SEQUENCE LISTING

<110> Neurimmune Holding AG

<120> Human-derived anti-dipeptide repeats (DPRs) antibody

<130> NE30A52/P-WO

<150> EP14187180.6
<151> 2014-09-30

<150> EP15180310.3
<151> 2015-08-07

<160> 86

<170> PatentIn version 3.5

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<213> Homo sapiens

<220>
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<223> NI-308.18F7-VH variable heavy chain (VH) sequence

<220>
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<223> complementarity determining region (CDR) VH-CDR1

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<223> complementarity determining region (CDR) VH-CDR2

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<222> (295)..(336)
<223> complementarity determining region (CDR) VH-CDR3

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

gag acc ctg tcc gtc acg tgc act gtc tct ggt ggc tcc atc aat gat 96
Glu Thr Leu Ser Val Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Asp
20 25 30

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tac tac tgg aac tgg atc cgg cag ccc gcc ggg aag gga ctg gag tgg        144
Tyr Tyr Trp Asn Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp
        35                  40                  45

att ggg cgt ata tat gcc agt ggg acc atc aat tac aac cct tcc ctc        192
Ile Gly Arg Ile Tyr Ala Ser Gly Thr Ile Asn Tyr Asn Pro Ser Leu
    50                  55                  60

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

cta gac ctc atc tct gtg tcc gcc gcg gac acg gcc gtc tac tat tgt        288
Leu Asp Leu Ile Ser Val Ser Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcg aga tgg ggc cag gtg gtc ggg gac tac tac tac ggg atg gac gtc        336
Ala Arg Trp Gly Gln Val Val Gly Asp Tyr Tyr Tyr Gly Met Asp Val
            100                 105                 110

tgg ggc cag ggg acc acg gtc acc gtc tcc tcg                            369
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 2
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<212> PRT
<213> Homo sapiens

<400> 2

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

Glu Thr Leu Ser Val Thr Cys Thr Val Ser Gly Gly Ser Ile Asn Asp
            20                  25                  30

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

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

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

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

Ala Arg Trp Gly Gln Val Val Gly Asp Tyr Tyr Tyr Gly Met Asp Val
            100                 105                 110


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


<210>  3
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<220>
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<222>  (1)..(336)
<223>  NI-308.18F7 VK variable light-kappa chain (VK) sequence

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<223>  complementarity determining region (CDR) VK-CDR1

<220>
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<222>  (166)..(186)
<223>  complementarity determining region (CDR) VK-CDR2

<220>
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<222>  (283)..(306)
<223>  complementarity determining region (CDR) VK-CDR3

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tgc gaa att gtg ctg act cag tct cca ctc tcc ctg tcc gtc acc cct         48
Cys Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Pro
1               5                   10                  15

gga gag ccg gcc tcc atc tcc tgc aag tct agt cag agc ctc caa cat         96
Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Gln His
            20                  25                  30

aca aat gga tac aat tac ttg gat tgg tac ctg ctg aag cca ggg cag        144
Thr Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln
        35                  40                  45

