SEQUENCE LISTING

<110> Neurimmune Holding AG

<120> Antibody-based therapy of transthyretin (TTR) amyloidosis and human-derived antibodies therefor

<130> NE30A43/P-WO

<150> EP 13199251.3
<151> 2013-12-20

<160> 91

<170> PatentIn version 3.5

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tcc ctg aga ctc tcc tgt gta gcc tct gga ttc act ttt agt aat tat 96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
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tgg atg agt tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtg 144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

gcc aat ata aat caa gat agt gag aaa tac tat gtg gac tct gtg aag 192
Ala Asn Ile Asn Gln Asp Ser Glu Lys Tyr Tyr Val Asp Ser Val Lys
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Gly Arg Phe Ala Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr Leu
65 70 75 80

caa atg aac agc ctg aga gtc gag gac acg ggc gtg tat tac tgt gcg 288
Gln Met Asn Ser Leu Arg Val Glu Asp Thr Gly Val Tyr Tyr Cys Ala
85 90 95

aga gat cgc tat tgc agt ggt ggg aga tgc tcc cgg ggt aac aac tgg 336
Arg Asp Arg Tyr Cys Ser Gly Gly Arg Cys Ser Arg Gly Asn Asn Trp
100 105 110

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

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

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

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

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

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

agt ggg tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag tct 240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

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

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

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

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

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

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

gcc atg agc tgg gtc cgc cag gtt cca ggg aag ggg ctg gag tgg gtc 144
Ala Met Ser Trp Val Arg Gln Val Pro Gly Lys Gly Leu Glu Trp Val
        35   40   45

tca tct att agt ggt agt ggt gat aca aca aaa tac aca gac tcc gtg 192
Ser Ser Ile Ser Gly Ser Gly Asp Thr Thr Lys Tyr Thr Asp Ser Val
    50   55   60

aag ggc cgg ttc acc atc tcc aga gac aat tcc aag aac acg gtg ttt 240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Phe
65   70   75   80

ctg caa atg agc agc ctg aga gcc gag gac acg gcc cta tat tac tgt 288
Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85   90   95

gtg aaa gat ggt agt gga cgg atc gat cct ttt gct tta tgg ggc caa 336
Val Lys Asp Gly Ser Gly Arg Ile Asp Pro Phe Ala Leu Trp Gly Gln
            100   105   110

ggg aca atg gtc acc gtc tct tcg   360
Gly Thr Met Val Thr Val Ser Ser
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            20   25   30

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

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

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
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Val Lys Asp Gly Ser Gly Arg Ile Asp Pro Phe Ala Leu Trp Gly Gln
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Gly Thr Met Val Thr Val Ser Ser
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cag ccg gcc tcc atc tcc tgc agg tct agt cgt agt ctc gta tac agt         96
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Arg Ser Leu Val Tyr Ser
            20                  25                  30

gat gga aac att tac ttg aat tgg ttt cag cag agg cca ggc caa tct        144
Asp Gly Asn Ile Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
        35                  40                  45

cca agg cgc cta att tat aag gtt tct aac cgg gac tct ggg gtc cca        192
Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Asp Ser Gly Val Pro
    50                  55                  60

gac aga ttc agt ggc agt ggg tca gac act gac ttc aca ctg aga atc        240
Asp Arg Phe Ser Gly Ser Gly Ser Asp Thr Asp Phe Thr Leu Arg Ile
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65                  70                  75                  80

agc agg gtg gag gct gag gat gtt ggg gtc tat tac tgc atg cag ggt        288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85                  90                  95

aca cac tgg cct agg acg ttc ggc caa ggg acc aag gtg gag atc aaa        336
Thr His Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


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


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


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


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
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Thr His Trp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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acc ctg tcc ctc acc tgc agt gtc tct ggt ggc tcc atc atc agt agg          96
Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ile Ser Arg
            20                  25                  30

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

tgg att ggg ggt atc tat cat agt ggg aac act tac gac aac ccg tcc         192
Trp Ile Gly Gly Ile Tyr His Ser Gly Asn Thr Tyr Asp Asn Pro Ser
    50                  55                  60

ctc aag agt cga ctc acc atg tcc gta gac acg tcg aag aac cag ttc         240
Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

tcc ctg aat ctg agg tct gtg acc gcc gca gac acg gct gtg tat tac         288
Ser Leu Asn Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg agg ata gtg ccg ggg ggt gat gct ttt gat atc tgg ggc caa         336
Cys Ala Arg Ile Val Pro Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln
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ggg aca atg gtc acc gtc tct tcg                                        360
Gly Thr Met Val Thr Val Ser Ser
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Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ile Ser Arg
            20                  25                  30

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

Trp Ile Gly Gly Ile Tyr His Ser Gly Asn Thr Tyr Asp Asn Pro Ser
    50                  55                  60

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

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

Cys Ala Arg Ile Val Pro Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

gac aga gtc aca atc gct tgc cgg gcc agt cag agc gtt ggc acc tat          96
Asp Arg Val Thr Ile Ala Cys Arg Ala Ser Gln Ser Val Gly Thr Tyr
            20                  25                  30

tta aat tgg tat cag cag aaa aga ggg aaa gcc cct aaa ctc ctc atc         144
Leu Asn Trp Tyr Gln Gln Lys Arg Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

ttt gct gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc         192
Phe Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

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

gaa gac ttt gca act tac tac tgt caa cag agt tac agt tct cct cca         288
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Pro
                85                  90                  95

acg ttc ggc caa ggg acc aag gtg gag atc aaa                             321
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105


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

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

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

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
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1               5                   10                  15

tcc ctg aga ctc tcc tgt gca acc tct gga ttc acc ttc agt aac tat          96
Ser Leu Arg Leu Ser Cys Ala Thr Ser Gly Phe Thr Phe Ser Asn Tyr
            20                  25                  30

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

gcc att att tca tat gat gga aac aat aaa tac tac gca gac tcc gtg         192
Ala Ile Ile Ser Tyr Asp Gly Asn Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

agg ggc cga ttc acc gtc tcc aga gac aat tcc aag aac aca ttc tat         240
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Arg Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Phe Tyr
65                  70                  75                  80

ctg caa atg aac agc ctg aga att gag gac acg gct gta tat ttt tgt        288
Leu Gln Met Asn Ser Leu Arg Ile Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

gcg aga ggg agc ggt aga gca gct cgt cac tgg ttc gac ccc tgg ggc        336
Ala Arg Gly Ser Gly Arg Ala Ala Arg His Trp Phe Asp Pro Trp Gly
            100                 105                 110

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Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


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


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


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


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


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


Ala Arg Gly Ser Gly Arg Ala Ala Arg His Trp Phe Asp Pro Trp Gly
            100                 105                 110


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

tcg atc acc atc tcc tgc act gga acc agc agt gac gtt ggt ggt tat 96
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

aac tat gtc tcc tgg tac caa caa tac cca ggc aaa gcc ccc aaa gtc 144
Asn Tyr Val Ser Trp Tyr Gln Gln Tyr Pro Gly Lys Ala Pro Lys Val
35 40 45

atg att ttt gat gtt ttt aat cgg cct tca ggg gtt tct aat cgc ttc 192
Met Ile Phe Asp Val Phe Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

cag gca gag gac gag gct gat tat tac tgc agt tca tat aca agc agc 288
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
85 90 95

gtc act cct cac tgg gtg ttc ggc gga ggg acc aag ctg acc gtc cta 336
Val Thr Pro His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

