Leu Lys Leu Pro
1425                1430                1435                1440
Glu Arg Asn Thr Pro Arg Asn Ser His Cys His Leu Ser Asn Ser Pro
                1445                1450                1455
Arg Ala Ile Glu His Ala Tyr Gln Tyr Gly Gly Thr Ala Asn Ser Arg
            1460                1465                1470
Gln Glu Phe Glu His Leu Lys Gly Asp Phe Gly Ala Lys Ser Gln Phe
        1475                1480                1485
Ser Ile Arg Leu Arg Thr Arg Ser Ser His Gly Met Ile Phe Tyr Val
    1490                1495                1500
Ser Asp Gln Glu Glu Asn Asp Phe Met Thr Leu Phe Leu Ala His Gly
1505                1510                1515                1520
Arg Leu Val Tyr Met Phe Asn Val Gly His Lys Lys Leu Lys Ile Arg
                1525                1530                1535
Ser Gln Glu Lys Tyr Asn Asp Gly Leu Trp His Asp Val Ile Phe Ile
            1540                1545                1550
Arg Glu Arg Ser Ser Gly Arg Leu Val Ile Asp Gly Leu Arg Val Leu
        1555                1560                1565
Glu Glu Ser Leu Pro Pro Thr Glu Ala Thr Trp Lys Ile Lys Gly Pro
    1570                1575                1580
Ile Tyr Leu Gly Gly Val Ala Pro Gly Lys Ala Val Lys Asn Val Gln
1585                1590                1595                1600
Ile Asn Ser Ile Tyr Ser Phe Ser Gly Cys Leu Ser Asn Leu Gln Leu
                1605                1610                1615
Asn Gly Ala Ser Ile Thr Ser Ala Ser Gln Thr Phe Ser Val Thr Pro
            1620                1625                1630
Cys Phe Glu Gly Pro Met Glu Thr Gly Thr Tyr Phe Ser Thr Glu Gly
        1635                1640                1645
Gly Tyr Val Val Leu Asp Glu Ser Phe Asn Ile Gly Leu Lys Phe Glu
    1650                1655                1660
Ile Ala Phe Glu Val Arg Pro Arg Ser Ser Ser Gly Thr Leu Val His
1665                1670                1675                1680
Gly His Ser Val Asn Gly Glu Tyr Leu Asn Val His Met Lys Asn Gly
                1685                1690                1695
Gln Val Ile Val Lys Val Asn Asn Gly Ile Arg Asp Phe Ser Thr Ser
            1700                1705                1710
```

```
Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Arg Trp His Arg Ile Thr
        1715                1720                1725
Val Ile Arg Asp Ser Asn Val Val Gln Leu Asp Val Asp Ser Glu Val
    1730                1735                1740
Asn His Val Val Gly Pro Leu Asn Pro Lys Pro Ile Asp His Arg Glu
1745                1750                1755                1760
Pro Val Phe Val Gly Gly Val Pro Glu Ser Leu Leu Thr Pro Arg Leu
                1765                1770                1775
Ala Pro Ser Lys Pro Phe Thr Gly Cys Ile Arg His Phe Val Ile Asp
            1780                1785                1790
Gly His Pro Val Ser Phe Ser Lys Ala Ala Leu Val Ser Gly Ala Val
        1795                1800                1805
Ser Ile Asn Ser Cys Pro Ala Ala
    1810                1815


<210> 29
<211> 334
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1174.1.3 - variable Light Chain


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

<400> 29
gac att gtg ctg aca cag tct cct gct tcc tta gct gta tct ctg ggg   48
Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15

cag agg gcc acc atc tca tgc agg gcc agc aaa agt gtc agt aca tct   96
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
             20                  25                  30

ggc tat agt tat atg tac tgg tac caa cag aaa cca gga cag cca ccc   144
Gly Tyr Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
         35                  40                  45

aaa ctc ctc atc tat ctt gca tcc aac cta gaa tct ggg gtc cct gcc   192
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
     50                  55                  60

agg ttc agt ggc agt ggg tct ggg aca gac ttc acc ctc aac atc cat   240
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65                  70                  75                  80
```

```
cct gtg gag gag gag gat gct gca acc tat tac tgt caa cac agt agg   288
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                 85                  90                  95

gag ctt cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa       333
Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

c                                                   334
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<210> 30
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 30

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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
 1               5                  10                  15
Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser
            20                  25                  30
Gly Tyr Ser Tyr Met Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
    50                  55                  60
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80
Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg
                85                  90                  95
Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> clone 1174.1.3 - CDR-L1

<400> 31

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Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr Met Tyr
 1               5                  10                  15
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<210> 32