tct cca caa ctc cta atc ttc ttg act tct aat cgg gcc tcc ggg gtc        192
Ser Pro Gln Leu Leu Ile Phe Leu Thr Ser Asn Arg Ala Ser Gly Val
    50                  55                  60
```

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cct gac agg ttc agt ggc agt gga tca ggc aca aat ttt aca ctg aaa        240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Lys
65                  70                  75                  80

atc agc aga gtg gag gct gag gat gtt ggg gtc tat tat tgc atg gaa        288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Glu
                85                  90                  95

ggt ata caa ttg tgg acg ttc ggc caa ggg acc aag ctg gag atc aaa        336
Gly Ile Gln Leu Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4

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Cys Glu Ile Val Leu Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Pro
1               5                   10                  15

Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Gln His
            20                  25                  30

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

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

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

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

Gly Ile Gln Leu Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110
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<210> 5
<211> 336
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(336)
<223> NI-308.18F7 VK-PIMC variable light-kappa chain (VK) sequence
after correction of primer induced mutations

<220>
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<222> (73)..(120)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (166)..(186)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (283)..(306)
<223> complementarity determining region (CDR) VK-CDR3

<400> 5

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tgc gac atc gtg atg acc cag tct cca ctc tcc ctg tcc gtc acc cct        48
Cys Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Ser Val Thr Pro
1               5                  10                  15

gga gag ccg gcc tcc atc tcc tgc aag tct agt cag agc ctc caa cat        96
Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Gln His
            20                  25                  30

aca aat gga tac aat tac ttg gat tgg tac ctg ctg aag cca ggg cag       144
Thr Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Leu Lys Pro Gly Gln
        35                  40                  45

tct cca caa ctc cta atc ttc ttg act tct aat cgg gcc tcc ggg gtc       192
Ser Pro Gln Leu Leu Ile Phe Leu Thr Ser Asn Arg Ala Ser Gly Val
    50                  55                  60

cct gac agg ttc agt ggc agt gga tca ggc aca aat ttt aca ctg aaa       240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asn Phe Thr Leu Lys
65                  70                  75                  80

atc agc aga gtg gag gct gag gat gtt ggg gtc tat tat tgc atg gaa       288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Glu
                85                  90                  95

ggt ata caa ttg tgg acg ttc ggc caa ggg acc aag gtg gag atc aaa       336
Gly Ile Gln Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> 6
<211> 112
<212> PRT
<213> Homo sapiens

<400> 6

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

Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Gln His
20 25 30

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

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

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

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

Gly Ile Gln Leu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 7
<211> 372
<212> DNA
<213> Homo sapiens

<220>
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<223> NI-308.15O7 VH variable heavy chain (VH) sequence

<220>
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<223> complementarity determining region (CDR) VH-CDR1

<220>
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<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
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<223> complementarity determining region (CDR) VH-CDR3

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tgc cag gtg cag ctg gtg gag tct ggg gga ggc gta gtc cag cct ggg 48
Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
1 5 10 15

agg tcc ctg aga ctg tcc tgt gca gcc tct gga ttc acc ttc agt aat 96
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn
20 25 30

cat gct atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg 144
His Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
35 40 45

gtg gca gtt ata tca tat gat ggc gag aac aca tat tat gca gac tcc 192
Val Ala Val Ile Ser Tyr Asp Gly Glu Asn Thr Tyr Tyr Ala Asp Ser
50 55 60

att gag ggc cga ttc acc att tcc aga gac aat ttc aag aac aca ctc 240
Ile Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Phe Lys Asn Thr Leu
65 70 75 80

ttt cta caa atg tac agc ctg aca gct gat gac acg gct atg tac ttc 288
Phe Leu Gln Met Tyr Ser Leu Thr Ala Asp Asp Thr Ala Met Tyr Phe
85 90 95

tgt gcg aga ggg ggc cgt cgg ggg cac ttc acc tca tac tac ctt gac 336
Cys Ala Arg Gly Gly Arg Arg Gly His Phe Thr Ser Tyr Tyr Leu Asp
100 105 110

tac tgg ggc cag gga acc ctg gtc acc gtc tcc tcg 372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 8
<211> 124
<212> PRT
<213> Homo sapiens

<400> 8

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

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

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

Val Ala Val Ile Ser Tyr Asp Gly Glu Asn Thr Tyr Tyr Ala Asp Ser
    50                  55                  60

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

Phe Leu Gln Met Tyr Ser Leu Thr Ala Asp Asp Thr Ala Met Tyr Phe
                85                  90                  95

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 9
<211> 324
<212> DNA
<213> Homo sapiens

<220>
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<222> (73)..(105)
<223> complementarity determining region (CDR) VK-CDR1

<220>
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<222> (151)..(171)
<223> complementarity determining region (CDR) VK-CDR2

<220>
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<222> (268)..(294)
<223> complementarity determining region (CDR) VK-CDR3

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tgc gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta 48
Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1 5 10 15

gga gac aga gtc acc atc act tgc cgg gca agc cag aac ata gac aag 96
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Lys
20 25 30

tac tta aat tgg tat cag cag ata ccg ggg aaa gcc cct aag ctc ctg 144
Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Lys Ala Pro Lys Leu Leu
35 40 45

atc tat gct gca tcg agt ttg cac agt ggg gtc cca tca agg ttc agt 192
Ile Tyr Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

ggc agt gga tct ggg aca gat ttc tct ctc acc atc agc agt ctg caa 240
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

cct gaa gat ttt gca att tac tac tgt caa cag agt tac agt tcc ttc 288
Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Phe
85 90 95

cgg acg ttc ggc caa ggg acc aag ctg gag atc aaa 324
Arg Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 10
<211> 108
<212> PRT
<213> Homo sapiens

<400> 10

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

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Lys
20 25 30

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

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

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


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


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


<210>  11
<211>  324
<212>  DNA
<213>  Homo sapiens


<220>
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<223>  NI-308.15O7 VK-PIMC variable light-kappa chain (VK) sequence
       after correction of primer induced mutations

<220>
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<220>
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<222>  (151)..(171)
<223>  complementarity determining region (CDR) VK-CDR2

<220>
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<223>  complementarity determining region (CDR) VK-CDR3

<400>  11
tgc gac atc cag atg acc cag tct ccg tcc tcc ctg tct gca tct gta         48
Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1               5                   10                  15

gga gac aga gtc acc atc act tgc cgg gca agc cag aac ata gac aag         96
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Lys
            20                  25                  30

tac tta aat tgg tat cag cag ata ccg ggg aaa gcc cct aag ctc ctg        144
Tyr Leu Asn Trp Tyr Gln Gln Ile Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45
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atc tat gct gca tcg agt ttg cac agt ggg gtc cca tca agg ttc agt        192
Ile Tyr Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser
    50                  55                  60

ggc agt gga tct ggg aca gat ttc tct ctc acc atc agc agt ctg caa        240
Gly Ser Gly Ser Gly Thr Asp Phe Ser Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

cct gaa gat ttt gca att tac tac tgt caa cag agt tac agt tcc ttc        288
Pro Glu Asp Phe Ala Ile Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Phe
                85                  90                  95

cgg acg ttc ggc caa ggg acc aag gtg gag atc aaa                        324
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 12
<211> 108
<212> PRT
<213> Homo sapiens

<400> 12

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

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Asp Lys
            20                  25                  30

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

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

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

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

Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 13

<211> 372
<212> DNA
<213> Homo sapiens

<220>
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<223> complementarity determining region (CDR) VH-CDR1

<220>
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<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
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<223> complementarity determining region (CDR) VH-CDR1

<220>
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<222> (298)..(339)
<223> complementarity determining region (CDR) VH-CDR1

<400> 13

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tgc gag gtg cag ctg gtg cag tct ggg gct gac ttg cgg aac cct ggg         48
Cys Glu Val Gln Leu Val Gln Ser Gly Ala Asp Leu Arg Asn Pro Gly
1               5                   10                  15

gcc tca gtg acg gtt tcc tgc acg gct tct gga tac cat ttc gct gac         96
Ala Ser Val Thr Val Ser Cys Thr Ala Ser Gly Tyr His Phe Ala Asp
            20                  25                  30

aat gct ata aac tgg ctg cgc cag gcc ccc gga caa agg ctt gag tgg        144
Asn Ala Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp
        35                  40                  45

atg ggg tgg atc aac att tac agt ggt aac aca aaa tat tca cag aac        192
Met Gly Trp Ile Asn Ile Tyr Ser Gly Asn Thr Lys Tyr Ser Gln Asn
    50                  55                  60

ttc cag ggc aga gtc acc ttt acc aga aac aca tcc gcg agc aca gcc        240
Phe Gln Gly Arg Val Thr Phe Thr Arg Asn Thr Ser Ala Ser Thr Ala
65                  70                  75                  80

ttc atg cac ctg cgc agc ctg aga tca gaa gac acg gct gtg tat ttc        288
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```
Phe Met His Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
                85                  90                  95

tgt gcg aga gac cct gat agc agt gga tat tac ttg ccc tat ttt gac        336
Cys Ala Arg Asp Pro Asp Ser Ser Gly Tyr Tyr Leu Pro Tyr Phe Asp
            100                 105                 110

tac tgg ggc caa gga acc ctg gtc acc gtc tcc tcg                        372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 14
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<212> PRT
<213> Homo sapiens

<400> 14

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

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

Asn Ala Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp
        35                  40                  45

Met Gly Trp Ile Asn Ile Tyr Ser Gly Asn Thr Lys Tyr Ser Gln Asn
    50                  55                  60

Phe Gln Gly Arg Val Thr Phe Thr Arg Asn Thr Ser Ala Ser Thr Ala
65                  70                  75                  80

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

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

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 15
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<220>
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<223> complementarity determining region (CDR) VK-CDR1

<220>
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<223> complementarity determining region (CDR) VK-CDR2

<220>
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<222> (286)..(312)
<223> complementarity determining region (CDR) VK-CDR3

<400> 15

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tgc gac atc cag ttg acc cag tct cca gac tcc ctg act ttg tct ctg         48
Cys Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Thr Leu Ser Leu
1               5                   10                  15

ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt ttc tac         96
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Phe Tyr
            20                  25                  30

aac tcc aac aat aag aac tac tta gct tgg tat cag cag aaa cca gga        144
Asn Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
        35                  40                  45

cag cct cct aag ttg ctc atg tac tgg gca tct acc cgg gag tcc ggg        192
Gln Pro Pro Lys Leu Leu Met Tyr Trp Ala Ser Thr Arg Glu Ser Gly
    50                  55                  60

gtc act gac cga ttc agt ggc agc ggg tct ggg aca gat ttt act ctc        240
Val Thr Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
65                  70                  75                  80

acc att acc aac ctg cag gct gaa gat gtg gca gtc tat tat tgt cag        288
Thr Ile Thr Asn Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
                85                  90                  95

caa ttt tat agt tct cct ctc act ttc ggc gga ggg acc aag gtg gag        336
Gln Phe Tyr Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
            100                 105                 110
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atc aaa 342
Ile Lys

<210> 16
<211> 114
<212> PRT
<213> Homo sapiens

<400> 16

Cys Asp Ile Gln Leu Thr Gln Ser Pro Asp Ser Leu Thr Leu Ser Leu
1 5 10 15

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

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

Gln Pro Pro Lys Leu Leu Met Tyr Trp Ala Ser Thr Arg Glu Ser Gly
50 55 60

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

Thr Ile Thr Asn Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
85 90 95

Gln Phe Tyr Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 17
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<212> DNA
<213> Homo sapiens

<220>
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<223> NI-308.5G2 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
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<223> complementarity determining region (CDR) VH-CDR1

<220>
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<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
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<223> complementarity determining region (CDR) VH-CDR2

<220>
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<223> complementarity determining region (CDR) VH-CDR3

<400> 17

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tgc cag gtg cag ctg gtg caa tct ggg gct gac ttg cgg aac cct ggg         48
Cys Gln Val Gln Leu Val Gln Ser Gly Ala Asp Leu Arg Asn Pro Gly
1               5                   10                  15

gcc tca gtg acg gtt tcc tgc acg gct tct gga tac cat ttc gct gac         96
Ala Ser Val Thr Val Ser Cys Thr Ala Ser Gly Tyr His Phe Ala Asp
            20                  25                  30

aat gct ata aac tgg ctg cgc cag gcc ccc gga caa agg ctt gag tgg        144
Asn Ala Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp
        35                  40                  45

atg ggg tgg atc aac att tac agt ggt aac aca aaa tat tca cag aac        192
Met Gly Trp Ile Asn Ile Tyr Ser Gly Asn Thr Lys Tyr Ser Gln Asn
    50                  55                  60

ttc cag ggc aga gtc acc ttt acc aga aac aca tcc gcg agc aca gcc        240
Phe Gln Gly Arg Val Thr Phe Thr Arg Asn Thr Ser Ala Ser Thr Ala
65                  70                  75                  80

ttc atg cac ctg cgc agc ctg aga tca gaa gac acg gct gtg tat ttc        288
Phe Met His Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
                85                  90                  95

tgt gcg aga gac cct gat agc agt gga tat tac ttg ccc tat ttt gac        336
Cys Ala Arg Asp Pro Asp Ser Ser Gly Tyr Tyr Leu Pro Tyr Phe Asp
            100                 105                 110
```

tac tgg ggc caa gga acc ctg gtc acc gtc tcc tcg 372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 18
<211> 124
<212> PRT
<213> Homo sapiens

<400> 18

Cys Gln Val Gln Leu Val Gln Ser Gly Ala Asp Leu Arg Asn Pro Gly
1 5 10 15

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

Asn Ala Ile Asn Trp Leu Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp
35 40 45

Met Gly Trp Ile Asn Ile Tyr Ser Gly Asn Thr Lys Tyr Ser Gln Asn
50 55 60

Phe Gln Gly Arg Val Thr Phe Thr Arg Asn Thr Ser Ala Ser Thr Ala
65 70 75 80

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

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

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

<210> 19
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(342)

<223> NI-308.5G2 VK-PIMC variable light-kappa chain (VK) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (73)..(123)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (169)..(189)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (286)..(312)
<223> complementarity determining region (CDR) VK-CDR3

<400> 19

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tgc gac atc gtg atg acc cag tct cca gac tcc ctg act ttg tct ctg         48
Cys Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Thr Leu Ser Leu
1               5                   10                  15

ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt gtt ttc tac         96
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Phe Tyr
            20                  25                  30

aac tcc aac aat aag aac tac tta gct tgg tat cag cag aaa cca gga        144
Asn Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
        35                  40                  45

cag cct cct aag ttg ctc atg tac tgg gca tct acc cgg gag tcc ggg        192
Gln Pro Pro Lys Leu Leu Met Tyr Trp Ala Ser Thr Arg Glu Ser Gly
    50                  55                  60

gtc act gac cga ttc agt ggc agc ggg tct ggg aca gat ttt act ctc        240
Val Thr Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
65                  70                  75                  80

acc att acc aac ctg cag gct gaa gat gtg gca gtc tat tat tgt cag        288
Thr Ile Thr Asn Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
                85                  90                  95

caa ttt tat agt tct cct ctc act ttc ggc gga ggg acc aag gtg gag        336
Gln Phe Tyr Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
            100                 105                 110

atc aaa                                                                342
Ile Lys
```

<210> 20

<211> 114
<212> PRT
<213> Homo sapiens

<400> 20

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

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

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

Gln Pro Pro Lys Leu Leu Met Tyr Trp Ala Ser Thr Arg Glu Ser Gly
50 55 60

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

Thr Ile Thr Asn Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln
85 90 95

Gln Phe Tyr Ser Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 21
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(369)
<223> NI-308.28G1-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(336)
<223> complementarity determining region (CDR) VH-CDR3

<400> 21

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tgc cag gtg cag ctg cag gag tcg ggc cca aga ctg gtg aag ccc tcg         48
Cys Gln Val Gln Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser
1               5                   10                  15

gag acc ctg tcg ctc acg tgc act gtc gct ggc ggc tcc gtc aat agt         96
Glu Thr Leu Ser Leu Thr Cys Thr Val Ala Gly Gly Ser Val Asn Ser
            20                  25                  30

tac tat tgg acc tgg atc cag cag tcc ccc ggg aag gga ctg gag tgg        144
Tyr Tyr Trp Thr Trp Ile Gln Gln Ser Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

ctt ggg cgt atc tat atc gct ggg agg acc aac tat aac ccc tcc ctc        192
Leu Gly Arg Ile Tyr Ile Ala Gly Arg Thr Asn Tyr Asn Pro Ser Leu
    50                  55                  60

acg agt cga atc gcc ctg tca gtg gac acg tcc agg aac cag ttg tcc        240
Thr Ser Arg Ile Ala Leu Ser Val Asp Thr Ser Arg Asn Gln Leu Ser
65                  70                  75                  80

ctg aag ctg acg tct gtg acc gcc gcg gac acg gcc ata tat tat tgt        288
Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
                85                  90                  95

gcg aga tgg gga gcg gag agt ggt gac tac tac tat gga gtg gac gtc        336
Ala Arg Trp Gly Ala Glu Ser Gly Asp Tyr Tyr Tyr Gly Val Asp Val
            100                 105                 110

tgg ggc cca ggc acc ctg gtc acc gtc tcc tcg                           369
Trp Gly Pro Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 22
<211> 123

<212> PRT
<213> Homo sapiens

<400> 22

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

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

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

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

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

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

Ala Arg Trp Gly Ala Glu Ser Gly Asp Tyr Tyr Tyr Gly Val Asp Val
100 105 110

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

<210> 23
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(339)
<223> NI-308.28G1 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (73)..(120)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (166)..(186)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (283)..(309)
<223> complementarity determining region (CDR) VK-CDR3

<400> 23
tgc gaa att gtg atg acg cag tct cca ctc tcc ctg ccc gtc acc cct 48
Cys Glu Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
1 5 10 15

gga gag ccg gcc tcc atc tcc tgc aag tct agt gag gga ctc ctg cat 96
Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Glu Gly Leu Leu His
20 25 30

agt aat ggt tac acc tat ttg gat tgg tac ctg cag aag cca ggg cag 144
Ser Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

gct ccg cag ctc ctg atc ttt ctg gct tct aat cgg gcc gcc ggg gtc 192
Ala Pro Gln Leu Leu Ile Phe Leu Ala Ser Asn Arg Ala Ala Gly Val
50 55 60

cct gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aag 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

atc agc aga gtg gag gct gag gat gtt ggc gtt tat tac tgc atg cag 288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

gct ata caa agt cct tgg acg ttc ggc cca ggg acc aag gtg gaa atc 336
Ala Ile Gln Ser Pro Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

aaa 339
Lys

<210> 24
<211> 113
<212> PRT
<213> Homo sapiens

<400> 24

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

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Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Glu Gly Leu Leu His
            20                  25                  30

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

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

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

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

Ala Ile Gln Ser Pro Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys
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<210> 25
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(369)
<223> NI-308.28G1 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(336)
<223> complementarity determining region (CDR) VH-CDR3

<400> 25
tgc cag gtg cag ctg cag gag tcg ggc cca aga ctg gtg aag ccc tcg 48
Cys Gln Val Gln Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser
1 5 10 15

gag acc ctg tcg ctc acg tgc act gtc gct ggc ggc tcc gtc aat agt 96
Glu Thr Leu Ser Leu Thr Cys Thr Val Ala Gly Gly Ser Val Asn Ser
20 25 30

tac tat tgg acc tgg atc cag cag tcc ccc ggg aag gga ctg gag tgg 144
Tyr Tyr Trp Thr Trp Ile Gln Gln Ser Pro Gly Lys Gly Leu Glu Trp
35 40 45

ctt ggg cgt atc tat atc gct ggg agg acc aac tat aac ccc tcc ctc 192
Leu Gly Arg Ile Tyr Ile Ala Gly Arg Thr Asn Tyr Asn Pro Ser Leu
50 55 60

acg agt cga atc gcc ctg tca gtg gac acg tcc agg aac cag ttg tcc 240
Thr Ser Arg Ile Ala Leu Ser Val Asp Thr Ser Arg Asn Gln Leu Ser
65 70 75 80

ctg aag ctg acg tct gtg acc gcc gcg gac acg gcc ata tat tat tgt 288
Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

gcg aga tgg gga gcg gag agt ggt gac tac tac tat gga gtg gac gtc 336
Ala Arg Trp Gly Ala Glu Ser Gly Asp Tyr Tyr Tyr Gly Val Asp Val
100 105 110

tgg ggc cca ggg acc acg gtc acc gtc tcc tca 369
Trp Gly Pro Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 26
<211> 123
<212> PRT
<213> Homo sapiens

<400> 26

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

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

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

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

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

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

Ala Arg Trp Gly Ala Glu Ser Gly Asp Tyr Tyr Tyr Gly Val Asp Val
            100                 105                 110

Trp Gly Pro Gly Thr Thr Val Thr Val Ser Ser
        115                 120
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<210> 27
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(339)
<223> NI-308.28G1 VK-PIMC variable light-kappa chain (VK) sequence after correction of primer induced mutations

<220>
<221> V-region
<222> (73)..(120)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V-region
<222> (166)..(186)
<223> complementarity determining region (CDR) VK-CDR2

<220>

<221> V-region
<222> (283)..(309)
<223> complementarity determining region (CDR) VK-CDR3

<400> 27
tgc gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct 48
Cys Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
1 5 10 15

gga gag ccg gcc tcc atc tcc tgc aag tct agt gag gga ctc ctg cat 96
Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Glu Gly Leu Leu His
20 25 30

agt aat ggt tac acc tat ttg gat tgg tac ctg cag aag cca ggg cag 144
Ser Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

gct ccg cag ctc ctg atc ttt ctg gct tct aat cgg gcc gcc ggg gtc 192
Ala Pro Gln Leu Leu Ile Phe Leu Ala Ser Asn Arg Ala Ala Gly Val
50 55 60

cct gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aag 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

atc agc aga gtg gag gct gag gat gtt ggc gtt tat tac tgc atg cag 288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

gct ata caa agt cct tgg acg ttc ggc cca ggg acc aag gtg gaa atc 336
Ala Ile Gln Ser Pro Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
100 105 110

aaa 339
Lys

<210> 28
<211> 113
<212> PRT
<213> Homo sapiens

<400> 28

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

Gly Glu Pro Ala Ser Ile Ser Cys Lys Ser Ser Glu Gly Leu Leu His
20 25 30

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

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

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

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

Ala Ile Gln Ser Pro Trp Thr Phe Gly Pro Gly Thr Lys Val Glu Ile
            100                 105                 110

Lys
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<210> 29
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(387)
<223> NI-308.45C2-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (79)..(114)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(114)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (157)..(210)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region

<222> (307)..(354)
<223> complementarity determining region (CDR) VH-CDR3

<400> 29
tgc cag ctg cag ctg cag gag tcg ggt cca gga ctg gtg aag ccc tcg 48
Cys Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

cag atc ctc tca ctc acc tgt gcc atc tcc ggg gac agt gtc ttc agc 96
Gln Ile Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Phe Ser
20 25 30

aac agt gct gct tgg aac tgg atc agg cag tcc cca tcg aga ggc ctt 144
Asn Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu
35 40 45

gag tgg ctg gga agg aca tac tac agg tcc aag tgg gat aat gat tat 192
Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Asp Asn Asp Tyr
50 55 60

gca cca tct gtg aaa agt cga ata agt atc aac cca gac aca tcc aag 240
Ala Pro Ser Val Lys Ser Arg Ile Ser Ile Asn Pro Asp Thr Ser Lys
65 70 75 80

aac cag ttc tcc ctg cag ttg aat tct gtg act ccc gag gac acg gct 288
Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala
85 90 95

gtg tat tat tgt gca aga gag gtc gca tat tgt ggt ggt gac tgc tat 336
Val Tyr Tyr Cys Ala Arg Glu Val Ala Tyr Cys Gly Gly Asp Cys Tyr
100 105 110

tct gtt tcc ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc 384
Ser Val Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

tcg 387
Ser

<210> 30
<211> 129
<212> PRT
<213> Homo sapiens

<400> 30

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

Gln Ile Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Phe Ser

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            20                  25                  30

Asn Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu
        35                  40                  45

Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Asp Asn Asp Tyr
    50                  55                  60

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

Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala
                85                  90                  95

Val Tyr Tyr Cys Ala Arg Glu Val Ala Tyr Cys Gly Gly Asp Cys Tyr
            100                 105                 110

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

Ser
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<210> 31
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(339)
<223> NI-308.45C2 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (73)..(120)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (166)..(186)
<223> complementarity determining region (CDR) VK-CDR2

<220>

<221> V_region
<222> (283)..(309)
<223> complementarity determining region (CDR) VK-CDR3

<400> 31
tgc gaa att gtg atg aca cag tct cca ctc tcc ctg ccc gtc acc cct 48
Cys Glu Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
1 5 10 15

gga gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ctc cag 96
Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Gln
20 25 30

agt aat gga tac acc tat ttg gat tgg tac ctg cag aag cca ggg cag 144
Ser Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

tct cca cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc 192
Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val
50 55 60

cct gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

atc agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgc atg caa 288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

gct cta caa act ccg ctc act ttc ggc gga ggg acc aag gtg gag atc 336
Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

aaa 339
Lys

<210> 32
<211> 113
<212> PRT
<213> Homo sapiens

<400> 32

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

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

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

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

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

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

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

Lys
```