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20 25 30

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

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

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

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

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Val Thr Pro His Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
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Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

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

aat ttc tac tgg ggc tgg atc cgc cag ccc cca ggg aag ggg ctg gag         144
Asn Phe Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg att ggg gct att tat tct agt gga aac acc tac tac aac ccg tcc         192
Trp Ile Gly Ala Ile Tyr Ser Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

ctc aag agt cga gtc acc ata tcc gta gac acg tcc aag aaa aag ttc         240
Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Lys Lys Phe
65                  70                  75                  80

tcc ctg aag ctg agc tct gtg acc gcc gct gac acg gct gtc tat tac         288
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga cac tct tgt agt agt gcc agc tgc tat cct ccc ggt ttc         336
Cys Ala Arg His Ser Cys Ser Ser Ala Ser Cys Tyr Pro Pro Gly Phe
            100                 105                 110

tgg ttc gac ccc tgg ggc cag gga acc ctg gtc acc gtc tcc tcg             381
Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  18
<211>  127
<212>  PRT
<213>  Homo sapiens
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<400> 18

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

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

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

Trp Ile Gly Ala Ile Tyr Ser Ser Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

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

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

Cys Ala Arg His Ser Cys Ser Ser Ala Ser Cys Tyr Pro Pro Gly Phe
100 105 110

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

<210> 19
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)
<223> NI-301.28B3 variable K-light chain (VK) sequence

<220>
<221> V_region
<222> (70)..(102)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (148)..(168)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (265)..(294)
<223> complementarity determining region (CDR) VK-CDR3

<400> 19
gaa att gtg atg aca cag tct cca gcc acc ctg tct gcg tct cca ggg 48
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Ala Ser Pro Gly
1 5 10 15

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

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

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

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

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

tgg acg ttc ggc caa ggg acc aag gtg gaa atc aaa                        324
Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 20
<211> 108
<212> PRT
<213> Homo sapiens

<400> 20

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

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

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

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

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

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

Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 21
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(384)
<223> NI-301.119C12 variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (91)..(111)

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

<220>
<221> V_region
<222> (154)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(351)
<223> complementarity determining region (CDR) VH-CDR3

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

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

gtt tac tac tgg agc tgg atc cgc cag cac cca ggg aag ggc ctg gag 144
Val Tyr Tyr Trp Ser Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

tgg att gga tat att tct aat act ggg aac acc tac tac aac ccg tcc 192
Trp Ile Gly Tyr Ile Ser Asn Thr Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

ctc aag agt cga gtt acc ata tcg ata gac acc tcc aag aac cag ttc 240
Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

tcc ctc aac ctg cgc tct gtg act gcc gcg gac acg gcc gac tat ttc 288
Ser Leu Asn Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Asp Tyr Phe
85 90 95

tgt gcg aga gag tat tgt agt ggt ggt aat tgc tac tct cgc ttc tac 336
Cys Ala Arg Glu Tyr Cys Ser Gly Gly Asn Cys Tyr Ser Arg Phe Tyr
100 105 110

tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tcg 384
Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 22
<211> 128
<212> PRT
<213> Homo sapiens

<400> 22

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

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

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

Trp Ile Gly Tyr Ile Ser Asn Thr Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe

```
65                  70                  75                  80

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

Cys Ala Arg Glu Tyr Cys Ser Gly Gly Asn Cys Tyr Ser Arg Phe Tyr
            100                 105                 110

Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125


<210>  23
<211>  336
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(336)
<223>  NI-301.119C12 variable light chain (VL) sequence

<220>
<221>  V_region
<222>  (67)..(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)..(306)
<223>  complementarity determining region (CDR) VL-CDR3

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

agg gtc acc atc tcc tgc act ggg agc agc tcc aac atc ggg gca ggt          96
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Ala Gly
            20                  25                  30

tat ggt gta cac tgg tac cag caa ctt tca gga aca ccc ccc aaa ctc         144
Tyr Gly Val His Trp Tyr Gln Gln Leu Ser Gly Thr Pro Pro Lys Leu
        35                  40                  45

ctc atc tat gga gac aac aat cgg ccc tca ggg gtc cct gac cga ttc         192
Leu Ile Tyr Gly Asp Asn Asn Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

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

cag gct gag gat gag gct cat tat tac tgc cag tcc tat gac acc acc         288
Gln Ala Glu Asp Glu Ala His Tyr Tyr Cys Gln Ser Tyr Asp Thr Thr
                85                  90                  95

ttg agt ggt tcg agg gtg ttc ggc gga ggg acc aag ctg acc gtc cta         336
Leu Ser Gly Ser Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 24
<211> 112
<212> PRT
<213> Homo sapiens

<400> 24

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

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

Tyr Gly Val His Trp Tyr Gln Gln Leu Ser Gly Thr Pro Pro Lys Leu
35 40 45

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

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

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

Leu Ser Gly Ser Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 25
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(363)
<223> NI-301.5D8 variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (148)..(195)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (292)..(330)
<223> complementarity determining region (CDR) VH-CDR3

<400> 25
cag gtg cag cta cag cag tgg ggc gca gga cgg ttg aag cct tcg gag 48
Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Arg Leu Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acg tgc gct gtc tat ggt ggg tct ttc agt gct tac 96
Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Ala Tyr
20 25 30

```
tac tgg aat tgg atc cgc cag gcc cca ggg aag ggg ctg gag tgg att        144
Tyr Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
        35                  40                  45

ggt gaa gtc agt cat ggt ggc agc agc aac tac agc ccg tcc ctc agg        192
Gly Glu Val Ser His Gly Gly Ser Ser Asn Tyr Ser Pro Ser Leu Arg
    50                  55                  60

ggt cga gtc gcc att tct tta gac acg tcc aag agc cag ttc tcc ctg        240
Gly Arg Val Ala Ile Ser Leu Asp Thr Ser Lys Ser Gln Phe Ser Leu
65                  70                  75                  80

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

aga ggc agc cct gta gta cta cca ggt gcc aga ttc gac ccc tgg ggc        336
Arg Gly Ser Pro Val Val Leu Pro Gly Ala Arg Phe Asp Pro Trp Gly
            100                 105                 110

cag gga acc ctg gtc acc gtc tcc tcg                                   363
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 26
<211> 121
<212> PRT
<213> Homo sapiens

<400> 26

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

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

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

Gly Glu Val Ser His Gly Gly Ser Ser Asn Tyr Ser Pro Ser Leu Arg
    50                  55                  60

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

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

Arg Gly Ser Pro Val Val Leu Pro Gly Ala Arg Phe Asp Pro Trp Gly
            100                 105                 110

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

<210> 27
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(327)
<223> NI-301.5D8 variable light chain (VL) sequence

<220>
<221> V_region
<222> (91)..(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)..(297)
<223> complementarity determining region (CDR) VL-CDR3

