SEQUENCE LISTING

<110> Neurimmune Therapeutics AG

<120> Human anti-alpha-synuclein antibodies

<130> NE30A27/P-WO

<150> US 61/139,253
<151> 2008-12-19

<150> EP 08 022 188.0
<151> 2008-12-19

<160> 22

<170> PatentIn version 3.5

<210> 1
<211> 140
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(140)
<223> Amino acid sequence of alpha-synuclein; see, e.g., Ueda et al, Proc. Natl. Acad. Sci. U.S.A. 90 (1993), 1282-1286; GenBank swissprot: locus SYUA_HUMAN, accession number P37840

<400> 1

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Met Asp Val Phe Met Lys Gly Leu Ser Lys Ala Lys Glu Gly Val Val
1               5                  10                  15

Ala Ala Ala Glu Lys Thr Lys Gln Gly Val Ala Glu Ala Ala Gly Lys
            20                  25                  30

Thr Lys Glu Gly Val Leu Tyr Val Gly Ser Lys Thr Lys Glu Gly Val
        35                  40                  45

Val His Gly Val Ala Thr Val Ala Glu Lys Thr Lys Glu Gln Val Thr
    50                  55                  60

Asn Val Gly Gly Ala Val Val Thr Gly Val Thr Ala Val Ala Gln Lys
65                  70                  75                  80

Thr Val Glu Gly Ala Gly Ser Ile Ala Ala Ala Thr Gly Phe Val Lys
                85                  90                  95

Lys Asp Gln Leu Gly Lys Asn Glu Glu Gly Ala Pro Gln Glu Gly Ile
            100                 105                 110

Leu Glu Asp Met Pro Val Asp Pro Asp Asn Glu Ala Tyr Glu Met Pro
        115                 120                 125
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Ser Glu Glu Gly Tyr Gln Asp Tyr Glu Pro Glu Ala
    130                 135                 140


<210>  2
<211>  363
<212>  DNA
<213>  Homo sapiens


<220>
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<222>  (1)..(363)
<223>  NI-202.3G12-VHB1 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)..(330)
<223>  complementarity determining region (CDR) CDRH3

<220>
<221>  V_region
<222>  (295)..(330)
<223>  complementarity determining region (CDR) VH-CDR3

<400>  2
gag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag ccg ggg gcc         48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

tca gtg aga ctc tcc tgt agg gct tct gga tac aac ttc atc gac ttc         96
Ser Val Arg Leu Ser Cys Arg Ala Ser Gly Tyr Asn Phe Ile Asp Phe
            20                  25                  30

cat ata cac tgg gtg cga cag gcc cct gga gag ggg ctt gag tgg atg        144
His Ile His Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Glu Trp Met
        35                  40                  45

ggc tgg agt aat cct caa agt ggc aac tca agt tct gca cag agg ttt        192
Gly Trp Ser Asn Pro Gln Ser Gly Asn Ser Ser Ser Ala Gln Arg Phe
    50                  55                  60

cag ggc cgg gtc acc atg acc acg gac acg tcc atg tcc gcg gcc tac        240
Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Met Ser Ala Ala Tyr
65                  70                  75                  80

atg gac ctg aac tgg ctg aca ctt gac gac acg gcc gtg tat tac tgt        288
Met Asp Leu Asn Trp Leu Thr Leu Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

acg aga ccc cat gat ggc gca gga aac tac cga ttt gac acc tgg ggc        336
```

```
Thr Arg Pro His Asp Gly Ala Gly Asn Tyr Arg Phe Asp Thr 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>  3
<211>  121
<212>  PRT
<213>  Homo sapiens

<400>  3

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


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


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


Gly Trp Ser Asn Pro Gln Ser Gly Asn Ser Ser Ser Ala Gln Arg Phe
    50                  55                  60


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


Met Asp Leu Asn Trp Leu Thr Leu Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


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


Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  4
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<212>  PRT
<213>  Homo sapiens


<220>
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<222>  (1)..(121)
<223>  NI-202.3G12-VHB1-GL variable heavy chain (VH) sequence aligned to
       the Germ Line (GL) Sequence