<210> 33
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(387)
<223> NI-308.45C2 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (79)..(114)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(114)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (157)..(210)
<223> complementarity determining region (CDR) VH-CDR2

<220>

<221> V_region
<222> (307)..(354)
<223> complementarity determining region (CDR) VH-CDR3

<400> 33
tgc cag ctg cag ctg cag cag tca ggt cca gga ctg gtg aag ccc tcg 48
Cys Gln Leu Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

cag atc ctc tca ctc acc tgt gcc atc tcc ggg gac agt gtc ttc agc 96
Gln Ile Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Phe Ser
20 25 30

aac agt gct gct tgg aac tgg atc agg cag tcc cca tcg aga ggc ctt 144
Asn Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu
35 40 45

gag tgg ctg gga agg aca tac tac agg tcc aag tgg gat aat gat tat 192
Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Asp Asn Asp Tyr
50 55 60

gca cca tct gtg aaa agt cga ata agt atc aac cca gac aca tcc aag 240
Ala Pro Ser Val Lys Ser Arg Ile Ser Ile Asn Pro Asp Thr Ser Lys
65 70 75 80

aac cag ttc tcc ctg cag ttg aat tct gtg act ccc gag gac acg gct 288
Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala
85 90 95

gtg tat tat tgt gca aga gag gtc gca tat tgt ggt ggt gac tgc tat 336
Val Tyr Tyr Cys Ala Arg Glu Val Ala Tyr Cys Gly Gly Asp Cys Tyr
100 105 110

tct gtt tcc ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc 384
Ser Val Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125

tcg 387
Ser

<210> 34
<211> 129
<212> PRT
<213> Homo sapiens

<400> 34

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

```
Gln Ile Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Phe Ser
            20                  25                  30

Asn Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu
        35                  40                  45

Glu Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Asp Asn Asp Tyr
    50                  55                  60

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

Asn Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala
                85                  90                  95

Val Tyr Tyr Cys Ala Arg Glu Val Ala Tyr Cys Gly Gly Asp Cys Tyr
            100                 105                 110

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

Ser
```

<210> 35
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(339)
<223> NI-308.45C2 VK-PIMC variable light-kappa chain (VK) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (73)..(120)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (166)..(186)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (283)..(309)
<223> complementarity determining region (CDR) VK-CDR3

<400> 35
tgc gat att gtg atg act cag tct cca ctc tcc ctg ccc gtc acc cct 48
Cys Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
1 5 10 15

gga gag ccg gcc tcc atc tcc tgc agg tct agt cag agc ctc ctc cag 96
Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu Gln
20 25 30

agt aat gga tac acc tat ttg gat tgg tac ctg cag aag cca ggg cag 144
Ser Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
35 40 45

tct cca cag ctc ctg atc tat ttg ggt tct aat cgg gcc tcc ggg gtc 192
Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val
50 55 60

cct gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa 240
Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
65 70 75 80

atc agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgc atg caa 288
Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
85 90 95

gct cta caa act ccg ctc act ttc ggc gga ggg acc aag gtg gag atc 336
Ala Leu Gln Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
100 105 110

aaa 339
Lys

<210> 36
<211> 113
<212> PRT
<213> Homo sapiens

<400> 36

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

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

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

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

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

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

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

Lys
```

<210> 37
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(381)
<223> NI-308.24E11-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(348)
<223> complementarity determining region (CDR) VH-CDR3

<400> 37
tgc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg 48
Cys Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1 5 10 15

gag acc ctg tcc ctc acc tgc act gtc tct act act tcc ctc aga agt 96
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Thr Thr Ser Leu Arg Ser
20 25 30

tat ttc tgg agt tgg atc cgg cag ccc cca ggg aag ggg ctg gag tgg 144
Tyr Phe Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

att ggg tat gtc tat tac agt ggg agt acc atc tac aat ccg tcc ctc 192
Ile Gly Tyr Val Tyr Tyr Ser Gly Ser Thr Ile Tyr Asn Pro Ser Leu
50 55 60

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

ctg aac ctg cgc tct gtg acc gct gcg gat acg gcc atg tat ttc tgt 288
Leu Asn Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Met Tyr Phe Cys
85 90 95

gcg aga ggc gtc ccg gct gag act gat gcg cgg gac ttc ccg ccc tac 336
Ala Arg Gly Val Pro Ala Glu Thr Asp Ala Arg Asp Phe Pro Pro Tyr
100 105 110

tac ttt gat cac tgg ggc cag gga acc ctg gtc acc gtc tcc tcg 381
Tyr Phe Asp His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 38
<211> 127
<212> PRT
<213> Homo sapiens

<400> 38

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

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

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

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

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

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

Ala Arg Gly Val Pro Ala Glu Thr Asp Ala Arg Asp Phe Pro Pro Tyr
            100                 105                 110

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


<210>  39
<211>  324
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(324)
<223>  NI-308.24E11 VK variable light-kappa chain (VK) sequence

<220>
<221>  V_region
<222>  (73)..(105)
<223>  complementarity determining region (CDR) VK-CDR1

<220>
<221>  V_region
<222>  (151)..(171)
<223>  complementarity determining region (CDR) VK-CDR2

<220>
<221>  V_region
<222>  (268)..(294)
<223>  complementarity determining region (CDR) VK-CDR3

<400>  39
tgc gac atc cag ttg acc cag tct cca tcc tcc ctg tct gcg tca gta         48
```

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

gga aac aga atc acc ttc act tgc cag gcg agt cag gac att aga tat         96
Gly Asn Arg Ile Thr Phe Thr Cys Gln Ala Ser Gln Asp Ile Arg Tyr
            20                  25                  30

tat tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aaa ctc ctg        144
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45

atc tac gat gtg tcc aat ttg gat aca ggg gtg cca cca agg ttc agt        192
Ile Tyr Asp Val Ser Asn Leu Asp Thr Gly Val Pro Pro Arg Phe Ser
    50                  55                  60

gga agt gga tct ggg aca aat ttc act ttc acc atc agc agc ctg cag        240
Gly Ser Gly Ser Gly Thr Asn Phe Thr Phe Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

cct gaa gat att gca gtt tat tac tgt caa cag tat gaa gga ctc cct        288
Pro Glu Asp Ile Ala Val Tyr Tyr Cys Gln Gln Tyr Glu Gly Leu Pro
                85                  90                  95

gtg acc ttc ggc ggg ggg acc aag gtg gag atc aaa                        324
Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210>  40
<211>  108
<212>  PRT
<213>  Homo sapiens

<400>  40

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


Gly Asn Arg Ile Thr Phe Thr Cys Gln Ala Ser Gln Asp Ile Arg Tyr
            20                  25                  30


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


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


Gly Ser Gly Ser Gly Thr Asn Phe Thr Phe Thr Ile Ser Ser Leu Gln
65                  70                  75                  80
```

```
Pro Glu Asp Ile Ala Val Tyr Tyr Cys Gln Gln Tyr Glu Gly Leu Pro
                85                  90                  95


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


<210>  41
<211>  324
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(324)
<223>  NI-308.24E11 VK-PIMC variable light-kappa chain (VK) sequence
       after correction of primer induced mutations

<220>
<221>  V_region
<222>  (73)..(105)
<223>  complementarity determining region (CDR) VK-CDR1

<220>
<221>  V_region
<222>  (151)..(171)
<223>  complementarity determining region (CDR) VK-CDR2

<220>
<221>  V_region
<222>  (268)..(294)
<223>  complementarity determining region (CDR) VK-CDR3

<400>  41
tgc gac atc cag atg acc cag tct cca tcc tcc ctg tct gcg tca gta         48
Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1               5                   10                  15

gga aac aga atc acc ttc act tgc cag gcg agt cag gac att aga tat         96
Gly Asn Arg Ile Thr Phe Thr Cys Gln Ala Ser Gln Asp Ile Arg Tyr
            20                  25                  30

tat tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aaa ctc ctg        144
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45

atc tac gat gtg tcc aat ttg gat aca ggg gtg cca cca agg ttc agt        192
Ile Tyr Asp Val Ser Asn Leu Asp Thr Gly Val Pro Pro Arg Phe Ser
    50                  55                  60
```

```
gga agt gga tct ggg aca aat ttc act ttc acc atc agc agc ctg cag        240
Gly Ser Gly Ser Gly Thr Asn Phe Thr Phe Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

cct gaa gat att gca gtt tat tac tgt caa cag tat gaa gga ctc cct        288
Pro Glu Asp Ile Ala Val Tyr Tyr Cys Gln Gln Tyr Glu Gly Leu Pro
                85                  90                  95

gtg acc ttc ggc ggg ggg acc aag gtg gag atc aaa                        324
Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 42
<211> 108
<212> PRT
<213> Homo sapiens

<400> 42

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

Gly Asn Arg Ile Thr Phe Thr Cys Gln Ala Ser Gln Asp Ile Arg Tyr
            20                  25                  30