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

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1174.1.3 - CDR-L2

<400> 32
Ala Ser Asn Leu Glu Ser
 1   5

<210> 33
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1174.1.3 - CDR-L3

<400> 33
Gln His Ser Arg Glu Leu Pro Phe Thr
 1   5

<210> 34
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> clone 1174.1.3 - Variable Heavy chain
<220>
<221> CDS
<222> (1)...(363)

<400> 34
cag att cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag   48
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1   5   10   15

aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc aca aac tat   96

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

gga atg aac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg   144
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
         35                  40                  45

ggc tgg ata aac acc tac act gga gag cca aca tat gct gat gac ttc   192
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
     50                  55                  60

aag gga cgg ttt gcc ttg tct ttg gaa acc tct gcc agc act gcc tat   240
Lys Gly Arg Phe Ala Leu Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65                  70                  75                  80

ttg cag atc aac aac ctc aaa aat gag gac atg gct aca tat ttc tgt   288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
                 85                  90                  95

gca aga tat agg tat aat aaa tac gag agg gct atg gac tac tgg ggt   336
Ala Arg Tyr Arg Tyr Asn Lys Tyr Glu Arg Ala Met Asp Tyr Trp Gly
            100                 105                 110

caa gga acc tca gtc acc gtc tcc tca                               363
Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120


<210> 35
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 35
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 Asn Tyr
            20                  25                  30
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
        35                  40                  45
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
    50                  55                  60
Lys Gly Arg Phe Ala Leu Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
65                  70                  75                  80
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Met Ala Thr Tyr Phe Cys
                85                  90                  95
Ala Arg Tyr Arg Tyr Asn Lys Tyr Glu Arg Ala Met Asp Tyr Trp Gly
            100                 105                 110
Gln Gly Thr Ser Val Thr Val Ser Ser
        115                 120
```

<210> 36
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1174.1.3 - CDR-H1

<400> 36
Gly Tyr Thr Phe Thr Asn Tyr Gly Met Asn
 1   5   10

<210> 37
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1174.1.3 - CDR-H2

<400> 37
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
 1   5   10   15
Gly

<210> 38
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1174.1.3 - CDR-H3

<400> 38
Tyr Arg Tyr Asn Lys Tyr Glu Arg Ala Met Asp Tyr
 1   5   10

<210> 39
<211> 338
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1414.1.2 - variable Light Chain

<220>
<221> CDS
<222> (1)...(336)

<400> 39
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gac att gtg atg tca cag tct cca tcc tcc ctg gct gtg tca gca gga   48
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 1               5                  10                  15

gag aag gtc act atg agc tgc aaa tcc agt cag agt ctg ctc aac agt   96
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Asn Ser
             20                  25                  30

agc acc cga aag aac ttc ttg gct tgg tac cag cag aaa cca ggg cag   144
Ser Thr Arg Lys Asn Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
         35                  40                  45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggg gtc   192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
     50                  55                  60

cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc   240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65                  70                  75                  80

atc agc agt gtg cag gct gaa gac ctg gca gtt tat tac tgc aag caa   288
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
                 85                  90                  95

tct tat aat cgg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa   336
Ser Tyr Asn Arg Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110

cg                                                                338
```

<210> 40
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Construct

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

<210> 41
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> clone 1414.1.2 - CDR-L1

<400> 41
Lys Ser Ser Gln Ser Leu Leu Asn Ser Ser Thr Arg Lys Asn Phe Leu
 1   5   10   15
Ala

<210> 42
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> clone 1414.1.2 - CDR-L2

<400> 42
Trp Ala Ser Thr Arg Glu Ser
 1   5

<210> 43
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1414.1.2 - CDR-L3

<400> 43
Lys Gln Ser Tyr Asn Arg Tyr Thr
 1   5

<210> 44
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1414.1.2 - variable Heavy chain

<220>
<221> CDS
<222> (1)...(351)

<400> 44
gag atc cag ctg cag cag act gga cct gag ctg gtg aag cct ggg gct   48
Glu Ile Gln Leu Gln Gln Thr Gly Pro Glu Leu Val Lys Pro Gly Ala
 1   5   10   15

tca gtg aag ata tcc tgc aag gct tct ggt tat tca ttc act gac tac   96
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Asp Tyr
             20   25   30

atc atg ctc tgg gtg aag cag agc cat gga aag agc ctt gag tgg att   144
Ile Met Leu Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
         35   40   45

gga aat att aat cct tac tct ggt agt agt ggc tac aat ctg aag ttc   192
Gly Asn Ile Asn Pro Tyr Ser Gly Ser Ser Gly Tyr Asn Leu Lys Phe
     50   55   60