<220>
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<222>  (31)..(35)
<223>  complementarity determining region (CDR) VH-CDR1
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<220>
<221> MISC_FEATURE
<222> (50)..(66)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> MISC_FEATURE
<222> (99)..(110)
<223> complementarity determining region (CDR) VH-CDR3

<400> 4

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

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

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

Gly Trp Ser Asn Pro Gln Ser Gly Asn Ser Ser Ser Ala Gln Arg Phe
    50                  55                  60

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

Met Asp Leu Asn Trp Leu Thr Leu Asp Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

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

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<210> 5
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
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<223> NI-202.3G12-VLc1 variable light chain (VL) sequence

<220>
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<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> 5
cag tct gtg ttg acg cag ccg ccc tcg gtg tca gtg gcc cca gga cag 48
Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
1 5 10 15

acg gcc agg atc acc tgc tct ggt gat gcc ttg cca aaa cac tat gct 96
Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys His Tyr Ala
20 25 30

cat tgg tac cag cag aag cca ggc cag gtc cct ata gtg gtc atc tat 144
His Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Ile Val Val Ile Tyr
35 40 45

aaa gac act gag agg ccc tca ggg atc cct gag cga ttc tct ggt tcc 192
Lys Asp Thr Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

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

gac gag gct cat tat tat tgt caa tca gca gac gtc agt tca act tat 288
Asp Glu Ala His Tyr Tyr Cys Gln Ser Ala Asp Val Ser Ser Thr Tyr
85 90 95

gtt gtg ttt ggc gga ggg acc aag ctg acc gtc cta 324
Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 6
<211> 108
<212> PRT
<213> Homo sapiens

<400> 6

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

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

His Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Ile Val Val Ile Tyr
35 40 45

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

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

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

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

<210> 7
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(108)
<223> NI-202.3G12-VLc1-GL variable light chain (VL) sequence aligned to the Germ Line (GL) Sequence

<220>
<221> MISC_FEATURE
<222> (23)..(33)
<223> complementarity determining region (CDR) VL-CDR1

<220>
<221> MISC_FEATURE
<222> (49)..(55)
<223> complementarity determining region (CDR) VL-CDR2

<220>
<221> MISC_FEATURE
<222> (88)..(98)
<223> complementarity determining region (CDR) VL-CDR3

<400> 7

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

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

His Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Ile Val Val Ile Tyr
        35                  40                  45

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

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

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

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


<210>  8
<211>  339
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(339)
<223>  NI-202.12F4-VHA1b variable heavy chain (VH) sequence

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

<220>
<221>  V_region
<222>  (147)..(204)
<223>  complementarity determining region (CDR) VH-CDR2

<220>
<221>  V_region
<222>  (301)..(306)
<223>  complementarity determining region (CDR) VH-CDR3

<220>
<221>  misc_feature
<222>  (319)..(339)
<223>  The nucleotide sequence at positions 319 to 339 may alternatively
       read "tcc cgg gtc acc gtc gcc tca" and encode the amino acids
       "Ser Arg Val Thr Val Ala Ser"

<400>  8
gag gtg cag ctg gtg cag tct ggg gga ggt ctg gtc gag ccg ggg ggg         48
Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Glu Pro Gly Gly
1               5                   10                  15

tcc cta aga ctc tcc tgt gca gtc tcc gga ttc gat ttc gaa aaa gcc         96
Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Phe Asp Phe Glu Lys Ala
            20                  25                  30

tgg atg agt tgg gtc cgc cag gct cca ggg cag ggg cta cag tgg gtt        144
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Gln Trp Val
        35                  40                  45

gcc cgt atc aag agc aca gct gat ggt ggg aca aca agc tac gcc gcc        192
Ala Arg Ile Lys Ser Thr Ala Asp Gly Gly Thr Thr Ser Tyr Ala Ala
    50                  55                  60

ccc gtg gaa ggc agg ttc atc atc tca aga gat gat tcg aga aac atg        240
Pro Val Glu Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Arg Asn Met
65                  70                  75                  80

ctt tat ctg caa atg aac agt ctg aaa act gaa gac aca gcc gtc tat        288
Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
                85                  90                  95

tat tgt aca tca gcc cac tgg ggc cag gga acc ctg gtc acc gtc tcc        336
```

```
Tyr Cys Thr Ser Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            100                 105                 110

tcg                                                                 339
Ser
```

<210> 9
<211> 113
<212> PRT
<213> Homo sapiens

<400> 9

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

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

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

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

Pro Val Glu Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Arg Asn Met
65                  70                  75                  80

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

Tyr Cys Thr Ser Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
            100                 105                 110

Ser
```