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

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

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

Pro Glu Asp Ile Ala Val Tyr Tyr Cys Gln Gln Tyr Glu Gly Leu Pro
                85                  90                  95

Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 43
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(372)
<223> NI-308.46E9-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (79)..(114)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(114)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (157)..(204)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (301)..(339)
<223> complementarity determining region (CDR) VH-CDR3

<400> 43

```
tgc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg         48
Cys Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1               5                   10                  15

gag acc ctg tcc ctc act tgc act gtc tct ggt gcc tcc atc agc ggt         96
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Gly
            20                  25                  30

agt acc tac tac tgg ggc tgg atc cgc cag ccc cca ggg aag ggg ctg        144
Ser Thr Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
        35                  40                  45

gag tat att ggg aga atc tac tat agt ggg agc acc tac tac aac ccg        192
Glu Tyr Ile Gly Arg Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro
    50                  55                  60

tcc ctc aag agt cga gcc acc ata tct gta gac acg tcc aag aac cag        240
Ser Leu Lys Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
65                  70                  75                  80

ctc tcc ctg aca ctg agt tct gtg acc gcc gca gat acg gct gtg tat        288
Leu Ser Leu Thr Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                85                  90                  95
```

```
tat tgt gtg aga ccc ttt tac gct ggt tcg ggg aac tcc ccc ttt gac        336
Tyr Cys Val Arg Pro Phe Tyr Ala Gly Ser Gly Asn Ser Pro Phe Asp
            100                 105                 110

tac tgg ggc cag gga acc ctg gtc acc gtc tcc tcg                        372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 44
<211> 124
<212> PRT
<213> Homo sapiens

<400> 44

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

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

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

Glu Tyr Ile Gly Arg Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro
    50                  55                  60

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

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

Tyr Cys Val Arg Pro Phe Tyr Ala Gly Ser Gly Asn Ser Pro Phe Asp
            100                 105                 110

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

<210> 45
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)
<223> NI-308.46E9 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (73)..(105)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (151)..(171)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (268)..(294)
<223> complementarity determining region (CDR) VK-CDR3

<400> 45
```
tgc gaa att gtg ctg act cag tct cca gcc acc gtg tct gtg tct cca         48
Cys Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Val Ser Val Ser Pro
1               5                   10                  15

ggg gag aga gcc acc ctc tcc tgc agg gcc agc cag agt gtt agc acc         96
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr
            20                  25                  30

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

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

ggc agt ggg tct ggg gca gag ttc acc ctc acc atc agc agc ctg cag        240
Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

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

ccg gct ttc ggc gga ggg acc aag gtg gaa atc aaa                       324
Pro Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 46
<211> 108

<212> PRT
<213> Homo sapiens

<400> 46

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

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

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

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

Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

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

Pro Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 47
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(372)
<223> NI-308.46E9 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (79)..(114)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(114)

<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (157)..(204)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (301)..(339)
<223> complementarity determining region (CDR) VH-CDR3

<400> 47

```
tgc cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg         48
Cys Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser
1               5                  10                  15

gag acc ctg tcc ctc act tgc act gtc tct ggt gcc tcc atc agc ggt         96
Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Ile Ser Gly
            20                  25                  30

agt acc tac tac tgg ggc tgg atc cgc cag ccc cca ggg aag ggg ctg        144
Ser Thr Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
        35                  40                  45

gag tat att ggg aga atc tac tat agt ggg agc acc tac tac aac ccg        192
Glu Tyr Ile Gly Arg Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro
    50                  55                  60

tcc ctc aag agt cga gcc acc ata tct gta gac acg tcc aag aac cag        240
Ser Leu Lys Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
65                  70                  75                  80

ctc tcc ctg aca ctg agt tct gtg acc gcc gca gat acg gct gtg tat        288
Leu Ser Leu Thr Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
                85                  90                  95

tat tgt gtg aga ccc ttt tac gct ggt tcg ggg aac tcc ccc ttt gac        336
Tyr Cys Val Arg Pro Phe Tyr Ala Gly Ser Gly Asn Ser Pro Phe Asp
            100                 105                 110

tac tgg ggc cag gga acc ctg gtc acc gtc tcc tcg                        372
Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 48
<211> 124
<212> PRT
<213> Homo sapiens

<400> 48

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

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

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

Glu Tyr Ile Gly Arg Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro
    50                  55                  60

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

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

Tyr Cys Val Arg Pro Phe Tyr Ala Gly Ser Gly Asn Ser Pro Phe Asp
            100                 105                 110

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

<210> 49
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)
<223> NI-308.46E9 VK-PIMC variable light-kappa chain (VK) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (73)..(105)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (151)..(171)

<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (268)..(294)
<223> complementarity determining region (CDR) VK-CDR3

<400> 49
tgc gaa ata gtg atg acg cag tct cca gcc acc gtg tct gtg tct cca 48
Cys Glu Ile Val Met Thr Gln Ser Pro Ala Thr Val Ser Val Ser Pro
1 5 10 15

ggg gag aga gcc acc ctc tcc tgc agg gcc agc cag agt gtt agc acc 96
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr
20 25 30

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

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

ggc agt ggg tct ggg gca gag ttc acc ctc acc atc agc agc ctg cag 240
Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

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

ccg gct ttc ggc gga ggg acc aag gtg gag atc aaa 324
Pro Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 50
<211> 108
<212> PRT
<213> Homo sapiens

<400> 50

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

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

Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Arg Leu Leu

```
        35                  40                  45

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

Gly Ser Gly Ser Gly Ala Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

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

Pro Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 51
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(387)
<223> NI-308.6B11-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(354)
<223> complementarity determining region (CDR) VH-CDR3

<400> 51
tgc gag gtg cag ctg gtg cag tct ggg gct gag gtg aag agg cct ggg 48

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

gcc tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc act gaa         96
Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu
            20                  25                  30

tta tcc atg cac tgg gtg cga cag gct cct gga aaa ggg ctt gag tgg        144
Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

atg gga ggt ttt gat cct gaa gat ggt gaa aca gtc tac gca cag aag        192
Met Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Val Tyr Ala Gln Lys
    50                  55                  60

ttc cag ggc aga gtc acc atg acc gag gac aca tct aca gac aca gcc        240
Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala
65                  70                  75                  80

tac atg gag ctg agc agc ctg aga tct gag gac acg gcc ttg tat cac        288
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr His
                85                  90                  95

tgt gca aca tac ggc agc agc tgg cac tgg aat gag gga aat gag ggg        336
Cys Ala Thr Tyr Gly Ser Ser Trp His Trp Asn Glu Gly Asn Glu Gly
            100                 105                 110

tcc tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc        384
Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

tcg                                                                    387
Ser
```

<210> 52
<211> 129
<212> PRT
<213> Homo sapiens

<400> 52

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


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


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

```
Met Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Val Tyr Ala Gln Lys
    50                  55                  60

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

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

Cys Ala Thr Tyr Gly Ser Ser Trp His Trp Asn Glu Gly Asn Glu Gly
            100                 105                 110

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

Ser
```

<210> 53
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)
<223> NI-308.6B11 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (73)..(105)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (151)..(171)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (268)..(294)
<223> complementarity determining region (CDR) VK-CDR3

<400> 53

```
tgc gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta         48
Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
1               5                   10                  15

gga gac aga gtc acc atc act tgc cag gcg agt cag gac att agc att         96
Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Ile
            20                  25                  30

tat tta aat tgg tat cag caa aaa cca ggg aaa gcc cct aag ctc ctg        144
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
        35                  40                  45

atc tac gat gca tcc aat ttg gaa aca ggg gtc cca tca agg ttc agt        192
Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser
    50                  55                  60

gga agt gga tct ggg aca gat ttt act ttc acc atc agc ggc ctg cag        240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Gly Leu Gln
65                  70                  75                  80

cct gaa gat gtt gca aga tat tat tgt caa cag tat gat gat ctc ccc        288
Pro Glu Asp Val Ala Arg Tyr Tyr Cys Gln Gln Tyr Asp Asp Leu Pro
                85                  90                  95

atc acc ttc ggc caa ggg aca cga ctg gag att aaa                        324
Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105
```

<210> 54
<211> 108
<212> PRT
<213> Homo sapiens

<400> 54

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


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


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


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


Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Gly Leu Gln
```

65 70 75 80

Pro Glu Asp Val Ala Arg Tyr Tyr Cys Gln Gln Tyr Asp Asp Leu Pro
85 90 95

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

<210> 55
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(387)
<223> NI-308.6B11 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(354)
<223> complementarity determining region (CDR) VH-CDR3

<400> 55
tgc cag gtc cag ctg gta cag tct ggg gct gag gtg aag agg cct ggg 48
Cys Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Arg Pro Gly
1 5 10 15

gcc tca gtg aag gtc tcc tgc aag gtt tcc gga tac acc ctc act gaa 96
Ala Ser Val Lys Val Ser Cys Lys Val Ser Gly Tyr Thr Leu Thr Glu
20 25 30

```
tta tcc atg cac tgg gtg cga cag gct cct gga aaa ggg ctt gag tgg        144
Leu Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

atg gga ggt ttt gat cct gaa gat ggt gaa aca gtc tac gca cag aag        192
Met Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Val Tyr Ala Gln Lys
    50                  55                  60

ttc cag ggc aga gtc acc atg acc gag gac aca tct aca gac aca gcc        240
Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala
65                  70                  75                  80

tac atg gag ctg agc agc ctg aga tct gag gac acg gcc ttg tat cac        288
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Leu Tyr His
                85                  90                  95

tgt gca aca tac ggc agc agc tgg cac tgg aat gag gga aat gag ggg        336
Cys Ala Thr Tyr Gly Ser Ser Trp His Trp Asn Glu Gly Asn Glu Gly
            100                 105                 110

tcc tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc        384
Ser Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
        115                 120                 125

tcg                                                                    387
Ser
```