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

```
atg cag ctc aac agt ctg aca tct gag gac tct gca gtc tat tac tgt   288
Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                 85                  90                  95

gca aga ggg aag gac ttt gct atg gac tac tgg ggt caa gga acc tca   336
Ala Arg Gly Lys Asp Phe Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser
            100                 105                 110

gtc acc gtc tcc tca                                               351
Val Thr Val Ser Ser
        115
```

<210> 45
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 45

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

<210> 46
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1414.1.2 - CDR-H1

<400> 46

```
Gly Tyr Ser Phe Thr Asp Tyr Ile Met Leu
```

1 5 10

<210> 47
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1414.1.2 - CDR-H2

<400> 47
Asn Ile Asn Pro Tyr Ser Gly Ser Ser Gly Tyr Asn Leu Lys Phe Lys
1 5 10 15
Gly

<210> 48
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1414.1.2 - CDR-H3

<400> 48
Gly Lys Asp Phe Ala Met Asp
1 5

<210> 49
<211> 322
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1415.1.1 - variable Light Chain

<220>
<221> CDS

<222> (1)...(321)

<400> 49
```
gac att gtg atg act cag tct cca gcc acc ctg tct gtg act cca gga   48
Asp Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
 1               5                  10                  15

gat aga gtc tct ctt tca tgc agg gcc agc cag agt att agc gac tac   96
Asp Arg Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asp Tyr
            20                  25                  30

tta cac tgg tat caa caa aaa tca cat gag tct cca agg ctt ctc atc   144
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
         35                  40                  45

aaa tat gct tcc caa tcc atc tct ggg atc ccc tcc agg ttc agt ggc   192
Lys Tyr Ala Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
     50                  55                  60

agt gga tca ggg tca gat ttc act ctc agt atc aac agt gtg gaa cct   240
Ser Gly Ser Gly Ser Asp Phe Thr Leu Ser Ile Asn Ser Val Glu Pro
 65                  70                  75                  80

gaa gat gtt gga gtg tat tac tgt caa aat ggt cac aac ttt cct cgg   288
Glu Asp Val Gly Val Tyr Tyr Cys Gln Asn Gly His Asn Phe Pro Arg
                85                  90                  95

acg ttc ggt gga ggc acc aag ctg gaa atc aaa c                    322
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

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

<220>
<223> Synthetic Construct

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 51
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1415.1.1 - CDR-L1

<400> 51
Arg Ala Ser Gln Ser Ile Ser Asp Tyr Leu His
1 5 10

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

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1415.1.1 - CDR-L2

<400> 52
Tyr Ala Ser Gln Ser Ile Ser
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1415.1.1 - CDR-L3

<400> 53
Gln Asn Gly His Asn Phe Pro Arg Thr
1 5

<210> 54
<211> 366
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1415.1.1 - variable Heavy chain

<220>
<221> CDS
<222> (1)...(366)

<400> 54
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cag gtc caa ctg cag cag cct ggg gct gag ctt gtg cag cct ggg gct   48
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Gln Pro Gly Ala
 1               5                  10                  15

cca gtg aag ctg tcc tgc aag gct tct ggc tac att ttc acc agc tac   96
Pro Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Ser Tyr
            20                  25                  30

tgg atg aac tgg gtg aag cag agg cct gga cga ggc ctc gag tgg att   144
Trp Met Asn Trp Val Lys Gln Arg Pro Gly Arg Gly Leu Glu Trp Ile
         35                  40                  45

gga agg att gat cct tcc gat agt aaa att cac tac aat caa aag ttc   192
Gly Arg Ile Asp Pro Ser Asp Ser Lys Ile His Tyr Asn Gln Lys Phe
     50                  55                  60

aaa gac aag gcc aca ctg act gta gac aga tcc tcc agc aca gcc tac   240
Lys Asp Lys Ala Thr Leu Thr Val Asp Arg Ser Ser Ser Thr Ala Tyr
 65                  70                  75                  80

atc caa ctc ggc agc ctg aca tct gag gac tct gcg gtc tat tat tgt   288
Ile Gln Leu Gly Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
                 85                  90                  95

gca aaa gag ggg ggt tta cga cgg ggg gac tat gct atg gac tac tgg   336
Ala Lys Glu Gly Gly Leu Arg Arg Gly Asp Tyr Ala Met Asp Tyr Trp
            100                 105                 110

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

<210> 55
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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

<210> 56
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> clone 1415.1.1 - CDR-H1

<400> 56
Gly Tyr Ile Phe Thr Ser Tyr Trp Met Asn
 1   5   10

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1415.1.1 - CDR-H2

<400> 57
Arg Ile Asp Pro Ser Asp Ser Lys Ile His Tyr Asn Gln Lys Phe Lys

```
 1               5                  10                  15
Asp
```

<210> 58
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1415.1.1 - CDR-H3

<400> 58