<210> 10
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(113)
<223> NI-202.12F4-VHA1b-GL variable heavy chain (VH) sequence aligned to the Germ Line (GL) Sequence

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

<220>
<221> MISC_FEATURE
<222> (50)..(68)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> MISC_FEATURE
<222> (101)..(102)
<223> complementarity determining region (CDR) VH-CDR3

<220>
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<222> (107)..(113)
<223> The amino acid sequence at positions 107 to 113 may alternatively read "Ser Arg Val Thr Val Ala Ser"

<400> 10

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

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

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

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

Pro Val Glu Gly Arg Phe Ile Ile Ser Arg Asp Asp Ser Arg Asn Met
65 70 75 80

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

Tyr Cys Thr Ser Ala His Trp Gly Gln Gly Thr Leu Val Thr Val Ser
100 105 110

Ser

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

<220>
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<222> (1)..(324)
<223> NI-202.12F4-VLa1 variable light chain (VL) sequence

<220>

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<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> 11

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cag tct gtg ctg act cag cca ccc tcg gtg tca gtg tcc cca gga cag          48
Gln Ser Val 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 gaa gca ttg cca atg caa ttt gct          96
Thr Ala Arg Ile Thr Cys Ser Gly Glu Ala Leu Pro Met Gln Phe Ala
            20                  25                  30

cat tgg tac caa cag agg cca ggc aag gcc cca gtg ata gtg gtg tac         144
His Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Val Ile Val Val Tyr
        35                  40                  45

aaa gac agt gag aga ccg tca ggt gtc cct gag cga ttc tct ggc tcc         192
Lys Asp Ser Glu Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

agc tca ggg aca aca gcc acg ttg acc atc act gga gtc cag gca gaa         240
Ser Ser Gly Thr Thr Ala Thr Leu Thr Ile Thr Gly Val Gln Ala Glu
65                  70                  75                  80

gat gag gct gac tat tac tgc cag tcg cca gac agc act aac act tat         288
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Pro Asp Ser Thr Asn Thr Tyr
                85                  90                  95

gaa gtc ttc ggc gga ggg acc aag ctg acc gtc cta                         324
Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105
```

<210> 12
<211> 108
<212> PRT
<213> Homo sapiens

<400> 12

```
Gln Ser Val 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 Glu Ala Leu Pro Met Gln Phe Ala
            20                  25                  30

His Trp Tyr Gln Gln Arg Pro Gly Lys Ala Pro Val Ile Val Val Tyr
        35                  40                  45
```

```
Lys Asp Ser Glu Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

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

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

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

<210> 13
<211> 108
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(108)
<223> NI-202.12F4-VLa1-GL variable light chain (VL) sequence aligned to the Germ Line (GL) Sequence

<220>
<221> MISC_FEATURE
<222> (23)..(33)
<223> complementarity determining region (CDR) VL-CDR1

<220>
<221> MISC_FEATURE
<222> (49)..(55)
<223> complementarity determining region (CDR) VL-CDR2

<220>
<221> MISC_FEATURE
<222> (88)..(98)
<223> complementarity determining region (CDR) VL-CDR3

<400> 13

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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 Glu Ala Leu Pro Met Gln Phe Ala
            20                  25                  30

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

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

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

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

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

<210> 14
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(369)
<223> NI-202.3D8-VHE1 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)..(336)
<223> complementarity determining region (CDR) VH-CDR3

<400> 14

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

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

gcc att tcc tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg         144
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

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

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

ctg gaa atg aac agc ctg aga gat gag gac acg gct gtg tat tac tgt         288
Leu Glu Met Asn Ser Leu Arg Asp Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

gcg aaa aaa cga ggg acg tat gcc agc agg tgc aaa gcc ttt gac ttc         336
Ala Lys Lys Arg Gly Thr Tyr Ala Ser Arg Cys Lys Ala Phe Asp Phe
```

```
            100                 105                 110

tgg ggc cag gga acc ctg gtc acc gtc tcc tcg                          369
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  15
<211>  123
<212>  PRT
<213>  Homo sapiens

