SEQUENCE LISTING

<110> Chen, Feng
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Nitsch, Roger
Hock, Christoph
Panima Pharmaceuticals AG
University of Zurich

<120> HUMAN ANTI-TAU ANTIBODIES

<130> 2159.341PCO2

<140> To be assigned
<141> Herewith

<150> EP 10 013 494.9
<151> 2010-10-11

<150> 61/391,751
<151> 2010-10-11

<160> 93

<170> PatentIn version 3.5

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

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<222> (1)..(352)
<223> Isoform Fetal-Tau

<300>
<301> Goedert M., Wischik C., Crowther R., Walker J., Klug A.
<302> Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau.
<303> Proc. Natl. Acad. Sci. U.S.A.
<304> 85
<306> 4051-4055
<307> 1988-06-01

<300>
<308> P10636-2
<309> 2010-10-05
<313> (1)..(352)

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Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
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Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu Ala
35 40 45

Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val
50 55 60

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

Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro
                85                  90                  95

Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg
            100                 105                 110

Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly
        115                 120                 125

Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser
    130                 135                 140

Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro
145                 150                 155                 160

Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys
                165                 170                 175

Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met
            180                 185                 190

Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu
        195                 200                 205

Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Val Tyr Lys Pro Val
    210                 215                 220

Asp Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His
225                 230                 235                 240

His Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp
                245                 250                 255

Phe Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr
            260                 265                 270

His Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr
        275                 280                 285

Phe Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val
    290                 295                 300

Tyr Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser
305                 310                 315                 320

Asn Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu
                325                 330                 335
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Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
            340                 345                 350


<210>  2
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<213>  Homo sapiens


<220>
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<222>  (1)..(381)
<223>  Isoform Tau-B

<300>
<301>  Goedert M., Spillantini M.G., Jakes R., Rutherford D., Crowther
       R.A.
<302>  Multiple isoforms of human microtubule-associated protein tau:
       sequences and localization in neurofibrillary tangles of
       Alzheimer's disease.
<303>  Neuron
<304>  3
<306>  519-526
<307>  1989-10-01

<300>
<308>  P10636-4
<309>  2010-10-05
<313>  (1)..(381)

<400>  2

Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                   10                  15


Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30


Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45


Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60


Asp Ala Lys Ser Thr Pro Thr Ala Glu Ala Glu Glu Ala Gly Ile Gly
65                  70                  75                  80


Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala
                85                  90                  95


Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys
            100                 105                 110


Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala
        115                 120                 125


Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala
    130                 135                 140
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Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro
145                 150                 155                 160

Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr
                165                 170                 175

Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg
            180                 185                 190

Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser
        195                 200                 205

Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu
    210                 215                 220

Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln
225                 230                 235                 240

Pro Gly Gly Gly Lys Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser
                245                 250                 255

Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro
            260                 265                 270

Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp
        275                 280                 285

Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro
    290                 295                 300

Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu
305                 310                 315                 320

Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser
                325                 330                 335

Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser
            340                 345                 350

Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu
        355                 360                 365

Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
    370                 375                 380

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<213>  Homo sapiens

<220>
<221>  PEPTIDE
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<222> (1)..(410)
<223> Isoform Tau-C

<300>
<301> Goedert M., Spillantini M.G., Jakes R., Rutherford D., Crowther R.A.
<302> Multiple isoforms of human microtubule-associated protein tau: sequences and localization in neurofibrillary tangles of Alzheimer's disease.
<303> Neuron
<304> 3
<306> 519-526
<307> 1989-10-01

<300>
<308> P10636-5
<309> 2010-10-05
<313> (1)..(410)

<400> 3

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1               5                  10                  15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65                  70                  75                  80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
                85                  90                  95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
            100                 105                 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
        115                 120                 125

Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
    130                 135                 140

Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145                 150                 155                 160

Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
                165                 170                 175

Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
            180                 185                 190
```

```
Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
        195                 200                 205

Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
    210                 215                 220

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225                 230                 235                 240

Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
                245                 250                 255

Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
            260                 265                 270

Gly Lys Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr
        275                 280                 285

Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly
    290                 295                 300

Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln
305                 310                 315                 320

Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly
                325                 330                 335

Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys
            340                 345                 350

Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val
        355                 360                 365

Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly
    370                 375                 380

Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu
385                 390                 395                 400

Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
                405                 410


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


<220>
<221>  PEPTIDE
<222>  (1)..(383)
<223>  Isoform Tau-D

<300>
<301>  Goedert M., Spillantini M.G., Potier M.-C., Ulrich J., Crowther
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R.A.
<302> Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain.
<303> EMBO J.
<304> 8
<306> 393-399
<307> 1989-02-01

<300>
<308> P10636-6
<309> 2010-10-05
<313> (1)..(383)

<400> 4

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Met Ala Glu Pro Arg Gln Glu Phe Glu Val Met Glu Asp His Ala Gly
1               5                  10                  15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Ala Glu Glu Ala
        35                  40                  45

Gly Ile Gly Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val
    50                  55                  60

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

Asp Lys Lys Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro
                85                  90                  95

Arg Gly Ala Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg
            100                 105                 110

Ile Pro Ala Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly
        115                 120                 125

Glu Pro Pro Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser
    130                 135                 140

Pro Gly Thr Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro
145                 150                 155                 160

Pro Thr Arg Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys
                165                 170                 175

Ser Pro Ser Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met
            180                 185                 190

Pro Asp Leu Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu
        195                 200                 205
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Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu
    210                 215                 220

Asp Leu Ser Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys
225                 230                 235                 240

His Val Pro Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val Asp
                245                 250                 255

Leu Ser Lys Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His
            260                 265                 270

Lys Pro Gly Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe
        275                 280                 285

Lys Asp Arg Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His
    290                 295                 300

Val Pro Gly Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe
305                 310                 315                 320

Arg Glu Asn Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr
                325                 330                 335

Lys Ser Pro Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn
            340                 345                 350

Val Ser Ser Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala
        355                 360                 365

Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
    370                 375                 380


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<211>  412
<212>  PRT
<213>  Homo sapiens


<220>
<221>  PEPTIDE
<222>  (1)..(412)
<223>  Isoform Tau-E

<300>
<301>  Goedert M., Spillantini M.G., Jakes R., Rutherford D., Crowther
       R.A.
<302>  Multiple isoforms of human microtubule-associated protein tau:
       sequences and localization in neurofibrillary tangles of
       Alzheimer's disease.
<303>  Neuron
<304>  3
<306>  519-526
<307>  1989-10-01

<300>
<308>  P10636-7
<309>  2010-10-05
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1               5                  10                  15

Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Ala Glu Glu Ala Gly Ile Gly
65                  70                  75                  80

Asp Thr Pro Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala
                85                  90                  95

Arg Met Val Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys
            100                 105                 110

Ala Lys Gly Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala
        115                 120                 125

Ala Pro Pro Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala
    130                 135                 140

Lys Thr Pro Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro
145                 150                 155                 160

Lys Ser Gly Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr
                165                 170                 175

Pro Gly Ser Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg
            180                 185                 190

Glu Pro Lys Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser
        195                 200                 205

Ser Ala Lys Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu
    210                 215                 220

Lys Asn Val Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln
225                 230                 235                 240

Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser
                245                 250                 255

Asn Val Gln Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro
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```
            260                 265                 270

Gly Gly Gly Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys
        275                 280                 285

Val Thr Ser Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly
    290                 295                 300

Gly Gly Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg
305                 310                 315                 320

Val Gln Ser Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly
                325                 330                 335

Gly Gly Asn Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn
            340                 345                 350

Ala Lys Ala Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro
        355                 360                 365

Val Val Ser Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser
    370                 375                 380

Thr Gly Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala
385                 390                 395                 400

Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
                405                 410


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


<220>
<221>  PEPTIDE
<222>  (1)..(441)
<223>  Isoform Tau-F

<300>
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       R.A.
<302>  Multiple isoforms of human microtubule-associated protein tau:
       sequences and localization in neurofibrillary tangles of
       Alzheimer's disease.
<303>  Neuron
<304>  3
<306>  519-526
<307>  1989-10-01

<300>
<308>  P10636-8
<309>  2010-10-05
<313>  (1)..(441)