```
Glu Gly Gly Leu Arg Arg Gly Asp Tyr Ala Met Asp Tyr
 1               5                  10
```

<210> 59
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1749.1.3 - Variable Light Chain

<220>
<221> CDS
<222> (1)...(336)

<400> 59

```
gac att gtg atg tca cag tct cca tcc tcc ctg gct gtg tca gca gga   48
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 1               5                  10                  15

gag aag gtc act atg aac tgc aaa tcc agt cgg agt ctg ctc aac agt   96
Glu Lys Val Thr Met Asn Cys Lys Ser Ser Arg Ser Leu Leu Asn Ser
             20                  25                  30

aga atc cga aag aac tac ttg gct tgg tac cag cag aaa cca ggg cag   144
Arg Ile Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
         35                  40                  45

tct cct aaa ctg ctg atc tac tgg gca tcc act agg gaa tct ggg gtc   192
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
```

```
     50                  55                  60

cct gat cgc ttc aca ggc agt gga tct ggg aca gat ttc act ctc acc   240
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65                  70                  75                  80

atc agc agt gtg cag gct gaa gac ctg gca gtt tat tac tgc aag caa   288
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
                 85                  90                  95
tct tat aat ctg ctc acg ttc ggt gct ggg acc aag ctg gag ctg aaa   336
Ser Tyr Asn Leu Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105                 110

c                                                     337
```

<210> 60
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 60

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

<210> 61
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1749.1.3 - CDR-L1

<400> 61

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

<210> 62
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> clone 1749.1.3 - CDR-L2

<400> 62
Trp Ala Ser Thr Arg Glu Ser
 1   5

<210> 63
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1749.1.3 - CDR-L3

<400> 63
Lys Gln Ser Tyr Asn Leu Leu Thr
 1   5

<210> 64
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 1749.1.3 - variable Heavy chain

<220>

<221> CDS
<222> (1)...(360)

<400> 64
gac gtg aag ctg gtg gag tct ggg gga gac tta gtg aag cct gga ggg 48
Asp Val Lys Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 1   5   10   15

tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc agt agc tat 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30

atc atg tct tgg gtt cgt cag act ccg gag aag agg ctg gag tgg gtc 144
Ile Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
         35   40   45

gca acc att agt agt ggt ggt agt tcc acc tac tat cca gac agt gtg 192
Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
     50   55   60

aag ggc cga ttc acc atc tcc aga gac aat gcc aag aac acc ctg tac 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65   70   75   80

ctg caa atg agc agt ctg aag tct gag gac aca gcc atg tat tac tgt 288
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85   90   95

aca aga gat gat gat tac gac gta aag gta ttt gct tac tgg ggc caa 336
Thr Arg Asp Asp Asp Tyr Asp Val Lys Val Phe Ala Tyr Trp Gly Gln
            100   105   110

ggg act ctg gtc act gtc tct gca 360
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 65
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 65
Asp Val Lys Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 1   5   10   15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ile 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 Ser Ser 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 Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
Thr Arg Asp Asp Asp Tyr Asp Val Lys Val Phe Ala Tyr Trp Gly Gln
            100                 105                 110
Gly Thr Leu Val Thr Val Ser Ala
        115                 120
```

<210> 66
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Peptide

<220>
<223> Clone 1749.1.3 - CDR-H1

<400> 66
```
Gly Phe Thr Phe Ser Ser Tyr Ile Met Ser
 1               5                  10
```

<210> 67
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1749.1.3 - CDR-H2

<400> 67
```
Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val Lys
 1               5                  10                  15
Gly
```

<210> 68
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 1749.1.3 - CDR-H3

<400> 68
Asp Asp Asp Tyr Asp Val Lys Val Phe Ala Tyr
 1   5   10

<210> 69
<211> 319
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide
<220>
<223> Clone 2120.4.19 - variable Light Chain

<220>
<221> CDS
<222> (1)...(318)

<400> 69
gat atc cgg atg act cag tct cct tca ctc ctg tct gca tct gtg ggg   48
Asp Ile Arg Met Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1   5   10   15

gac aga gtc act ctc aac tgc aaa gca agt cag aat att tat aac agc   96
Asp Arg Val Thr Leu Asn Cys Lys Ala Ser Gln Asn Ile Tyr Asn Ser
             20   25   30

tta gcc tgg tat cag caa aag ctt gga gaa ggt ccc aaa gtc ctg att   144
Leu Ala Trp Tyr Gln Gln Lys Leu Gly Glu Gly Pro Lys Val Leu Ile
         35   40   45

ttt aat gca aac agt ttg caa acg ggc atc cca tca agg ttc agt ggc   192
Phe Asn Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser Arg Phe Ser Gly
     50   55   60

agt gga tct ggt aca gat ttc aca ctc acc atc agc agc ctg cag cct   240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65   70   75   80

gaa gat ttt gcc aca tat ttc tgc cag cag ttt tat agc ggg tac acg   288
Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Phe Tyr Ser Gly Tyr Thr
                 85   90   95

ttt gga gct ggg acc aag ctg gaa ctg aaa c   319
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 70
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