<210> 56
<211> 129
<212> PRT
<213> Homo sapiens

<400> 56

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

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

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

Met Gly Gly Phe Asp Pro Glu Asp Gly Glu Thr Val Tyr Ala Gln Lys
    50                  55                  60

Phe Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp Thr Ala
```

65 70 75 80

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

Cys Ala Thr Tyr Gly Ser Ser Trp His Trp Asn Glu Gly Asn Glu Gly
100 105 110

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

Ser

<210> 57
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(378)
<223> NI-308.46F8-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(345)
<223> complementarity determining region (CDR) VH-CDR3

<400> 57
tgc cag gtg cag ctg gtg gag tct ggg gga ggt gtg gta cgg cct ggg 48

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

ggg tcc ctg aga ctc tcc tgt aca gcc tct gga ttc acg ttt gat gaa         96
Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Glu
            20                  25                  30

tat ggc atg agc tgg gtc cgc caa gtt cca ggg aag ggg ctg gag tgg        144
Tyr Gly Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

gtc tct ggc att aat tgg aat gga gca acc aca cgt tat gca gac tct        192
Val Ser Gly Ile Asn Trp Asn Gly Ala Thr Thr Arg Tyr Ala Asp Ser
    50                  55                  60

gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctc        240
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65                  70                  75                  80

tat ctg caa atg aac agt ctg aga gcc gag gac acg gcc ttg tat cac        288
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His
                85                  90                  95

tgt gcg aga gat ggg tgt agg aat acc agc tgc tat atc tgg gac tgg        336
Cys Ala Arg Asp Gly Cys Arg Asn Thr Ser Cys Tyr Ile Trp Asp Trp
            100                 105                 110

ttc gat ccc tgg ggc cag gga acc ctg gtc acc gtc tcc tcg                378
Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  58
<211>  126
<212>  PRT
<213>  Homo sapiens

<400>  58

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


Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Glu
            20                  25                  30


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


Val Ser Gly Ile Asn Trp Asn Gly Ala Thr Thr Arg Tyr Ala Asp Ser
    50                  55                  60
```

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


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


Cys Ala Arg Asp Gly Cys Arg Asn Thr Ser Cys Tyr Ile Trp Asp Trp
            100                 105                 110


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


<210>  59
<211>  333
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(333)
<223>  NI-308.46F8 VL variable light-lambda chain (VL) sequence

<220>
<221>  V_region
<222>  (70)..(108)
<223>  complementarity determining region (CDR) VL-CDR1

<220>
<221>  V_region
<222>  (154)..(174)
<223>  complementarity determining region (CDR) VL-CDR2

<220>
<221>  V_region
<222>  (271)..(303)
<223>  complementarity determining region (CDR) VL-CDR3

<400>  59
tgc cag tct gtg ttg acg cag ccg ccc tca gtg tct gcg gcc cca gga         48
Cys Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly
1               5                   10                  15

cag aag gtc acc atc tcc tgc tct gga agc agc tcc aac att gga aat         96
Gln Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn
            20                  25                  30
```

```
aat tat gta tgc tgg tac cag aac ctc cca gga aca gcc ccc aaa ctc        144
Asn Tyr Val Cys Trp Tyr Gln Asn Leu Pro Gly Thr Ala Pro Lys Leu
        35                  40                  45

ctc att tat gac gat aat aag cga ccc tca ggg att cct gac cga ttc        192
Leu Ile Tyr Asp Asp Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe
    50                  55                  60

tct ggc tcc aag tct ggc acg tca gcc acc ctg ggc atc acc gga ctc        240
Ser Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu
65                  70                  75                  80

cag act ggg gac gag gcc gat tat tac tgc gga aca tgg gac agc agc        288
Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser
                85                  90                  95

ctg agt gtt gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta            333
Leu Ser Val Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  60
<211>  111
<212>  PRT
<213>  Homo sapiens

<400>  60

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


Gln Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn
            20                  25                  30


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


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


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


Gln Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser
                85                  90                  95


Leu Ser Val Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
```

100 105 110

<210> 61
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(378)
<223> NI-308.46F8 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (79)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1 according to the numbering conventions set forth by Kabat et al. 1983

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(345)
<223> complementarity determining region (CDR) VH-CDR3

<400> 61
tgc gag gtg cag ctg gtg gag tct ggg gga ggt gtg gta cgg cct ggg 48
Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Arg Pro Gly
1 5 10 15

ggg tcc ctg aga ctc tcc tgt aca gcc tct gga ttc acg ttt gat gaa 96
Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Glu
20 25 30

tat ggc atg agc tgg gtc cgc caa gtt cca ggg aag ggg ctg gag tgg 144
Tyr Gly Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp
35 40 45

gtc tct ggc att aat tgg aat gga gca acc aca cgt tat gca gac tct 192
Val Ser Gly Ile Asn Trp Asn Gly Ala Thr Thr Arg Tyr Ala Asp Ser
50 55 60

```
gtg aag ggc cga ttc acc atc tcc aga gac aac gcc aag aac tcc ctc        240
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu
65                  70                  75                  80

tat ctg caa atg aac agt ctg aga gcc gag gac acg gcc ttg tat cac        288
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr His
                85                  90                  95

tgt gcg aga gat ggg tgt agg aat acc agc tgc tat atc tgg gac tgg        336
Cys Ala Arg Asp Gly Cys Arg Asn Thr Ser Cys Tyr Ile Trp Asp Trp
            100                 105                 110

ttc gat ccc tgg ggc cag gga acc ctg gtc acc gtc tcc tcg                378
Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 62
<211> 126
<212> PRT
<213> Homo sapiens

<400> 62

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

Gly Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe Asp Glu
            20                  25                  30

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

Val Ser Gly Ile Asn Trp Asn Gly Ala Thr Thr Arg Tyr Ala Asp Ser
    50                  55                  60

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

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

Cys Ala Arg Asp Gly Cys Arg Asn Thr Ser Cys Tyr Ile Trp Asp Trp
            100                 105                 110

Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
```

115 120 125

<210> 63
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(381)
<223> NI-308.4M1-VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(348)
<223> complementarity determining region (CDR) VH-CDR3

<400> 63

```
tgc gag gtg cag ctg gtg gag act ggg gga ggc gtg gtc cag ccg ggg         48
Cys Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly
1               5                   10                  15

ggg tcc ctg cga ctc tcc tgt gaa gcc tct gga ttc acc atc ggc acc         96
Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Ile Gly Thr
            20                  25                  30

tat gcc atg cac tgg gtc cgc cag ttt cca ggc aag ggc ctg gat tgg        144
Tyr Ala Met His Trp Val Arg Gln Phe Pro Gly Lys Gly Leu Asp Trp
        35                  40                  45

gtg gca gta ata tcg ttc gat gga act act gag tac tac aca gac gcc        192
Val Ala Val Ile Ser Phe Asp Gly Thr Thr Glu Tyr Tyr Thr Asp Ala
    50                  55                  60

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

tat ctg caa atg aac tac ttg aga ggt gac gac acg gct ata tat ttc        288
Tyr Leu Gln Met Asn Tyr Leu Arg Gly Asp Asp Thr Ala Ile Tyr Phe
                85                  90                  95
```

```
tgt gcg cga gat ttc acc tcc tcg ggg gag acc ggt tcg tgg aca caa        336
Cys Ala Arg Asp Phe Thr Ser Ser Gly Glu Thr Gly Ser Trp Thr Gln
            100                 105                 110

gta cct gat ctc tgg ggc cag ggc acc ctg gtc acc gtc tcc tcg           381
Val Pro Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 64
<211> 127
<212> PRT
<213> Homo sapiens

<400> 64

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

Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Ile Gly Thr
            20                  25                  30

Tyr Ala Met His Trp Val Arg Gln Phe Pro Gly Lys Gly Leu Asp Trp
        35                  40                  45

Val Ala Val Ile Ser Phe Asp Gly Thr Thr Glu Tyr Tyr Thr Asp Ala
    50                  55                  60

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

Tyr Leu Gln Met Asn Tyr Leu Arg Gly Asp Asp Thr Ala Ile Tyr Phe
                85                  90                  95

Cys Ala Arg Asp Phe Thr Ser Ser Gly Glu Thr Gly Ser Trp Thr Gln
            100                 105                 110

Val Pro Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 65
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(327)
<223> NI-308.4M1 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (73)..(105)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (151)..(171)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (268)..(297)
<223> complementarity determining region (CDR) VK-CDR3

<400> 65
tgc gaa att gtg atg aca cag tct cca gcc acc ctg tct ctg tct cca 48
Cys Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
1 5 10 15

ggg gaa aga gcc acg ctc tcc tgc agg gcc agt cag agt gtt act aaa 96
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Lys
20 25 30

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

atc tat gat gta tct tac agg gcc gct ggc acc cca gcc agg ttc agt 192
Ile Tyr Asp Val Ser Tyr Arg Ala Ala Gly Thr Pro Ala Arg Phe Ser
50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gat ttt gca gtt tat tac tgt cac caa cgt agc agc tgg cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Arg Ser Ser Trp Pro
85 90 95

ccg gtc act ttc ggc gga ggg acc aag gtg gag atc aaa 327
Pro Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 66