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Thr Tyr Gly Leu Gly Asp Arg Lys Asp Gln Gly Gly Tyr Thr Met His
            20                  25                  30

Gln Asp Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Pro Leu
        35                  40                  45

Gln Thr Pro Thr Glu Asp Gly Ser Glu Glu Pro Gly Ser Glu Thr Ser
    50                  55                  60

Asp Ala Lys Ser Thr Pro Thr Ala Glu Asp Val Thr Ala Pro Leu Val
65                  70                  75                  80

Asp Glu Gly Ala Pro Gly Lys Gln Ala Ala Ala Gln Pro His Thr Glu
                85                  90                  95

Ile Pro Glu Gly Thr Thr Ala Glu Glu Ala Gly Ile Gly Asp Thr Pro
            100                 105                 110

Ser Leu Glu Asp Glu Ala Ala Gly His Val Thr Gln Ala Arg Met Val
        115                 120                 125

Ser Lys Ser Lys Asp Gly Thr Gly Ser Asp Asp Lys Lys Ala Lys Gly
    130                 135                 140

Ala Asp Gly Lys Thr Lys Ile Ala Thr Pro Arg Gly Ala Ala Pro Pro
145                 150                 155                 160

Gly Gln Lys Gly Gln Ala Asn Ala Thr Arg Ile Pro Ala Lys Thr Pro
                165                 170                 175

Pro Ala Pro Lys Thr Pro Pro Ser Ser Gly Glu Pro Pro Lys Ser Gly
            180                 185                 190

Asp Arg Ser Gly Tyr Ser Ser Pro Gly Ser Pro Gly Thr Pro Gly Ser
        195                 200                 205

Arg Ser Arg Thr Pro Ser Leu Pro Thr Pro Pro Thr Arg Glu Pro Lys
    210                 215                 220

Lys Val Ala Val Val Arg Thr Pro Pro Lys Ser Pro Ser Ser Ala Lys
225                 230                 235                 240

Ser Arg Leu Gln Thr Ala Pro Val Pro Met Pro Asp Leu Lys Asn Val
                245                 250                 255

Lys Ser Lys Ile Gly Ser Thr Glu Asn Leu Lys His Gln Pro Gly Gly
            260                 265                 270

Gly Lys Val Gln Ile Ile Asn Lys Lys Leu Asp Leu Ser Asn Val Gln
        275                 280                 285
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Ser Lys Cys Gly Ser Lys Asp Asn Ile Lys His Val Pro Gly Gly Gly
    290                 295                 300

Ser Val Gln Ile Val Tyr Lys Pro Val Asp Leu Ser Lys Val Thr Ser
305                 310                 315                 320

Lys Cys Gly Ser Leu Gly Asn Ile His His Lys Pro Gly Gly Gly Gln
                325                 330                 335

Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg Val Gln Ser
            340                 345                 350

Lys Ile Gly Ser Leu Asp Asn Ile Thr His Val Pro Gly Gly Gly Asn
        355                 360                 365

Lys Lys Ile Glu Thr His Lys Leu Thr Phe Arg Glu Asn Ala Lys Ala
    370                 375                 380

Lys Thr Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro Val Val Ser
385                 390                 395                 400

Gly Asp Thr Ser Pro Arg His Leu Ser Asn Val Ser Ser Thr Gly Ser
                405                 410                 415

Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu Val
            420                 425                 430

Ser Ala Ser Leu Ala Lys Gln Gly Leu
        435                 440


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<220>
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<400>  7

Val Glu Val Lys Ser Glu Lys
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<210>  8
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<212>  DNA
<213>  Homo sapiens


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<222> (91)..(105)
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<220>
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<222> (148)..(204)
<223> complementarity determining region (CDR) VH-CDR2

<220>
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<222> (301)..(330)
<223> complementarity determining region (CDR) VH-CDR3