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

<210> 71
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> clone 2120.4.19 - variable Light Chain

<400> 71
Asp Ile Gln Val Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Leu Asn Cys Lys Ala Ser Gln Asn Ile Tyr Asn Ser
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Leu Gly Glu Gly Pro Lys Val Leu Ile
        35   40   45
Phe Asn Ala Asn Ser Leu Gln Thr Gly Ile 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 Phe Cys Gln Gln Phe Tyr Ser Gly Tyr Thr
                85   90   95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 72
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - variable Light chain

<400> 72
Asp Ile Val Leu Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Leu Asn Cys Lys Ala Ser Gln Asn Ile Tyr Asn Ser
            20   25   30
Leu Ala Trp Tyr Gln Gln Lys Leu Gly Glu Gly Pro Lys Val Leu Ile
        35   40   45
Phe Asn Ala Asn Ser Leu Gln Thr Gly Ile 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 Phe Cys Gln Gln Phe Tyr Ser Gly Tyr Thr
                85   90   95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 73
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - CDR-L1

<400> 73
Lys Ala Ser Gln Asn Ile Tyr Asn Ser Leu Ala
 1   5   10

<210> 74
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - CDR-L2

<400> 74
Asn Ala Asn Ser Leu Gln Thr
 1   5

<210> 75
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - CDR-L3
<400> 75
Gln Gln Phe Tyr Ser Gly Tyr Thr
 1   5

<210> 76
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 2120.4.19 - variable Heavy Chain

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

<400> 76
cag gtg cag ctg aag gag tca gga cct ggt ctg gtg cag ccc tca cag   48
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1   5   10   15

acc ctg tct ctc acc tgc act gtc tct gga ttc tca tta acc agc aat   96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20   25   30

ggt gta agc tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg att   144
Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
         35   40   45

```
gca gca ata tca tct ggt gga acc aca tat tat aat tca gcg ttc aaa   192
Ala Ala Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Asn Ser Ala Phe Lys
     50                  55                  60

tcc cga ctg agc atc agc agg aac acc tcc aag agc caa gtt ctc tta   240
Ser Arg Leu Ser Ile Ser Arg Asn Thr Ser Lys Ser Gln Val Leu Leu
 65                  70                  75                  80

aaa atg aac agt ctg caa act gaa gac aca gcc atg tac ttc tgt gcc   288
Lys Met Asn Ser Leu Gln Thr Glu Asp Thr Ala Met Tyr Phe Cys Ala
                 85                  90                  95

aga cgg tat ggg tac ggg tgg tac ttt gac ttc tgg ggc cca gga acc   336
Arg Arg Tyr Gly Tyr Gly Trp Tyr Phe Asp Phe Trp Gly Pro Gly Thr
            100                 105                 110

atg gtc aca gtc tcc tca                                          354
Met Val Thr Val Ser Ser
        115
```

<210> 77
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 77

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

<210> 78
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - CDR-H1

<400> 78
Gly Phe Ser Leu Thr Ser Asn Gly Val Ser
 1   5   10

<210> 79
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - CDR-H2

<400> 79
Ala Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Asn Ser Ala Phe Lys Ser
 1   5   10   15

<210> 80
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2120.4.19 - CDR-H3

<400> 80
Arg Tyr Gly Tyr Gly Trp Tyr Phe Asp Phe
 1   5   10

<210> 81
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 2107.4.10 - variable Light Chain

<220>
<221> CDS
<222> (1)...(318)

<400> 81
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gac atc cgg gtg act cag tct cct tca ctc ctg tct gca tct gtg gga   48
Asp Ile Arg Val Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1               5                  10                  15

gac aga gtc act ctc aac tgc aaa gga agt cag aat att tat aag agc   96
Asp Arg Val Thr Leu Asn Cys Lys Gly Ser Gln Asn Ile Tyr Lys Ser
             20                  25                  30

tta gcc tgg ttt cgg cta aag cgt gga gaa gct ccc aag ctc ctg att   144
Leu Ala Trp Phe Arg Leu Lys Arg Gly Glu Ala Pro Lys Leu Leu Ile
         35                  40                  45

tat gat gca aac agt ttg caa acg ggc atc cca tca agg ttc agt ggc   192
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser Arg Phe Ser Gly
     50                  55                  60

agt gga tct ggt aca gat ttc aca ctc acc atc acc agc cta cag cct   240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
 65                  70                  75                  80