<400> 27
cag tct gcc ctg act cag cct gcc tcc gtg tct ggg ttt cct gga cag 48
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Phe Pro Gly Gln
1 5 10 15

tcg atc acc atc tcc tgc act gga acc agc agt gat gtt ggg agt tat 96
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr
20 25 30

aac ctt gtc tcc tgg tac caa caa cac cca ggc aaa gcc ccc aaa ctc 144
Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
35 40 45

ttg att tat gag gtc aat aag cgg ccc tca gga gtt tct act cgc ttc 192
Leu Ile Tyr Glu Val Asn Lys Arg Pro Ser Gly Val Ser Thr Arg Phe
50 55 60

tct ggc tcc aag tct ggc aac acg gcc tcc ctg acg atc tct ggg ctc 240
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

cag act gag gac gag gct gat tat tac tgc tgc tca tat gca ggt agt 288
Gln Thr Glu Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Tyr Ala Gly Ser
85 90 95

act aag gtc ttc gga att ggg acc aag gtc acc gtc cta 327
Thr Lys Val Phe Gly Ile Gly Thr Lys Val Thr Val Leu
100 105

<210> 28
<211> 109
<212> PRT
<213> Homo sapiens

<400> 28

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Ser Tyr
20 25 30

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

```
Leu Ile Tyr Glu Val Asn Lys Arg Pro Ser Gly Val Ser Thr Arg Phe
    50                  55                  60


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


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


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


<210>  29
<211>  372
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(372)
<223>  NI-301.9D5 variable heavy chain (VH) sequence

<220>
<221>  V_region
<222>  (91)..(111)
<223>  complementarity determining region (CDR) VH-CDR1

<220>
<221>  V_region
<222>  (154)..(201)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (298)..(339)
<223>  complementarity determining region (CDR) VH-CDR3

<400>  29
cag gtg cag ctg cag gag tcg ggc cca ggc ctg gtg aag cct tca gag          48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1               5                   10                  15

acc ctg tcc ctc acc tgc att gtc tct ggt gtc tcc atc aga agt ggt          96
Thr Leu Ser Leu Thr Cys Ile Val Ser Gly Val Ser Ile Arg Ser Gly
            20                  25                  30

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

tgg gtt ggg ttc atc tat tac act ggg aac acc tac tac aac ccg tcc         192
Trp Val Gly Phe Ile Tyr Tyr Thr Gly Asn Thr Tyr Tyr Asn Pro Ser
    50                  55                  60

ctc aag agt cga gct acc ata tca gta gac acc tct aag aac cag ttc         240
Leu Lys Ser Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65                  70                  75                  80

tcc ctg agg ctg acc gct gtg act gcc gcg gac acg gcc gtg tat tac         288
Ser Leu Arg Leu Thr Ala Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt gcg aga gat tgt agt ggt ggc agc tgc ccc gag tcc tac ttt gac         336
Cys Ala Arg Asp Cys Ser Gly Gly Ser Cys Pro Glu Ser Tyr Phe Asp
            100                 105                 110
```

tcc tgg ggt cgg ggc acc ctg gtc acc gtc tcc tcg 372
Ser Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 30
<211> 124
<212> PRT
<213> Homo sapiens

<400> 30

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

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

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

Trp Val Gly Phe Ile Tyr Tyr Thr Gly Asn Thr Tyr Tyr Asn Pro Ser
50 55 60

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

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

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

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

<210> 31
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(327)
<223> NI-301.9D5 variable K-light chain (VK) sequence

<220>
<221> V_region
<222> (70)..(102)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (148)..(168)
<223> complementarity determining region (CDR) VK-CDR2

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

<400> 31
gaa att gtg atg aca cag tct cca gcc acc ctg tct ttg tct cca ggg 48
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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

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

tat gat gca tcc aag agg gcc act ggc atc cca gcc agg ttc agt gac 192
Tyr Asp Ala Ser Lys Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Asp
50 55 60

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

gaa gac tct gcg gtt tat tac tgt cag cag cgt acc aac tgg cct cca 288
Glu Asp Ser Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Pro
85 90 95

cac ctc act ttc ggc gga ggg acc aag gtg gaa atc aaa 327
His Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 32
<211> 109
<212> PRT
<213> Homo sapiens

<400> 32

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

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

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

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

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

Glu Asp Ser Ala Val Tyr Tyr Cys Gln Gln Arg Thr Asn Trp Pro Pro
85 90 95

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

<210> 33
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(357)
<223> NI-301.104F5 variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (148)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(324)
<223> complementarity determining region (CDR) VH-CDR3

<400> 33
cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct gag agg 48
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Glu Arg
1 5 10 15

tcc ctg aga ctc tcc tgt gca gcg tct gga ttc acc ttc agg agc tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Ser Tyr
20 25 30

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

gca gtt ata tgg ttt gat gga agt aat aaa tac tat gca gac tcc gtg 192
Ala Val Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
50 55 60

aag ggc cga ttc acc gtc tcc aga gac aat tcc aag aac acg ctg tat 240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

ctg caa atg aac agc ctg aga gcc gag gac acg gct gtc tac tac tgt 288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gca aga gat ggt ata gca gcc act tat gcg gac tac tgg ggc cag gga 336
Ala Arg Asp Gly Ile Ala Ala Thr Tyr Ala Asp Tyr Trp Gly Gln Gly
100 105 110

acc ctg gtc acc gtc tcc tcg 357
Thr Leu Val Thr Val Ser Ser
115

<210> 34
<211> 119
<212> PRT
<213> Homo sapiens

<400> 34

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

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

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

Ala Val Ile Trp Phe Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

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

Ala Arg Asp Gly Ile Ala Ala Thr Tyr Ala Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
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<210> 35
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(321)
<223> NI-301.104F5 variable K-light chain (VK) sequence

<220>
<221> V_region
<222> (70)..(102)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (148)..(168)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (265)..(291)
<223> complementarity determining region (CDR) VK-CDR3

<400> 35

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gaa att gtg ttg aca cag tct cca gcc acc ctg tct ttg tct cca ggg          48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5                   10                  15

gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt gtt cgc agc tac          96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr
            20                  25                  30

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

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

agt ggg tct ggg aca gac ttc act ctc acc atc agc agc ctg gag cct         240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
```

```
65                  70                  75                  80

gaa gat ttt gca gtt tat tac tgt cag caa cgt agc aac tgg ccg atc        288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
                85                  90                  95

acc ttc ggc caa ggg aca cga ctg gag att aaa                            321
Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100                 105


<210>  36
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  36

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


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


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


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


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


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


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


<210>  37
<211>  375
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(375)
<223>  NI-301.21F10 variable heavy chain (VH) sequence

<220>
<221>  V_region
<222>  (91)..(114)
<223>  complementarity determining region (CDR) VH-CDR1

<220>
<221>  V_region
<222>  (157)..(207)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (304)..(342)
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<223> complementarity determining region (CDR) VH-CDR3

<400> 37
cag gtg cag ctg gtg gag tcg ggg gga ggt ttg gtc cag cct ggg ggg 48
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ttg aga ctg tcc tgt gcg gtc tct gga ttc acc ctt agt agt ctt 96
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Thr Leu Ser Ser Leu
20 25 30

agt tct tat tac atg agt tgg gtc cgc cag gct cca ggg aag ggg ctg 144
Ser Ser Tyr Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
35 40 45

gag tgg gtg gcc act ata aac cca ggt gga agt gag aag tcc tat gtg 192
Glu Trp Val Ala Thr Ile Asn Pro Gly Gly Ser Glu Lys Ser Tyr Val
50 55 60

gac tct gtg aag ggc cga ttc acc gtc tcc aga gac aac gcc agg agc 240
Asp Ser Val Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Arg Ser
65 70 75 80

tca gta tat ttg caa atg gac agc ctg aca gtc gag gac acg gct att 288
Ser Val Tyr Leu Gln Met Asp Ser Leu Thr Val Glu Asp Thr Ala Ile
85 90 95

tat tac tgt gcg aga cca aga tat tgc act agt ggt ggt tgc tat ttt 336
Tyr Tyr Cys Ala Arg Pro Arg Tyr Cys Thr Ser Gly Gly Cys Tyr Phe
100 105 110

gac aac tgg ggc cag gga acc ctg gtc acc gtc tcc tcg 375
Asp Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 38
<211> 125
<212> PRT
<213> Homo sapiens