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

tcc ctg aaa ctc tcc tgt gca gcc tct ggg ttc aat ttc aac atc tct 96
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Asn Ile Ser
20 25 30

gct ata cac tgg gtc cgc cag gct tcc ggg aaa ggg ctg gag tgg gtt 144
Ala Ile His Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val
35 40 45

ggc cga ata aga agt aaa tct cac aat tac gcg act tta tat gct gcg 192
Gly Arg Ile Arg Ser Lys Ser His Asn Tyr Ala Thr Leu Tyr Ala Ala
50 55 60

tcc ctg aaa ggc cgg ttc acc ctc tcc aga gat gat tca agg aac acg 240
Ser Leu Lys Gly Arg Phe Thr Leu Ser Arg Asp Asp Ser Arg Asn Thr
65 70 75 80

gcg tat ctg caa atg agc agc ctg caa acc gag gat atg gcc gtc tat 288
Ala Tyr Leu Gln Met Ser Ser Leu Gln Thr Glu Asp Met Ala Val Tyr
85 90 95

tac tgt act gtt ctg agt gcg aat tac gac acc ttt gac tac tgg ggc 336
Tyr Cys Thr Val Leu Ser Ala Asn Tyr Asp Thr Phe 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> 9
<211> 121
<212> PRT
<213> Homo sapiens

<400> 9

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

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

Ala Ile His Trp Val Arg Gln Ala Ser Gly Lys Gly Leu Glu Trp Val

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        35                  40                  45

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

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

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

Tyr Cys Thr Val Leu Ser Ala Asn Tyr Asp Thr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
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<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(321)
<223> NI-105.4E4-VL variable light chain (VL) sequence wherein amino acid sequence Ser-Tyr-Glu at positions 1-3 may also be Leu-Pro-Val

<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)..(291)
<223> complementarity determining region (CDR) VL-CDR3

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

acg gcc agg atc tcc tgc ttt gga gat aca ttg cca aag caa tat act         96
Thr Ala Arg Ile Ser Cys Phe Gly Asp Thr Leu Pro Lys Gln Tyr Thr
            20                  25                  30

tat tgg tat cag cag aag cct ggc cag gcc cct gtg tta gtg att tat        144
Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45

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

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

gac gag gct gac tat tac tgt cta tca gct gac aac agt gct act tgg        288
Asp Glu Ala Asp Tyr Tyr Cys Leu Ser Ala Asp Asn Ser Ala Thr Trp
                85                  90                  95

gtg ttc ggc gga ggg acc aag gtg acc gtc cta                            321
Val Phe Gly Gly Gly Thr Lys Val Thr Val Leu
            100                 105


<210>  11
<211>  107
<212>  PRT
<213>  Homo sapiens

<400>  11

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


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


Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu 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


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


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


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


<210>  12
<211>  345
<212>  DNA
<213>  Homo sapiens


<220>
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<222>  (1)..(345)
<223>  NI-105.24B2-VH variable heavy chain (VH) sequence wherein Gln at
       position 1 of the sequence may also be Glu

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

<220>
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<222>  (148)..(198)
<223>  complementarity determining region (CDR) VH-CDR2
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<220>
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<222> (295)..(312)
<223> complementarity determining region (CDR) VH-CDR3

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

tcg gtg aag gtt tcc tgt aag gca tct gga tac acc ttc gtc aat tac 96
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Val Asn Tyr
20 25 30

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

gga atc atc aat cct aat ggc gga aac aca agt tat gca gag aaa ttc 192
Gly Ile Ile Asn Pro Asn Gly Gly Asn Thr Ser Tyr Ala Glu Lys Phe
50 55 60

cag gcc cga gtc acc ttg acc agc gac acg tct acg agt acg gtg tac 240
Gln Ala Arg Val Thr Leu Thr Ser Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

atg gac ctg agc agc ctg aca tct gag gac acg gcc gtc tat tac tgt 288
Met Asp Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

gcc gtc ctt tcc cct tcg aat ccc tgg ggc cag ggg acc acg gtc acc 336
Ala Val Leu Ser Pro Ser Asn Pro Trp Gly Gln Gly Thr Thr Val Thr
100 105 110