gaa gat gtt gcc aca tat ttc tgc cag cag tat tat agc ggt tac acg   288
Glu Asp Val Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
                 85                  90                  95

ttt gga gct ggg acc aag ctg gaa ctg aaa                          318
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100                 105
```

<210> 82
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 82
```
Asp Ile Arg Val Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1               5                  10                  15
Asp Arg Val Thr Leu Asn Cys Lys Gly Ser Gln Asn Ile Tyr Lys Ser
            20                  25                  30
Leu Ala Trp Phe Arg Leu Lys Arg Gly Glu Ala Pro Lys Leu Leu Ile
        35                  40                  45
```

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


<210> 83
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 2107.4.10 - variable Light Chain


<220>
<221> CDS
<222> (1)...(318)

<400> 83
gac atc cag gtg act cag tct cct tca ctc ctg tct gca tct gtg gga   48
Asp Ile Gln Val Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1               5                  10                  15

gac aga gtc act ctc aac tgc aaa gga agt cag aat att tat aag agc   96
Asp Arg Val Thr Leu Asn Cys Lys Gly Ser Gln Asn Ile Tyr Lys Ser
             20                  25                  30

tta gcc tgg ttt cgg cta aag cgt gga gaa gct ccc aag ctc ctg att   144
Leu Ala Trp Phe Arg Leu Lys Arg Gly Glu Ala Pro Lys Leu Leu Ile
         35                  40                  45

tat gat gca aac agt ttg caa acg ggc atc cca tca agg ttc agt ggc   192
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser Arg Phe Ser Gly
     50                  55                  60

agt gga tct ggt aca gat ttc aca ctc acc atc acc agc cta cag cct   240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
 65                  70                  75                  80

gaa gat gtt gcc aca tat ttc tgc cag cag tat tat agc ggt tac acg   288
Glu Asp Val Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
                 85                  90                  95

ttt gga gct ggg acc aag ctg gaa ctg aaa                          318
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
```

100 105

<210> 84
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 84
Asp Ile Gln Val Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
1 5 10 15
Asp Arg Val Thr Leu Asn Cys Lys Gly Ser Gln Asn Ile Tyr Lys Ser
20 25 30
Leu Ala Trp Phe Arg Leu Lys Arg Gly Glu Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
65 70 75 80
Glu Asp Val Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
85 90 95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105

<210> 85
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2107.4.10 - CDR-L1

<400> 85
Lys Gly Ser Gln Asn Ile Tyr Lys Ser Leu Ala
1 5 10

<210> 86
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2107.4.10 - CDR-L2

<400> 86
Asp Ala Asn Ser Leu Gln Thr
 1   5

<210> 87
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2107.4.10 - CDR-L3

<400> 87
Gln Gln Tyr Tyr Ser Gly Tyr Thr
 1   5

<210> 88
<211> 348
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Polynucleotide

<220>
<223> Clone 2107.4.10 - variable Heavy Chain

<220>
<221> CDS
<222> (1)...(348)

<400> 88
cag gtg cag ctg aag gag tca gga cct ggt ctg gtg cag tcc tca cag   48
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Gln Ser Ser Gln
 1   5   10   15

acc ctg tct ctc acc tgc act gtc tct gga ttc tca tta acc agt aat   96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
             20   25   30

ggt gta agc tgg gtt cgc cag cct cca gga aag ggt ctg gag tgg att   144
Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile

```
         35                  40                  45

gca gca ata tca agt ggt gga agc aca tat tat aat tca gcg ttc aaa   192
Ala Ala Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Asn Ser Ala Phe Lys
     50                  55                  60

tcc cga ctg agc atc agc agg aac acc tcc aag agc caa gtt ctc tta   240
Ser Arg Leu Ser Ile Ser Arg Asn Thr Ser Lys Ser Gln Val Leu Leu
 65                  70                  75                  80

aaa atg aac agt ctg caa act gaa gac aca ggc atg tac ttc tgt gcc   288
Lys Met Asn Ser Leu Gln Thr Glu Asp Thr Gly Met Tyr Phe Cys Ala
                85                  90                  95

aga cat aga ccg ttc tac ttt gat tac tgg ggc caa gga gtc atg gtc   336
Arg His Arg Pro Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Val Met Val
            100                 105                 110

aca gtc tcc tca                                                  348
Thr Val Ser Ser
        115
```

<210> 89
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 89

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

<210> 90
<211> 10
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2107.4.10 - CDR-H1

<400> 90
Gly Phe Ser Leu Thr Ser Asn Gly Val Ser
 1   5   10

<210> 91
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<220>
<223> Clone 2107.4.10 - CDR-H2

<400> 91
Ala Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Asn Ser Ala Phe Lys Ser
 1   5   10   15