<400> 38

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

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

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

Glu Trp Val Ala Thr Ile Asn Pro Gly Gly Ser Glu Lys Ser Tyr Val
50 55 60

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

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

Tyr Tyr Cys Ala Arg Pro Arg Tyr Cys Thr Ser Gly Gly Cys Tyr Phe
100 105 110

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


<210>  39
<211>  327
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(327)
<223>  NI-301.21F10 variable light chain (VL) sequence

<220>
<221>  V_region
<222>  (67)..(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)..(297)
<223>  complementarity determining region (CDR) VL-CDR3

<400>  39
cag tct gcc ctg act cag cct cgc tca gtg tcc ggg tct cct gga cag         48
Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
1               5                   10                  15

tca gtc acc atc tcc tgc act gca acc aat agt gat gtt ggc gat tat         96
Ser Val Thr Ile Ser Cys Thr Ala Thr Asn Ser Asp Val Gly Asp Tyr
            20                  25                  30

aag tct gtc tcc tgg tac caa caa cac cca ggc aaa gcc ccc aaa ctc        144
Lys Ser Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

atg att tat gat gtc ggt agg cgg ccc tca ggg gtc cct gat cgc ttc        192
Met Ile Tyr Asp Val Gly Arg Arg Pro Ser Gly Val Pro Asp Arg Phe
    50                  55                  60

tct ggc tcc aaa tct gac aac acg gcc ttc ctg acc atc tct ggg ctc        240
Ser Gly Ser Lys Ser Asp Asn Thr Ala Phe Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

cag act gag gat gaa gct gat tac ttt tgc tgt ata tat gta ggc agg        288
Gln Thr Glu Asp Glu Ala Asp Tyr Phe Cys Cys Ile Tyr Val Gly Arg
                85                  90                  95

tct tcg gtg ttc ggc gga ggg acc aag ttg acc gtc ctg                    327
Ser Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  40
<211>  109
<212>  PRT
<213>  Homo sapiens

<400>  40

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

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

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

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

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

Gln Thr Glu Asp Glu Ala Asp Tyr Phe Cys Cys Ile Tyr Val Gly Arg
                85                  90                  95

Ser Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

<210> 41
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(372)
<223> NI-301.9G12 variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (91)..(108)
<223> complementarity determining region (CDR) VH-CDR1

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

<220>
<221> V_region
<222> (295)..(339)
<223> complementarity determining region (CDR) VH-CDR3

<400> 41

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

acc ctg tcc ctc acc tgc gct gtc tct ggt ttc tcc atc agc agt ggt         96
Thr Leu Ser Leu Thr Cys Ala Val Ser Gly Phe Ser Ile Ser Ser Gly
            20                  25                  30

tac tac tgg ggc tgg atc cgg cag ccc cca ggg acg ggg ctg gag tgg        144
Tyr Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Thr Gly Leu Glu Trp
        35                  40                  45

att ggg agt atg tat cat agt ggg agg acc tac tac aac ccg tcc ctc        192
Ile Gly Ser Met Tyr His Ser Gly Arg Thr Tyr Tyr Asn Pro Ser Leu
    50                  55                  60

aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag ttg tcc        240
```

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

ctg aag ctg agc tct gtg acc gcc gca gac acg gcc gtg tat tac tgt        288
Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcg agg ggc ttc gat act agt ggt tcc cat cgg ccc ctc tcg act gac        336
Ala Arg Gly Phe Asp Thr Ser Gly Ser His Arg Pro Leu Ser Thr Asp
            100                 105                 110

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


<210>  42
<211>  124
<212>  PRT
<213>  Homo sapiens

<400>  42

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


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


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


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


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


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


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


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


<210>  43
<211>  330
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(330)
<223>  NI-301.9G12 variable light chain (VL) sequence

<220>
<221>  V_region
<222>  (67)..(105)
<223>  complementarity determining region (CDR) VL-CDR1
```

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

<220>
<221> V_region
<222> (268)..(300)
<223> complementarity determining region (CDR) VL-CDR3

<400> 43
cag tct gtg ttg acg cag ccg ccc tca gtg tct gcg gcc cca gga cag 48
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1 5 10 15

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

tat gta tcc tgg tac cag cag ctc cca gga aca gcc ccc aaa ctc ctc 144
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

att tat gac aat aat aag cga ccc tca ggg att cct gac cga atc tct 192
Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Ile Ser
50 55 60

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

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

agt gct tat gtc ttc gga act ggg acc aag gtc acc gtc cta 330
Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
100 105 110

<210> 44
<211> 110
<212> PRT
<213> Homo sapiens

<400> 44

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

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

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

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

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

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

```
Ser Ala Tyr Val Phe Gly Thr Gly Thr Lys Val Thr Val Leu
            100                 105                 110


<210>  45
<211>  357
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(357)
<223>  NI-301.12D3 variable heavy chain (VH) sequence

<220>
<221>  V_region
<222>  (91)..(105)
<223>  complementarity determining region (CDR) VH-CDR1

<220>
<221>  V_region
<222>  (148)..(198)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (295)..(324)
<223>  complementarity determining region (CDR) VH-CDR3

<400>  45
gag gtg cag ctg gtg gag act ggg gga ggc gtg gtc cag cct ggg agg          48
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Val Val Gln Pro Gly Arg
1               5                   10                  15

tcc ctg aga ctc tcc tgt gta gcg tct gga ttc acc ttc agg aac tat          96
Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Arg Asn Tyr
            20                  25                  30

ggc atg cac tgg gtc cgc cgg gcc cca ggc agg ggg ctg gag tgg gta         144
Gly Met His Trp Val Arg Arg Ala Pro Gly Arg Gly Leu Glu Trp Val
        35                  40                  45

gca gtt ata tgg tct gat gga agt gat aaa tac tat gca gac tcc gtg         192
Ala Val Ile Trp Ser Asp Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

gag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg gtg ttt         240
Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Val Phe
65                  70                  75                  80

ctc caa atg aac agc ctg aga gcc gac gac acg gct gta tac ttc tgt         288
Leu Gln Met Asn Ser Leu Arg Ala Asp Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

gcg aga gag ccg agc agc acc tgg gct ttt gac tac tgg ggc cag gga         336
Ala Arg Glu Pro Ser Ser Thr Trp Ala Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

acc ctg gtc acc gtc tcc tcg                                            357
Thr Leu Val Thr Val Ser Ser
        115


<210>  46
<211>  119
<212>  PRT
<213>  Homo sapiens
```

<400> 46

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

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

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

Ala Val Ile Trp Ser Asp Gly Ser Asp Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Thr Leu Val Thr Val Ser Ser
115

<210> 47
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)
<223> NI-301.12D3 variable light chain (VL) sequence