gtc tcc tcg 345
Val Ser Ser
115

<210> 13
<211> 115
<212> PRT
<213> Homo sapiens

<400> 13

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

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

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

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

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

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

```
Ala Val Leu Ser Pro Ser Asn Pro Trp Gly Gln Gly Thr Thr Val Thr
            100                 105                 110


Val Ser Ser
        115


<210>  14
<211>  324
<212>  DNA
<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(324)
<223>  NI-105.24B2-VL variable light chain (VL) sequence wherein Glu at
       position 3 in the sequence may also be Val

<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>  14
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 ggg atc acc tgc tct gga gat gct ttg cca aag caa ttt gtt         96
Thr Ala Gly Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Gln Phe Val
            20                  25                  30

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

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

acc tca ggg aca aca gtc gcg ttg acc atc aat ggg gtc cag gca gag        240
Thr Ser Gly Thr Thr Val Ala Leu Thr Ile Asn Gly Val Gln Ala Glu
65                  70                  75                  80

gac gag gct gac tat tac tgt caa tca gcc gac cgc agt ggt gct ctt        288
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Ala Asp Arg Ser Gly Ala Leu
                85                  90                  95

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


<210>  15
<211>  108
<212>  PRT
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<213> Homo sapiens

<400> 15

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

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

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

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

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

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

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

<210> 16
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(378)
<223> NI-105.4A3-VH variable heavy chain (VH) sequence wherein Gln at positon 1 of the sequence may also be Glu and Ser at position 7 of the sequence may also be Thr

<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)..(345)
<223> complementarity determining region (CDR) VH-CDR3

<400> 16
cag gtg cag ctg gtg gag tct ggg gga ggc gcg gtc cag cct ggg ggg 48
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ala Val Gln Pro Gly Gly
1 5 10 15

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

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

gca gtt ata tcg tat gag gga act tat aaa tac tat gca gac tcc gtg        192
Ala Val Ile Ser Tyr Glu Gly Thr Tyr Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60

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

ttg cag atg agc agc ctg aga gtt gaa gac acg gct gtg tat ttc tgt        288
Leu Gln Met Ser Ser Leu Arg Val Glu Asp Thr Ala Val Tyr Phe Cys
                85                  90                  95

gtg aaa gct cga gcc ttt gcc tcc gga cag cga agc acc tcc acc gta        336
Val Lys Ala Arg Ala Phe Ala Ser Gly Gln Arg Ser Thr Ser Thr Val
            100                 105                 110

cct gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tcg                378
Pro Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 17
<211> 126
<212> PRT
<213> Homo sapiens

<400> 17

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

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

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

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

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

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

Val Lys Ala Arg Ala Phe Ala Ser Gly Gln Arg Ser Thr Ser Thr Val
            100                 105                 110

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

<210> 18
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(324)
<223> NI-105.4A3-VL 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> 18
tcc tat gag ctg act cag cca ccc tcg gtg tca gtg tcc cca gga caa 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 gca ttg cca aaa aaa tat gct 96
Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Lys Tyr Ala
20 25 30

tat tgg tac cag cag aag tca ggc cag gcc cct gtg ttg gtc atc tat 144
Tyr Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

gag gac aac aaa cga ccc tcc ggg atc cct gag aga ttc tct ggc tcc 192
Glu Asp Asn Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

agc tca ggg aca gtg gcc acc ttg act atc agt ggg gcc cag gtg gac 240
Ser Ser Gly Thr Val Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Asp
65 70 75 80

gat gaa gct gac tac tac tgc tac tcg aca gac atc agt ggt gac ctt 288
Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Ile Ser Gly Asp Leu
85 90 95

cgg gtg ttc ggc gga ggg acc aag ctg acc gtc ctc 324
Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105

<210> 19
<211> 108
<212> PRT
<213> Homo sapiens

<400> 19

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 Lys Lys Tyr Ala
20 25 30

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

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

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

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

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

<210> 20
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> mature ch4E4 heavy chain (mouse IgG2a)

<400> 20

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

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

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

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

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

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

Tyr Cys Thr Val Leu Ser Ala Asn Tyr Asp Thr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser
        115                 120                 125

Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val
    130                 135                 140

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu
145                 150                 155                 160

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175
```

```
Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr
            180                 185                 190

Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro
        195                 200                 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr
    210                 215                 220

Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met
                245                 250                 255

Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu
            260                 265                 270

Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val
        275                 280                 285

His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu
    290                 295                 300

Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly
305                 310                 315                 320

Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile
                325                 330                 335

Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val
            340                 345                 350

Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr
        355                 360                 365

Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu
    370                 375                 380

Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val
                405                 410                 415

Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val
            420                 425                 430

His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr
        435                 440                 445
```