<400>  15

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


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


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


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


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


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


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


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


<210>  16
<211>  123
<212>  PRT
<213>  Homo sapiens


<220>
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<222>  (1)..(123)
<223>  NI-202.3D8-VHE1-GL variable heavy chain (VH) sequence aligned to
       the Germ Line (GL) Sequence

<220>
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<222>  (31)..(35)
<223>  complementarity determining region (CDR) VH-CDR1
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<220>
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<222> (50)..(66)
<223> complementarity determining region (CDR) VH-CDR2

<220>
<221> MISC_FEATURE
<222> (99)..(112)
<223> complementarity determining region (CDR) VH-CDR3

<400> 16

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

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

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

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

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

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

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

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

<210> 17
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(318)
<223> NI-202.3D8-VKa1 variable light chain (VL) sequence

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

<220>
<221> V_region
<222> (148)..(168)

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

<220>
<221> V_region
<222> (265)..(288)
<223> complementarity determining region (CDR) VL-CDR3

<400> 17

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gac atc cag ttg acc cag tct cct tcc acc ctg tct gca tct gta gga          48
Asp Ile Gln Leu 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 ggc tgg          96
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Gly Trp
            20                  25                  30

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

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

agt gga 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 ttt gca act tat tat tgc caa cag tat gat aat tat tgg acg         288
Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Tyr Trp Thr
                85                  90                  95

ttc ggc caa ggg acc aag gtg gaa atc aaa                                 318
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 18
<211> 106
<212> PRT
<213> Homo sapiens

<400> 18

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Asp Ile Gln Leu 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 Gly Trp
            20                  25                  30

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

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

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105
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<210> 19
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(106)
<223> NI-202.3D8-VKa1-GL variable light chain (VL) sequence aligned to the Germ Line (GL) Sequence

<220>
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<222> (24)..(34)
<223> complementarity determining region (CDR) VL-CDR1

<220>
<221> MISC_FEATURE
<222> (50)..(56)
<223> complementarity determining region (CDR) VL-CDR2

<220>
<221> MISC_FEATURE
<222> (89)..(96)
<223> complementarity determining region (CDR) VL-CDR3

<400> 19

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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 Gly Trp
            20                  25                  30

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

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

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

<210> 20
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(321)
<223> NI-202.3D8-VKc1 variable light chain (VL) sequence

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

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

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

<400> 20
gaa att gtg atg acg cag tct cca tcc tca ctg tct gca tct att gga 48
Glu Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Ile Gly
1 5 10 15

gac aga gtc acc ttc act tgt cgg gcg agt cac gac att agc aat tat 96
Asp Arg Val Thr Phe Thr Cys Arg Ala Ser His Asp Ile Ser Asn Tyr
20 25 30

tta gcc tgg ttt cgg cag caa cca ggg aaa gcc cct aag tcc ctg atc 144
Leu Ala Trp Phe Arg Gln Gln Pro Gly Lys Ala Pro Lys Ser Leu Ile
35 40 45

tat gct gca tct agt ctg caa agt ggg gtc cca tca aga ttc agc gcc 192
Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ala
50 55 60

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

gaa gat ttt gca act tat tat tgt gtt caa tat agg act tac ccc ctc 288
Glu Asp Phe Ala Thr Tyr Tyr Cys Val Gln Tyr Arg Thr Tyr Pro Leu
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> 21
<211> 107
<212> PRT
<213> Homo sapiens

<400> 21

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

Asp Arg Val Thr Phe Thr Cys Arg Ala Ser His Asp Ile Ser Asn Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ala
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 Val Gln Tyr Arg Thr Tyr Pro Leu
85 90 95

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

<210> 22
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
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<223> NI-202.3D8-VKc1-GL variable light chain (VL) sequence aligned to the Germ Line (GL) Sequence

<220>
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<220>
<221> MISC_FEATURE
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<220>
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<223> complementarity determining region (CDR) VL-CDR3

<400> 22

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

```
Asp Arg Val Thr Phe Thr Cys Arg Ala Ser His Asp Ile Ser Asn Tyr
            20                  25                  30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Ala
    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 Val Gln Tyr Arg Thr Tyr Pro Leu
                85                  90                  95

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