<220>
<221> V_region
<222> (67)..(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)..(300)
<223> complementarity determining region (CDR) VL-CDR3

<400> 47
cag tct gcc ctg act cag cct gcc tcc gtg tct ggg tct cct gga cag 48
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
1 5 10 15

tcg atc acc atc tcc tgc act gga acc agc agt gat gtt ggg ggt tat 96
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

```
aac ctt gtc tcc tgg tac caa cag cac cca ggc aaa gcc ccc aaa ctc        144
Asn Leu Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

atg att tat gag gac att aag ggg ccc tca ggg gtt tct aat cgc ttc        192
Met Ile Tyr Glu Asp Ile Lys Gly Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

tct ggc tcc aag tct ggc aac acg gcc tcc ctg aca atc tct ggg ctc        240
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

cag gct gag gac gag gct gat tat ttc tgc tgc tca tat gca ggt act        288
Gln Ala Glu Asp Glu Ala Asp Tyr Phe Cys Cys Ser Tyr Ala Gly Thr
                85                  90                  95

ggc act ctg gta ttc ggc gga ggg acc aag ctg acc gtc cta                330
Gly Thr Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  48
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  48

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


Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30


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


Met Ile Tyr Glu Asp Ile Lys Gly Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60


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


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


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


<210>  49
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Epitope recognized by NI-301.59F1 antibody


<220>
<221>  PEPTIDE
<222>  (1)..(9)
<223>  Epitope of NI-301.59F1 antibody, aa 61to aa 69
```

<220>
<221> PEPTIDE
<222> (1)..(9)
<223> Epitope of NI-301.59F1 antibody, aa 61 to aa 69

<400> 49

Glu Glu Glu Phe Val Glu Gly Ile Tyr
1   5

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognized by NI-301.35G11 antibody

<220>
<221> PEPTIDE
<222> (1)..(11)
<223> Epitope of NI-301.35G11 antibody, aa 53 to aa 63

<400> 50

Gly Glu Leu His Gly Leu Thr Thr Glu Glu Glu
1   5   10

<210> 51
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope recognized by NI-301.37F1 antibody

<220>
<221> PEPTIDE
<222> (1)..(5)
<223> Epitope of NI-301.37F1 antibody, aa 41 to aa 45

<400> 51

Trp Glu Pro Phe Ala
1   5

<210> 52
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(360)
<223> NI-301.37F1-PIMC variable heavy chain (VH) sequence after
       correction of primer induced mutations

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region

<222> (154)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(327)
<223> complementarity determining region (CDR) VH-CDR3

<400> 52
cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag 48
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

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

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

tgg att ggg ggt atc tat cat agt ggg aac act tac gac aac ccg tcc 192
Trp Ile Gly Gly Ile Tyr His Ser Gly Asn Thr Tyr Asp Asn Pro Ser
50 55 60

ctc aag agt cga ctc acc atg tcc gta gac acg tcg aag aac cag ttc 240
Leu Lys Ser Arg Leu Thr Met Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

tcc ctg aat ctg agg tct gtg acc gcc gca gac acg gct gtg tat tac 288
Ser Leu Asn Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

tgt gcg agg ata gtg ccg ggg ggt gat gct ttt gat atc tgg ggc caa 336
Cys Ala Arg Ile Val Pro Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

ggg aca atg gtc acc gtc tct tcg 360
Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 53
<211> 120
<212> PRT
<213> Homo sapiens

<400> 53

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

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

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

Trp Ile Gly Gly Ile Tyr His Ser Gly Asn Thr Tyr Asp Asn Pro Ser
50 55 60

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

Ser Leu Asn Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr

```
                85                  90                  95

Cys Ala Arg Ile Val Pro Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 54
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(360)
<223> NI-301.44E4 VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (148)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(327)
<223> complementarity determining region (CDR) VH-CDR3

<400> 54

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

tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt agc agc tat         96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

gcc atg atc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc        144
Ala Met Ile Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

tca ggt att agt ggc agt ggc agt acg aca tac tac gca gac tcc gtg        192
Ser Gly Ile Ser Gly Ser Gly Ser Thr Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

aag ggc cgg ttc gcc atc tcc aga gac aaa tcc aag aac acg ctg tcc        240
Lys Gly Arg Phe Ala Ile Ser Arg Asp Lys Ser Lys Asn Thr Leu Ser
65                  70                  75                  80

cta caa atg aac agc ctg aga gcc gag gac acg gcc gta tat tac tgt        288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gca aaa ggg gca tgg gag ata ccc acc tac ttt gac aac tgg ggc cag        336
Ala Lys Gly Ala Trp Glu Ile Pro Thr Tyr Phe Asp Asn Trp Gly Gln
            100                 105                 110

gga acc ctg gtc acc gtc tcc tcg                                      360
Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 55
<211> 120
<212> PRT
<213> Homo sapiens

<400> 55

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

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

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

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

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

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

Ala Lys Gly Ala Trp Glu Ile Pro Thr Tyr Phe Asp Asn Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 56
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(327)
<223> NI-301.44E4 VK variable light-kappa chain (VK) sequence

<220>
<221> V_region
<222> (70)..(102)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (148)..(168)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (265)..(297)
<223> complementarity determining region (CDR) VK-CDR3

<400> 56
gaa att gtg ctg act cag tct cca gcc acc ctg tct gtg tct cca ggg 48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

```
gaa aga gcc acc ctc tcc tgc agg gcc agt cag agt att agg aac aac          96
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Ile Arg Asn Asn
            20                  25                  30

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

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

act ggg tct ggg aca gag ttc act ctc atc gtc agc agc ctg cag tct         240
Thr Gly Ser Gly Thr Glu Phe Thr Leu Ile Val Ser Ser Leu Gln Ser
65                  70                  75                  80

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

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

<210> 57
<211> 109
<212> PRT
<213> Homo sapiens

<400> 57

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

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

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

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

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

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

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

<210> 58
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope of NI-301.59F1 antibody, aa 61to aa 68 after alanine scan

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<400> 58

Glu Glu Phe Xaa Glu Gly Ile Tyr
1 5

<210> 59
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope of NI-301.35G11 antibody, aa 54 to aa 61 after alanine scan

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 59

Glu Leu Xaa Gly Leu Thr Xaa Glu
1 5

<210> 60
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Epitope of NI-301.37F1 antibody, aa 41 to aa 45 after alanine scan

<400> 60

Trp Glu Pro Phe Ala
1 5

<210> 61
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(375)
<223> NI-301.18C4 VH variable heavy chain (VH) sequence

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region

<222> (148)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(342)
<223> complementarity determining region (CDR) VH-CDR3