<210> 92
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Peptide

<220>
<223> Clone 2107.4.10 - CDR-H3

<400> 92
His Arg Pro Phe Tyr Phe Asp Tyr
 1   5

<210> 93
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthetic Peptide

<400> 93
Asp Val Lys Leu Val Glu Ser Gly Gly Asp Leu Val Lys Pro Gly Gly
 1   5   10   15
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ile 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 Ser Ser 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 Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85   90   95
Thr Arg Asp Asp Asp Tyr Asp Val Lys Val Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Leu Val Thr Val Ser Ala
        115   120

<210> 94
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 94
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ile 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 Ser Ser Thr Tyr Tyr Pro Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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
Thr Arg Asp Asp Asp Tyr Asp Val Lys Val Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 95
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 95
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Ile Met Ser Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val
        35   40   45
Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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
Thr Arg Asp Asp Asp Tyr Asp Val Lys Val Phe Ala Tyr Trp Gly Gln
            100   105   110
Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 96
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 96
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1   5   10   15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20   25   30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
    50   55   60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser 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 Asp Gly Ala Ile Phe Gly Val Val Ser His Ile Trp Gly Gln
            100   105   110
Gly Thr Met Val Thr Val Ser Ser
        115   120

<210> 97
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 97
Asp Ile Val Met Ser Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly
 1   5   10   15
Glu Lys Val Thr Met Asn Cys Lys Ser Ser Arg Ser Leu Leu Asn Ser
            20   25   30
Arg Ile Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Lys Gln
                85   90   95
Ser Tyr Asn Leu Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105   110

<210> 98
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 98
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Arg Ser Leu Leu Asn Ser
            20   25   30
Arg Ile Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95
Ser Tyr Asn Leu Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 99
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 99
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1   5   10   15
Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Arg Ser Leu Leu Asn Ser
            20   25   30
Arg Ile Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50   55   60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65   70   75   80
Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Lys Gln
                85   90   95
Ser Tyr Asn Leu Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 100
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

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

<210> 101
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 101
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Gln Ser Ser Gln
 1   5   10   15

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

<210> 102
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 102

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

<210> 103
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 103

```
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
```

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

<210> 104
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 104

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

<210> 105
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 105

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

<210> 106
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 106

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

<210> 107
<211> 116
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 107
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20   25   30
Ala Val Ser Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Ile
        35   40   45
Ala Ala Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Asn Ser Ala Phe Lys
    50   55   60
Ser Arg Leu Thr Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Val Leu
65   70   75   80
Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala
                85   90   95
Arg His Arg Pro Phe Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
            100   105   110
Thr Val Ser Ser
        115

<210> 108
<211> 131
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 108
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser Asn Ala
            20   25   30
Arg Met Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
        35   40   45
Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
    50   55   60
Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Ser Gln Val
65   70   75   80
Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85   90   95
Cys Ala Arg Ile Gly Glu Ser Ala Ser Asp Arg Tyr Cys Ser Gly Gly
            100   105   110
Ser Cys Phe Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
        115   120   125
Val Ser Ser
    130

<210> 109
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 109
Asp Ile Gln Val Thr Gln Ser Pro Ser Leu Leu Ser Ala Ser Val Gly
 1   5   10   15
Asp Arg Val Thr Leu Asn Cys Lys Gly Ser Gln Asn Ile Tyr Lys Ser
            20   25   30
Leu Ala Trp Phe Arg Leu Lys Arg Gly Glu Ala Pro Lys Leu Leu Ile
        35   40   45
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile Pro Ser Arg Phe Ser Gly
    50   55   60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr Ser Leu Gln Pro
65   70   75   80
Glu Asp Val Ala Thr Tyr Phe Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
                85   90   95
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
            100   105

<210> 110
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 110
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 Gly Ser Gln Asn Ile Tyr Lys Ser
            20   25   30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35   40   45
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
                85   90   95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 111
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide
<400> 111

```
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 Gly Ser Gln Asn Ile Tyr Lys Ser
            20                  25                  30
Leu Ala Trp Phe Gln Leu Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 112
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 112

```
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 Asn Cys Lys Gly Ser Gln Asn Ile Tyr Lys Ser
            20                  25                  30
Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Asp Ala Asn Ser Leu Gln Thr Gly Ile 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 Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Gly Tyr Thr
                85                  90                  95
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 113
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 113

```
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 Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile
        35                  40                  45
Tyr Ala Ala Ser Thr 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 Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Asn Ser Ala Pro Pro
                85                  90                  95
Leu Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 114
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 114
Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Gln Pro Ser Gln
 1               5                  10                  15
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30
Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45
Ala Ala Ile Ser Ser Gly Gly Thr Thr Tyr Tyr Asn Ser Ala Phe Lys
    50                  55                  60
Ser Arg Leu Ser Ile Ser Arg Asn Thr Ser Lys Ser Gln Val Leu Leu
65                  70                  75                  80
Lys Met Asn Ser Leu Gln Thr Glu Asp Thr Ala Met Tyr Phe Cys Ala
                85                  90                  95
Arg Arg Tyr Gly Tyr Gly Trp Tyr Phe Asp Phe Trp Gly Pro Gly Thr
            100                 105                 110
Met Val Thr Val Ser Ser
        115


<210> 115
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 115
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
            20                  25                  30
```