<211> 109
<212> PRT
<213> Homo sapiens

<400> 66

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

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

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

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

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

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

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

<210> 67
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(381)
<223> NI-308.4M1 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region

<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(348)
<223> complementarity determining region (CDR) VH-CDR3

<400> 67
tgc cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag ccg ggg 48
Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
1 5 10 15

ggg tcc ctg cga ctc tcc tgt gaa gcc tct gga ttc acc atc ggc acc 96
Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Ile Gly Thr
20 25 30

tat gcc atg cac tgg gtc cgc cag ttt cca ggc aag ggc ctg gat tgg 144
Tyr Ala Met His Trp Val Arg Gln Phe Pro Gly Lys Gly Leu Asp Trp
35 40 45

gtg gca gta ata tcg ttc gat gga act act gag tac tac aca gac gcc 192
Val Ala Val Ile Ser Phe Asp Gly Thr Thr Glu Tyr Tyr Thr Asp Ala
50 55 60

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

tat ctg caa atg aac tac ttg aga ggt gac gac acg gct ata tat ttc 288
Tyr Leu Gln Met Asn Tyr Leu Arg Gly Asp Asp Thr Ala Ile Tyr Phe
85 90 95

tgt gcg cga gat ttc acc tcc tcg ggg gag acc ggt tcg tgg aca caa 336
Cys Ala Arg Asp Phe Thr Ser Ser Gly Glu Thr Gly Ser Trp Thr Gln
100 105 110

gta cct gat ctc tgg ggc cag ggc acc ctg gtc acc gtc tcc tcg 381
Val Pro Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 68
<211> 127
<212> PRT
<213> Homo sapiens

<400> 68

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

```
Gly Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Phe Thr Ile Gly Thr
            20                  25                  30

Tyr Ala Met His Trp Val Arg Gln Phe Pro Gly Lys Gly Leu Asp Trp
        35                  40                  45

Val Ala Val Ile Ser Phe Asp Gly Thr Thr Glu Tyr Tyr Thr Asp Ala
    50                  55                  60

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

Tyr Leu Gln Met Asn Tyr Leu Arg Gly Asp Asp Thr Ala Ile Tyr Phe
                85                  90                  95

Cys Ala Arg Asp Phe Thr Ser Ser Gly Glu Thr Gly Ser Trp Thr Gln
            100                 105                 110

Val Pro Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
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<210> 69
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(327)
<223> NI-308.4M1 VK-PIMC variable light-kappa chain (VK) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (73)..(105)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (151)..(171)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (268)..(297)

<223> complementarity determining region (CDR) VK-CDR3

<400> 69
tgc gaa att gtg ttg aca cag tct cca gcc acc ctg tct ctg tct cca 48
Cys Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro
1 5 10 15

ggg gaa aga gcc acg ctc tcc tgc agg gcc agt cag agt gtt act aaa 96
Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Thr Lys
20 25 30

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

atc tat gat gta tct tac agg gcc gct ggc acc cca gcc agg ttc agt 192
Ile Tyr Asp Val Ser Tyr Arg Ala Ala Gly Thr Pro Ala Arg Phe Ser
50 55 60

ggc agt ggg tct ggg aca gac ttc act ctc acc atc agc agc cta gag 240
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

cct gaa gat ttt gca gtt tat tac tgt cac caa cgt agc agc tgg cct 288
Pro Glu Asp Phe Ala Val Tyr Tyr Cys His Gln Arg Ser Ser Trp Pro
85 90 95

ccg gtc act ttc ggc gga ggg acc aag gtg gag atc aaa 327
Pro Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 70
<211> 109
<212> PRT
<213> Homo sapiens

<400> 70

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

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

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

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

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


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


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


<210>  71
<211>  381
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(381)
<223>  NI-308.12A3-VH variable heavy chain (VH) sequence

<220>
<221>  V_region
<222>  (94)..(108)
<223>  complementarity determining region (CDR) VH-CDR1

<220>
<221>  V_region
<222>  (151)..(201)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (298)..(348)
<223>  complementarity determining region (CDR) VH-CDR3

<400>  71
tgc gag gtg cag ctg gtg gag act ggg gga ggc ttg gta cag cct gga         48
Cys Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly
1               5                   10                  15

ggg tcc ctg aga ctc tcc tgc gta ggc tct gga ttt ctc ttc agt gat         96
Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Leu Phe Ser Asp
            20                  25                  30

ttt gaa atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg        144
Phe Glu Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45
```

```
att tca tat att agt ggt gac ggt aat atc ata tat cag aca gac tct        192
Ile Ser Tyr Ile Ser Gly Asp Gly Asn Ile Ile Tyr Gln Thr Asp Ser
    50                  55                  60

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

ttt cta caa atg gac agc ctg acc gtc gag gac acg gct gta tat tac        288
Phe Leu Gln Met Asp Ser Leu Thr Val Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga gac gcc cgt gaa aac tgt ggt ggt gac tgc tat tcc acg        336
Cys Ala Arg Asp Ala Arg Glu Asn Cys Gly Gly Asp Cys Tyr Ser Thr
            100                 105                 110

tcc ttt gat ttt tgg ggc cag ggc acc ctg gtc acc gtc tcc tcg           381
Ser Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

        115                 120                 125
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<210> 72
<211> 127
<212> PRT
<213> Homo sapiens

<400> 72

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Cys Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Val Gln Pro Gly
1               5                   10                  15


Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Leu Phe Ser Asp
            20                  25                  30


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


Ile Ser Tyr Ile Ser Gly Asp Gly Asn Ile Ile Tyr Gln Thr Asp Ser
    50                  55                  60


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


Phe Leu Gln Met Asp Ser Leu Thr Val Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95
```

```
Cys Ala Arg Asp Ala Arg Glu Asn Cys Gly Gly Asp Cys Tyr Ser Thr
            100                 105                 110


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


<210>  73
<211>  342
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(342)
<223>  NI-308.12A3 VK  variable light-kappa chain (VK) sequence

<220>
<221>  V_region
<222>  (73)..(123)
<223>  complementarity determining region (CDR) VK-CDR1

<220>
<221>  V_region
<222>  (169)..(189)
<223>  complementarity determining region (CDR) VK-CDR2

<220>
<221>  V_region
<222>  (286)..(312)
<223>  complementarity determining region (CDR) VK-CDR3

<400>  73
tgc gac atc cag atg acc cag tct cca gac tcc ctg gct gtg tct ctg         48
Cys Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
1               5                   10                  15

ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt ctt tta tac         96
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr
            20                  25                  30

act gcc aac aat agg aac tac tta gcc tgg tac cag aaa aaa gca gga        144
Thr Ala Asn Asn Arg Asn Tyr Leu Ala Trp Tyr Gln Lys Lys Ala Gly
        35                  40                  45

cag cct cct aag ctc ctc att cac tgg gca tct acc cgg gca tcc ggg        192
Gln Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Ala Ser Gly
    50                  55                  60

gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc att ctc        240
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu
```

65 70 75 80

acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat ttt tgt caa 288
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln
85 90 95

cat tat tat aat tct ccc cgg acg ttc ggc caa ggg acc aag gtg gag 336
His Tyr Tyr Asn Ser Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu

100 105 110

atc aaa 342
Ile Lys

<210> 74
<211> 114
<212> PRT
<213> Homo sapiens

<400> 74

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

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr
20 25 30

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

Gln Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Ala Ser Gly
50 55 60

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

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

His Tyr Tyr Asn Ser Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 75
<211> 381
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(381)
<223> NI-308.12A3 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(348)
<223> complementarity determining region (CDR) VH-CDR3

<400> 75

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tgc gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta cag cct gga         48
Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
1               5                   10                  15

ggg tcc ctg aga ctc tcc tgc gta ggc tct gga ttt ctc ttc agt gat         96
Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Leu Phe Ser Asp
            20                  25                  30

ttt gaa atg gac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg        144
Phe Glu Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

att tca tat att agt ggt gac ggt aat atc ata tat cag aca gac tct        192
Ile Ser Tyr Ile Ser Gly Asp Gly Asn Ile Ile Tyr Gln Thr Asp Ser
    50                  55                  60

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

ttt cta caa atg gac agc ctg acc gtc gag gac acg gct gta tat tac        288
Phe Leu Gln Met Asp Ser Leu Thr Val Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga gac gcc cgt gaa aac tgt ggt ggt gac tgc tat tcc acg        336
```

```
Cys Ala Arg Asp Ala Arg Glu Asn Cys Gly Gly Asp Cys Tyr Ser Thr
            100                 105                 110

tcc ttt gat ttt tgg ggc cag ggc acc ctg gtc acc gtc tcc tcg           381
Ser Phe Asp Phe Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser

        115                 120                 125


<210>  76
<211>  127
<212>  PRT
<213>  Homo sapiens

<400>  76

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


Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Leu Phe Ser Asp
            20                  25                  30


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


Ile Ser Tyr Ile Ser Gly Asp Gly Asn Ile Ile Tyr Gln Thr Asp Ser
    50                  55                  60


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


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


Cys Ala Arg Asp Ala Arg Glu Asn Cys Gly Gly Asp Cys Tyr Ser Thr
            100                 105                 110