<400> 61
gag gtg cag ctg gtg gag tct ggg gga acc ttg gtc cag ccg ggg ggg 48
Glu Val Gln Leu Val Glu Ser Gly Gly Thr Leu Val Gln Pro Gly Gly
1 5 10 15

tcc ctg agg ctc tcc tgc gca gcg tcg gga ttc aca ttc aac att tat 96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Ile Tyr
20 25 30

gcc atg acc tgg gtc cgc ctg tct cca gtg agg gga ctg gag tgg gtc 144
Ala Met Thr Trp Val Arg Leu Ser Pro Val Arg Gly Leu Glu Trp Val
35 40 45

tct act att act agt ggt ggc gtc agc ata tat tac gca gac tcc ata 192
Ser Thr Ile Thr Ser Gly Gly Val Ser Ile Tyr Tyr Ala Asp Ser Ile
50 55 60

aag ggc cgc ttc acc gtc tcc aga gac aat gcc aag aac atg gtg ttt 240
Lys Gly Arg Phe Thr Val Ser Arg Asp Asn Ala Lys Asn Met Val Phe
65 70 75 80

cta caa ctg gac aac ctg aca gtc gat gac acg gcc ata tat tac tgt 288
Leu Gln Leu Asp Asn Leu Thr Val Asp Asp Thr Ala Ile Tyr Tyr Cys
85 90 95

ggg aag gac gga aac tgc gat gag aca agt tgt tac tta agg ggg atg 336
Gly Lys Asp Gly Asn Cys Asp Glu Thr Ser Cys Tyr Leu Arg Gly Met
100 105 110

gac gtc 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> 62
<211> 125
<212> PRT
<213> Homo sapiens

<400> 62

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

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

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

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

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

Leu Gln Leu Asp Asn Leu Thr Val Asp Asp Thr Ala Ile Tyr Tyr Cys

```
                85                  90                  95

Gly Lys Asp Gly Asn Cys Asp Glu Thr Ser Cys Tyr Leu Arg Gly Met
            100                 105                 110

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

<210> 63
<211> 333
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(333)
<223> NI-301.18C4 VL variable light chain (VL) sequence

<220>
<221> V_region
<222> (67)..(105)
<223> complementarity determining region (CDR) VL-CDR1

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

<220>
<221> V_region
<222> (268)..(303)
<223> complementarity determining region (CDR) VL-CDR3

<400> 63

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

aag gtc acc atc tcc tgc tct ggt agc agg tcc gac att ggg tct aaa         96
Lys Val Thr Ile Ser Cys Ser Gly Ser Arg Ser Asp Ile Gly Ser Lys
            20                  25                  30

ctt gtt tcc tgg tac cag gta atc cca gga aga gcc ccc cgg ctc gtc        144
Leu Val Ser Trp Tyr Gln Val Ile Pro Gly Arg Ala Pro Arg Leu Val
        35                  40                  45

att ttt gac act tat aag cgg ccc tca ggg gta cct gcc cgc ttc tct        192
Ile Phe Asp Thr Tyr Lys Arg Pro Ser Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

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

cct ggg gac gag gcc gaa tat ttc tgc gga tca tgg ggt aac agt gag        288
Pro Gly Asp Glu Ala Glu Tyr Phe Cys Gly Ser Trp Gly Asn Ser Glu
                85                  90                  95

aat ttt tat tat gtc ttc gga tct ggg acc cgg gtc acc gtc ctg            333
Asn Phe Tyr Tyr Val Phe Gly Ser Gly Thr Arg Val Thr Val Leu
            100                 105                 110
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<210> 64
<211> 111
<212> PRT

<213> Homo sapiens

<400> 64

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

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

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

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

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

Pro Gly Asp Glu Ala Glu Tyr Phe Cys Gly Ser Trp Gly Asn Ser Glu
85 90 95

Asn Phe Tyr Tyr Val Phe Gly Ser Gly Thr Arg Val Thr Val Leu
100 105 110

<210> 65
<211> 354
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(354)
<223> NI-301.11A10 variable heavy chain (VH) sequence (PIMC by default)

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (154)..(201)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (298)..(321)
<223> complementarity determining region (CDR) VH-CDR3

<400> 65
cag ctg cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag 48
Gln Leu Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

acc ctg tcc ctc acc tgc act gtg tct ggt ggc tcc atc agc agt aga 96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Arg
20 25 30

agt tac tac tgg ggc tgg atg cgc cag ccc cca ggg aag ggg ctg gag 144
Ser Tyr Tyr Trp Gly Trp Met Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

```
tgg att ggg agt att tat tat agt ggg agc acc ctc tac aat ccg tcc        192
Trp Ile Gly Ser Ile Tyr Tyr Ser Gly Ser Thr Leu Tyr Asn Pro Ser
    50                  55                  60

ctc aag agt cga gtc acc atg tca ata gtc acg tcg agg aac cag ttc        240
Leu Lys Ser Arg Val Thr Met Ser Ile Val Thr Ser Arg Asn Gln Phe
65                  70                  75                  80

tcc ctg aag ctg agt tct gtg acc gcc gcg gac acg gcc gtg tat tat        288
Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
                85                  90                  95

tgt acc cga atg ggg gag ggg ggg cgg gac tac tgg ggc cag gga acc        336
Cys Thr Arg Met Gly Glu Gly Gly Arg Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

ctg gtc acc gtc tcc tcg                                               354
Leu Val Thr Val Ser Ser
        115
```

<210> 66
<211> 118
<212> PRT
<213> Homo sapiens

<400> 66

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

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

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

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

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

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

Cys Thr Arg Met Gly Glu Gly Gly Arg Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
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<210> 67
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(321)

<223> NI-301.11A10 variable K-light chain (VK) sequence

<220>
<221> V_region
<222> (70)..(102)
<223> complementarity determining region (CDR) VK-CDR1

<220>
<221> V_region
<222> (148)..(168)
<223> complementarity determining region (CDR) VK-CDR2

<220>
<221> V_region
<222> (265)..(291)
<223> complementarity determining region (CDR) VK-CDR3

<400> 67
gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct gta gga 48
Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

gac aga gtc acc atc act tgc cgg gcc agt cag agt att agt agt tgg 96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

ttg gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag gtc ctg atc 144
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Val Leu Ile
35 40 45

tat gat gcc tcc agt ttg gaa aga ggg gtc cca tca agg ttc agc ggc 192
Tyr Asp Ala Ser Ser Leu Glu Arg Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

agt ggg tct ggg aca gaa ttc act ctc acc atc agc agc ctg cag cct 240
Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

gat gat tct gca act tat tac tgc caa cac tat aat ggt tat tca agg 288
Asp Asp Ser Ala Thr Tyr Tyr Cys Gln His Tyr Asn Gly Tyr Ser Arg
85 90 95

acg ttc ggc cgc ggg acc aag gtg gaa atc aaa 321
Thr Phe Gly Arg Gly Thr Lys Val Glu Ile Lys
100 105

<210> 68
<211> 107
<212> PRT
<213> Homo sapiens

<400> 68

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

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

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

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

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


Asp Asp Ser Ala Thr Tyr Tyr Cys Gln His Tyr Asn Gly Tyr Ser Arg
                85                  90                  95


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


<210>  69
<211>  372
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(372)
<223>  NI-301.3C9 variable heavy chain (VH) sequence (PIMC by default)

<220>
<221>  V_region
<222>  (91)..(111)
<223>  complementarity determining region (CDR) VH-CDR1

<220>
<221>  V_region
<222>  (154)..(201)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (298)..(339)
<223>  complementarity determining region (CDR) VH-CDR3

<400>  69
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag tct tcg cag         48
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Ser Ser Gln
1               5                   10                  15

acc ctg tcc ctc acc tgc act gtc tct ggt gcc tcc ttc acc agg ggt         96
Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Phe Thr Arg Gly
            20                  25                  30

gat ttc tac tgg agt tgg atc cgc cag gtc cca ggg aag ggc ctg gaa        144
Asp Phe Tyr Trp Ser Trp Ile Arg Gln Val Pro Gly Lys Gly Leu Glu
        35                  40                  45

tgg att ggt tac ata tat tcc act ggg gac gtc tac tac aat ccg tct        192
Trp Ile Gly Tyr Ile Tyr Ser Thr Gly Asp Val Tyr Tyr Asn Pro Ser
    50                  55                  60

ctc aag agt cga gca aac atc tcg gtc gac acg ccc aag aag cag ttc        240
Leu Lys Ser Arg Ala Asn Ile Ser Val Asp Thr Pro Lys Lys Gln Phe
65                  70                  75                  80

ttc ctg aaa ttg acc tct ttg act gcc gca gac acg gcc gtc tat ttt        288
Phe Leu Lys Leu Thr Ser Leu Thr Ala Ala Asp Thr Ala Val Tyr Phe
                85                  90                  95

tgt gcc agg gaa gga caa tat tgt agc ggt ggt agt tgc tac cct gaa        336
Cys Ala Arg Glu Gly Gln Tyr Cys Ser Gly Gly Ser Cys Tyr Pro Glu
            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> 70
<211> 124
<212> PRT
<213> Homo sapiens

<400> 70

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

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

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

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

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

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

Cys Ala Arg Glu Gly Gln Tyr Cys Ser Gly Gly Ser Cys Tyr Pro Glu
100 105 110

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

<210> 71
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(318)
<223> NI-301.3C9 variable light chain (VL) sequence (PIMC by default)

<220>
<221> V_region
<222> (67)..(99)
<223> complementarity determining region (CDR) VL-CDR1

<220>
<221> V_region
<222> (145)..(165)
<223> complementarity determining region (CDR) VL-CDR2

<220>
<221> V_region
<222> (262)..(288)
<223> complementarity determining region (CDR) VL-CDR3

<400> 71
tcc tat gag ctg act cag cca ccc tca gtg tcc gtg tcc cca gga cag 48
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln

```
1               5                   10                  15

aca gcc acc atc acc tgc tct gga gat aat ttg gga cat aaa ttt act          96
Thr Ala Thr Ile Thr Cys Ser Gly Asp Asn Leu Gly His Lys Phe Thr
            20                  25                  30

tgc tgg tat cag cag aag cca ggc cag tcc cct gtc ctg gtc atc tat         144
Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
        35                  40                  45

caa gat cac aag cgg ccc tca ggg atc cct gag cga ttc tcc ggc tcc         192
Gln Asp His Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

aac tct ggg gac aca gcc act ctg acc atc agc ggg acc cag gct atg         240
Asn Ser Gly Asp Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80

gat gag gct gag tat tac tgt cag gcg tgg gcc ttc ccc tat gtg gtc         288
Asp Glu Ala Glu Tyr Tyr Cys Gln Ala Trp Ala Phe Pro Tyr Val Val
                85                  90                  95

ttc ggc gga ggg acc aag ctg acc gtc cta                                 318
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  72
<211>  106
<212>  PRT
<213>  Homo sapiens

<400>  72

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


Thr Ala Thr Ile Thr Cys Ser Gly Asp Asn Leu Gly His Lys Phe Thr
            20                  25                  30


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


Gln Asp His Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60


Asn Ser Gly Asp Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65                  70                  75                  80


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


Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105


<210>  73
<211>  372
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
```

<222> (1)..(372)
<223> NI-301.14D8 variable heavy chain (VH) sequence (not PIMC)

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (148)..(198)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (295)..(339)
<223> complementarity determining region (CDR) VH-CDR3

<400> 73

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gag gtg cag ctg gtg gag act ggg gga cgc ttg gtc cag ccg ggg ggg          48
Glu Val Gln Leu Val Glu Thr Gly Gly Arg Leu Val Gln Pro Gly Gly
1               5                   10                  15

tcc gtg aga ctc tcc tgt ata gcc tct gga ttt ccc ttt agg aat tat          96
Ser Val Arg Leu Ser Cys Ile Ala Ser Gly Phe Pro Phe Arg Asn Tyr
            20                  25                  30

tgg atg agt tgg gtc cgc cag cct cca ggg aag ggg ctg gag tgg gtg         144
Trp Met Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

gcc aac ata aag gaa gat ggc agt gac aga tac tat gtg gac tct gtg         192
Ala Asn Ile Lys Glu Asp Gly Ser Asp Arg Tyr Tyr Val Asp Ser Val
    50                  55                  60

aag ggc cgc ttc acc atc ttt aga gac aac gcc aag aat ttt ctg agt         240
Lys Gly Arg Phe Thr Ile Phe Arg Asp Asn Ala Lys Asn Phe Leu Ser
65                  70                  75                  80

cta caa atg aat cgc ctg aga gcc gag gac acg gcg gta tac ttc tgt         288
Leu Gln Met Asn Arg Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

gcg aga att gta ggg gta atc ccg tcc gct gac cca tac tac ctt gac         336
Ala Arg Ile Val Gly Val Ile Pro Ser Ala Asp Pro Tyr Tyr Leu Asp
            100                 105                 110

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

<210> 74
<211> 124
<212> PRT
<213> Homo sapiens

<400> 74

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


Ser Val Arg Leu Ser Cys Ile Ala Ser Gly Phe Pro Phe Arg Asn Tyr
            20                  25                  30


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

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

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

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

Ala Arg Ile Val Gly Val Ile Pro Ser Ala Asp Pro Tyr Tyr Leu Asp
            100                 105                 110

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

<210> 75
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(330)
<223> NI-301.14D8 variable light chain (VL) sequence (PIMC by default)

<220>
<221> V_region
<222> (67)..(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)..(300)
<223> complementarity determining region (CDR) VL-CDR3

<400> 75

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cag tct gcc ctg act cag cct gcc tcc gtg tct ggg ttt gct gga cag         48
Gln Ser Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Phe Ala Gly Gln
1               5                   10                  15

tcg gtc acc atc tcc tgc act gga acc agc ctt aac att ggg act tac         96
Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Leu Asn Ile Gly Thr Tyr
            20                  25                  30

aac ctt atc tcc tgg tac caa caa cac cca ggc aga gcc ccc aga ctc        144
Asn Leu Ile Ser Trp Tyr Gln Gln His Pro Gly Arg Ala Pro Arg Leu
        35                  40                  45

atc att ttt gag ggc aat agg cgg ccc ccc ggg att tct aat cgc ttc        192
Ile Ile Phe Glu Gly Asn Arg Arg Pro Pro Gly Ile Ser Asn Arg Phe
    50                  55                  60

tct gcc tcc aag tct ggc aac acg gcc tcc ttg aca gtc tct ggg ctg        240
Ser Ala Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65                  70                  75                  80

ctg gct ggc gac gag gct gat tat tac tgt tgc tca ttt gca gga aga        288
Leu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Phe Ala Gly Arg
```

```
                85                  90                  95

gtc tct ttg gtg ttt ggc gga ggg acc aag ttg acc gtc cta                330
Val Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  76
<211>  110
<212>  PRT
<213>  Homo sapiens

<400>  76

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


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


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


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


Ser Ala Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Val Ser Gly Leu
65                  70                  75                  80


Leu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Cys Ser Phe Ala Gly Arg
                85                  90                  95


Val Ser Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  77
<211>  348
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(348)
<223>  NI-301.9X4 variable heavy chain (VH) sequence (PIMC by default)

<220>
<221>  V_region
<222>  (91)..(105)
<223>  complementarity determining region (CDR) VH-CDR1

<220>
<221>  V_region
<222>  (148)..(195)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (292)..(315)
<223>  complementarity determining region (CDR) VH-CDR3

<400>  77
cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aaa cct tcg gag         48
```