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


<210> 116
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

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


<210> 117
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 117
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1               5                  10                  15
Thr Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Ser
```

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

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

<220>
<223> Synthetic Peptide

<400> 118

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

<210> 119
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 119

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

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

<210> 120
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 120

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

<210> 121
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 121

```
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 Asn Ile Tyr Asn Ser
```

```
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35                  40                  45
Phe Asn Ala Asn Ser Leu Gln Thr Gly Ile 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 Phe Tyr Ser Gly Tyr Thr
                85                  90                  95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 122
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 122
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 Asn Ile Tyr Asn Ser
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35                  40                  45
Phe Asn Ala Asn Ser Leu Gln Thr 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 Phe Tyr Ser Gly Tyr Thr
                85                  90                  95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 123
<211> 106
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 123
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 Asn Cys Lys Ala Ser Gln Asn Ile Tyr Asn Ser
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
        35                  40                  45
```

```
Phe Asn Ala Asn Ser Leu Gln Thr Gly Ile 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 Phe Tyr Ser Gly Tyr Thr
                85                  90                  95
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 124
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 124

```
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 Ser Ile Ser Ser Tyr
            20                  25                  30
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu 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 Ser Tyr Ser Thr Pro Arg
                85                  90                  95
Ser Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 125
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 125

```
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
 1               5                  10
```

<210> 126
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 126
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
 1   5   10   15
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Thr Arg
            20   25   30

<210> 127
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 127
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
 1   5   10

<210> 128
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 128
Trp Val Arg Gln Ala Pro Gly Lys Arg Leu Glu Trp Val Ala
 1   5   10

<210> 129
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 129
Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr
 1   5   10   15

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

<220>
<223> Synthetic Peptide

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

<210> 131
<211> 10
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Peptide

<400> 131
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 1   5   10

<210> 132
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 132
Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
            20   25   30

<210> 133
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 133
Gln Val Thr Leu Lys Glu Ser Gly Pro Val Leu Val Lys Pro Thr Glu
 1   5   10   15
Thr Leu Thr Leu Thr Cys Thr Val Ser
            20   25

<210> 134

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

<220>
<223> Synthetic Peptide

<400> 134
Trp Val Arg Gln Pro Pro Gly Lys Ala Leu Glu Trp Ile Ala
 1   5   10

<210> 135
<211> 32
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Peptide

<400> 135
Arg Leu Thr Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Val Leu Thr
 1   5   10   15
Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
            20   25   30

<210> 136
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 136
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 1   5   10

<210> 137
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 137
Arg Leu Ser Ile Ser Arg Asp Thr Ser Lys Ser Gln Val Val Leu Thr
 1   5   10   15
Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
            20   25   30

<210> 138
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 138
Arg Leu Thr Ile Ser Arg Asn Thr Ser Lys Ser Gln Val Val Leu Thr
 1   5   10   15
Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg
            20   25   30

<210> 139
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 139
Gly Phe Ser Leu Thr Ser Ser Gly Val Ser
 1   5   10

<210> 140
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 140
Gly Phe Ser Leu Thr Ser Gln Gly Val Ser
 1   5   10

<210> 141
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 141
Gly Phe Ser Leu Thr Ser Asn Ala Val Ser
 1   5   10

<210> 142
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 142
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
            20

<210> 143
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 143
Trp Phe Gln Gln Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
 1   5   10   15

<210> 144
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 144
Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
 1   5   10   15
Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys
            20   25   30

<210> 145
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 145
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys

1 5 10

<210> 146
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 146
Trp Phe Gln Leu Lys Pro Gly Lys Val Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 147
<211> 23
<212> PRT
<213> Artificial Sequence
<220>
<223> Synthetic Peptide

<400> 147
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 Asn Cys
20

<210> 148
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Peptide

<400> 148
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile Phe
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<210> 149
<211> 32
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<220>
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<400> 149
Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

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<211> 10
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<213> Artificial Sequence

<220>
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<210> 151
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<213> Artificial Sequence
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Ser Asn Gly Val Ser
 1               5


<210> 152
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<213> Artificial Sequence

<220>
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Ser Ser Gly Val Ser
 1               5


<210> 153
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<210> 154
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<220>
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<400> 155
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Ser Leu Arg Leu Ser Cys Ala Ala Ser
            20                  25
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