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


<210>  77
<211>  342
<212>  DNA
<213>  Homo sapiens
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<220>
<221> CDS
<222> (1)..(342)
<223> NI-308.12A3 VK-PIMC variable light-kappa chain (VK) sequence
after correction of primer induced mutations

<220>
<221> V_region
<222> (73)..(123)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (169)..(189)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (286)..(312)
<223> complementarity determining region (CDR) VK-CDR3

<400> 77
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tgc gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg         48
Cys Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu
1               5                   10                  15

ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt ctt tta tac         96
Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr
            20                  25                  30

act gcc aac aat agg aac tac tta gcc tgg tac cag aaa aaa gca gga        144
Thr Ala Asn Asn Arg Asn Tyr Leu Ala Trp Tyr Gln Lys Lys Ala Gly
        35                  40                  45

cag cct cct aag ctc ctc att cac tgg gca tct acc cgg gca tcc ggg        192
Gln Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Ala Ser Gly
    50                  55                  60

gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat ttc att ctc        240
Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Ile Leu
65                  70                  75                  80

acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat ttt tgt caa        288
Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Phe Cys Gln
                85                  90                  95

cat tat tat aat tct ccc cgg acg ttc ggc caa ggg acc aag gtg gag        336
His Tyr Tyr Asn Ser Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu

            100                 105                 110

atc aaa                                                                342
```

Ile Lys

<210> 78
<211> 114
<212> PRT
<213> Homo sapiens

<400> 78

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

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Leu Leu Tyr
20 25 30

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

Gln Pro Pro Lys Leu Leu Ile His Trp Ala Ser Thr Arg Ala Ser Gly
50 55 60

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

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

His Tyr Tyr Asn Ser Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu
100 105 110

Ile Lys

<210> 79
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)
<223> NI-308.16C10-VH variable heavy chain (VH) sequence

<220>

<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(342)
<223> complementarity determining region (CDR) VH-CDR3

<400> 79
tgc gag gtg cag ctg gtg gag act ggg gga ggc gtg gtc cag cct ggg 48
Cys Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly
1 5 10 15

atg tcc ctg agc ctc tcc tgt gca gcg act gga ttc acc ttc agc agt 96
Met Ser Leu Ser Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Ser Ser
20 25 30

tat ggc atg cac tgg gtc cgc caa ggt cca ggc aag ggg ccg gag tgg 144
Tyr Gly Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Pro Glu Trp
35 40 45

gtg gcg ggt ata tgg tac gat gga aca aat aag tat tat gga gac tcc 192
Val Ala Gly Ile Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Gly Asp Ser
50 55 60

gtg acg ggc aga gtc acc atc tcc aga gac aac tcc aag aac acg ctg 240
Val Thr Gly Arg Val Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65 70 75 80

ttt ctg caa atg atc aac gtg aga gtc gag gac acg gct gtg tat tac 288
Phe Leu Gln Met Ile Asn Val Arg Val Glu Asp Thr Ala Val Tyr Tyr
85 90 95

tgt gtg aag gat gca gag cgc gtc cag aaa tgg gct agt tac att atg 336
Cys Val Lys Asp Ala Glu Arg Val Gln Lys Trp Ala Ser Tyr Ile Met
100 105 110

gac gtg tgg ggc caa ggg acc acg gtc acc gtc tcc tcg 375
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 80
<211> 125
<212> PRT
<213> Homo sapiens

<400> 80

Cys Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly
1 5 10 15

Met Ser Leu Ser Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Ser Ser
20 25 30

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

Val Ala Gly Ile Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Gly Asp Ser
50 55 60

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

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

Cys Val Lys Asp Ala Glu Arg Val Gln Lys Trp Ala Ser Tyr Ile Met
100 105 110

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

<210> 81
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(315)
<223> NI-308.16C10 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (73)..(108)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (154)..(174)

<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (271)..(285)
<223> complementarity determining region (CDR) VK-CDR3

<400> 81
tgc gaa att gtg ctg act cag tct cca ggc atc ctg tct ttg tct cga 48
Cys Glu Ile Val Leu Thr Gln Ser Pro Gly Ile Leu Ser Leu Ser Arg
1 5 10 15

ggg aat cgg gtc gcc ctc tcc tgc agg gcc agt cgg agt gtt aat agc 96
Gly Asn Arg Val Ala Leu Ser Cys Arg Ala Ser Arg Ser Val Asn Ser
20 25 30

agc tac tta aat tgg tac cag caa aaa cca ggc cag gct ccc aga ctc 144
Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
35 40 45

ctc atc tat ggt gca tct aaa agg gcc act ggc atc tca gac agg ttc 192
Leu Ile Tyr Gly Ala Ser Lys Arg Ala Thr Gly Ile Ser Asp Arg Phe
50 55 60

cgt ggc act ggg tct ggg aca gac ttc act ctc acc gtc gcc aga ctg 240
Arg Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Ala Arg Leu
65 70 75 80

gag cct gaa gat att gcg gtt tac tac tgt cag cac tat ggt gcc ttc 288
Glu Pro Glu Asp Ile Ala Val Tyr Tyr Cys Gln His Tyr Gly Ala Phe
85 90 95

ggc caa ggg acc aag ctg gag atc aaa 315
Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 82
<211> 105
<212> PRT
<213> Homo sapiens

<400> 82

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

Gly Asn Arg Val Ala Leu Ser Cys Arg Ala Ser Arg Ser Val Asn Ser
20 25 30

Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu

```
        35                  40                  45

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

Arg Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Ala Arg Leu
65                  70                  75                  80

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

Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

<210> 83
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)
<223> NI-308.16C10 VH-PIMC variable heavy chain (VH) sequence after correction of primer induced mutations

<220>
<221> V_region
<222> (94)..(108)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (151)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(342)
<223> complementarity determining region (CDR) VH-CDR3

<400> 83

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tgc cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg        48
Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly
1               5                   10                  15

atg tcc ctg agc ctc tcc tgt gca gcg act gga ttc acc ttc agc agt        96
Met Ser Leu Ser Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Ser Ser
```

```
            20                  25                  30

tat ggc atg cac tgg gtc cgc caa ggt cca ggc aag ggg ccg gag tgg        144
Tyr Gly Met His Trp Val Arg Gln Gly Pro Gly Lys Gly Pro Glu Trp
        35                  40                  45

gtg gcg ggt ata tgg tac gat gga aca aat aag tat tat gga gac tcc        192
Val Ala Gly Ile Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Gly Asp Ser
    50                  55                  60

gtg acg ggc aga gtc acc atc tcc aga gac aac tcc aag aac acg ctg        240
Val Thr Gly Arg Val Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
65                  70                  75                  80

ttt ctg caa atg atc aac gtg aga gtc gag gac acg gct gtg tat tac        288
Phe Leu Gln Met Ile Asn Val Arg Val Glu Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gtg aag gat gca gag cgc gtc cag aaa tgg gct agt tac att atg        336
Cys Val Lys Asp Ala Glu Arg Val Gln Lys Trp Ala Ser Tyr Ile Met
            100                 105                 110

gac gtg tgg ggc caa ggg acc acg gtc acc gtc tcc tcg                    375
Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  84
<211>  125
<212>  PRT
<213>  Homo sapiens

<400>  84

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


Met Ser Leu Ser Leu Ser Cys Ala Ala Thr Gly Phe Thr Phe Ser Ser
            20                  25                  30


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


Val Ala Gly Ile Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Gly Asp Ser
    50                  55                  60


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

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


Cys Val Lys Asp Ala Glu Arg Val Gln Lys Trp Ala Ser Tyr Ile Met
            100                 105                 110


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


<210>  85
<211>  315
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(315)
<223>  NI-308.16C10 VK-PIMC variable light-kappa chain (VK) sequence
       after correction of primer induced mutations

<220>
<221>  V_region
<222>  (73)..(108)
<223>  complementarity determining region (CDR) VK-CDR1

<220>
<221>  V_region
<222>  (154)..(174)
<223>  complementarity determining region (CDR) VK-CDR2

<220>
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ggg aat cgg gtc gcc ctc tcc tgc agg gcc agt cgg agt gtt aat agc         96
Gly Asn Arg Val Ala Leu Ser Cys Arg Ala Ser Arg Ser Val Asn Ser
            20                  25                  30

agc tac tta aat tgg tac cag caa aaa cca ggc cag gct ccc aga ctc        144
Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu
        35                  40                  45
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ctc atc tat ggt gca tct aaa agg gcc act ggc atc tca gac agg ttc        192
Leu Ile Tyr Gly Ala Ser Lys Arg Ala Thr Gly Ile Ser Asp Arg Phe
    50                  55                  60

cgt ggc act ggg tct ggg aca gac ttc act ctc acc gtc gcc aga ctg        240
Arg Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Ala Arg Leu
65                  70                  75                  80

gag cct gaa gat att gcg gtt tac tac tgt cag cac tat ggt gcc ttc        288
Glu Pro Glu Asp Ile Ala Val Tyr Tyr Cys Gln His Tyr Gly Ala Phe
                85                  90                  95

ggc caa ggg acc aag gtg gaa atc aaa                                   315
Gly Gln Gly Thr Lys Val Glu Ile Lys
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<210> 86
<211> 105
<212> PRT
<213> Homo sapiens

<400> 86

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

Gly Asn Arg Val Ala Leu Ser Cys Arg Ala Ser Arg Ser Val Asn Ser
            20                  25                  30

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

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

Arg Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Val Ala Arg Leu
65                  70                  75                  80

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

Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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