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

acc ctg tcc ctc acc tgc agt gtc tct gct ggc tcc atc agt agt cac          96
Thr Leu Ser Leu Thr Cys Ser Val Ser Ala Gly Ser Ile Ser Ser His
            20                  25                  30

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

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

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

agg ttg acg tct gtg acc gcc gca gac acg gcc gtg tat tac tgt gcg         288
Arg Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
                85                  90                  95

aga gac tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc         336
Arg Asp Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
            100                 105                 110

acc gtc tcc tcg                                                        348
Thr Val Ser Ser
        115


<210>  78
<211>  116
<212>  PRT
<213>  Homo sapiens

<400>  78

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


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


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


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


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


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


Arg Asp Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val
            100                 105                 110


Thr Val Ser Ser
        115
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<210> 79
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)
<223> NI-301.9X4 variable light chain (VL) sequence (PIMC by default)

<220>
<221> V_region
<222> (67)..(99)
<223> complementarity determining region (CDR) VL-CDR1

<220>
<221> V_region
<222> (145)..(165)
<223> complementarity determining region (CDR) VL-CDR2

<220>
<221> V_region
<222> (262)..(294)
<223> complementarity determining region (CDR) VL-CDR3

<400> 79
tcc tat gag ctg act cag cca ccc tcg gtg tca gtg tcc cca gga cag 48
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

acg gcc agg atc acc tgc tct gga gat gcg ttg cca gac aag tat gct 96
Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Asp Lys Tyr Ala
20 25 30

tat tgg tac cag cag aag cca ggc cag gcc cct atg ttg gtt ata tat 144
Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Met Leu Val Ile Tyr
35 40 45

aag gac agt gag agg ccc tca ggg atc cct gag cga ttc tct ggc tcc 192
Lys Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

agt ttg ggg aca aca gtc atg ctg acc atc agt gga gtc cag gca gag 240
Ser Leu Gly Thr Thr Val Met Leu Thr Ile Ser Gly Val Gln Ala Glu
65 70 75 80

gac gag gct gac tat tac tgt aaa tca gca gac agc agt ggt act tat 288
Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Ala Asp Ser Ser Gly Thr Tyr
85 90 95

tgg gtg ttc ggc ggg ggg acc aag ctg acc gtc cta 324
Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 80
<211> 108
<212> PRT
<213> Homo sapiens

<400> 80

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

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Asp Lys Tyr Ala
20 25 30

```
Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Met Leu Val Ile Tyr
        35                  40                  45

Lys Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

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

Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Ala Asp Ser Ser Gly Thr Tyr
                85                  90                  95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
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<210> 81
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(363)
<223> NI-301.14C3 variable heavy chain (VH) sequence (PIMC by default)

<220>
<221> V_region
<222> (91)..(105)
<223> complementarity determining region (CDR) VH-CDR1

<220>
<221> V_region
<222> (148)..(195)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> V_region
<222> (292)..(330)
<223> complementarity determining region (CDR) VH-CDR3

<400> 81

```
gag gtg cag ctg gtg gag act gga gga ggc ttg atc cag cct ggg ggg         48
Glu Val Gln Leu Val Glu Thr Gly Gly Gly Leu Ile Gln Pro Gly Gly
1               5                   10                  15

tcc ctg aga ctc tcc tgt gca gcc tct ggg ttc acc gtc agt agc cac         96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser His
            20                  25                  30

tac atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc        144
Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

tca att att tat agc ggt ggt ggc aca tac tac gca gac tcc gtg aag        192
Ser Ile Ile Tyr Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60

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

caa atg aac agc ctg aga gcc gag gac acg gcc gtg tat tac tgt gcg        288
```

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

aag atc tac agg tcg ggt aat act ggt tat tct tac gac tac tgg ggc        336
Lys Ile Tyr Arg Ser Gly Asn Thr Gly Tyr Ser Tyr Asp Tyr Trp Gly
            100                 105                 110

cag gga acc ctg gtc acc gtc tcc tcg                                    363
Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  82
<211>  121
<212>  PRT
<213>  Homo sapiens

<400>  82

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


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Ser His
            20                  25                  30


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


Ser Ile Ile Tyr Ser Gly Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys
    50                  55                  60


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


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


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


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  83
<211>  324
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(324)
<223>  NI-301.14C3 variable light chain (VL) sequence

<220>
<221>  V_region
<222>  (67)..(99)
<223>  complementarity determining region (CDR) VL-CDR1

<220>
<221>  V_region
<222>  (145)..(165)
```

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

<220>
<221> V_region
<222> (262)..(294)
<223> complementarity determining region (CDR) VL-CDR3

<400> 83
tcc tat gag ctg act cag cca ccc tca gtg tcc gtg tcc cca ggg cag 48
Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
1 5 10 15

aca gcc agc atc acc tgc tct gga gat aaa ttg ggg agt aaa tat gct 96
Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Ser Lys Tyr Ala
20 25 30

tgc tgg tat cag cag aag cca ggc cag tcc cct gta ctg gtc atc tat 144
Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
35 40 45

gaa gat aag aag cgg ccc tca ggg atc cct gag cga ttc tct ggc tcc 192
Glu Asp Lys Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

aac tct ggg aac aca gcc act ctg acc atc agc ggg acc cag gct atg 240
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

gat gag gct gac tat ttc tgt cag gcg tgg gac agc agc act tct cat 288
Asp Glu Ala Asp Tyr Phe Cys Gln Ala Trp Asp Ser Ser Thr Ser His
85 90 95

gtg gta ttc ggc gga ggg acc agg ctg acc gtc cta 324
Val Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu
100 105

<210> 84
<211> 108
<212> PRT
<213> Homo sapiens

<400> 84

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

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

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

Glu Asp Lys Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met
65 70 75 80

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

Val Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu
100 105

<210> 85
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.59F1 in the epitope mapping - Spot 15

<400> 85

Gly Leu Thr Thr Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys Val
1 5 10 15

<210> 86
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.59F1 in the epitope mapping - Spot 16

<400> 86

Glu Glu Glu Phe Val Glu Gly Ile Tyr Lys Val Glu Ile Asp Thr
1 5 10 15

<210> 87
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.35G11 in the epitope mapping - Spot 13

<400> 87

Thr Ser Glu Ser Gly Glu Leu His Gly Leu Thr Thr Glu Glu Glu
1 5 10 15

<210> 88
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.35G11 in the epitope mapping - Spot 14

<400> 88

Gly Glu Leu His Gly Leu Thr Thr Glu Glu Glu Phe Val Glu Gly
1 5 10 15

<210> 89
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.37F1 in the epitope mapping - Spot 9

<400> 89

Phe Arg Lys Ala Ala Asp Asp Thr Trp Glu Pro Phe Ala Ser Gly
1 5 10 15

<210> 90
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.37F1 in the epitope mapping - Spot 10

<400> 90

Ala Asp Asp Thr Trp Glu Pro Phe Ala Ser Gly Lys Thr Ser Glu
1 5 10 15

<210> 91
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence recognized by NI-301.37F1 in the epitope mapping - Spot 11

<400> 91

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