Pro Gly Lys
450

<210> 21
<211> 213
<212> PRT
<213> Artificial sequence

<220>
<223> mature ch4E4 light chain (mouse lambda)

<400> 21

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

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

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu 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

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

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

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

Ser Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Glu Thr
115 120 125

Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp Phe Tyr Pro Gly Val
130 135 140

Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro Val Thr Gln Gly Met
145 150 155 160

Glu Thr Thr Gln Pro Ser Lys Gln Ser Asn Asn Lys Tyr Met Ala Ser
165 170 175

Ser Tyr Leu Thr Leu Thr Ala Arg Ala Trp Glu Arg His Ser Ser Tyr
180 185 190

Ser Cys Gln Val Thr His Glu Gly His Thr Val Glu Lys Ser Leu Ser
195 200 205

Arg Ala Asp Cys Ser
210

<210> 22
<211> 451
<212> PRT
<213> Artificial sequence

<220>
<223> mature ch4E4(N30Q) heavy chain (mouse IgG2a)

<400> 22

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Gln Ile Ser
            20                  25                  30

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

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

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

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

Tyr Cys Thr Val Leu Ser Ala Asn Tyr Asp Thr Phe Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser
        115                 120                 125

Val Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val
    130                 135                 140

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu
145                 150                 155                 160

Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala
                165                 170                 175

Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr
            180                 185                 190

Ser Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro
        195                 200                 205

Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr
    210                 215                 220

Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly
```

```
225                 230                 235                 240

Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met
                245                 250                 255

Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu
            260                 265                 270

Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val
        275                 280                 285

His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu
    290                 295                 300

Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly
305                 310                 315                 320

Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile
                325                 330                 335

Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val
            340                 345                 350

Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr
        355                 360                 365

Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu
    370                 375                 380

Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro
385                 390                 395                 400

Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val
                405                 410                 415

Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val
            420                 425                 430

His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr
        435                 440                 445

Pro Gly Lys
    450


<210>  23
<211>  5
<212>  PRT
<213>  Artificial sequence

<220>
<223>  NI-105.4E4-VH (variable heavy chain sequence VH) CDR1

<400>  23
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Ile Ser Ala Ile His
1 5

<210> 24
<211> 19
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4E4-VH (variable heavy chain sequence VH) CDR2

<400> 24

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

Leu Lys Gly

<210> 25
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4E4-VH (variable heavy chain sequence VH) CDR3

<400> 25

Leu Ser Ala Asn Tyr Asp Thr Phe Asp Tyr
1 5 10

<210> 26
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4E4-VL (variable light chain sequence VL) CDR1

<400> 26

Phe Gly Asp Thr Leu Pro Lys Gln Tyr Thr Tyr
1 5 10

<210> 27
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4E4-VL (variable light chain sequence VL) CDR2

<400> 27

Lys Asp Thr Glu Arg Pro Ser
1 5

<210> 28
<211> 10
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4E4-VL (variable light chain sequence VL) CD3

<400> 28

Leu Ser Ala Asp Asn Ser Ala Thr Trp Val
1   5   10

<210> 29
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.24B2-VH (variable heavy chain sequence VH) CDR1

<400> 29

Asn Tyr Ile Ile His
1   5

<210> 30
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.24B2-VH (variable heavy chain sequence VH) CD2

<400> 30

Ile Ile Asn Pro Asn Gly Gly Asn Thr Ser Tyr Ala Glu Lys Phe Gln
1   5   10   15

Ala

<210> 31
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.24B2-VH (variable heavy chain sequence VH) CDR3

<400> 31

Leu Ser Pro Ser Asn Pro
1   5

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

<220>
<223> NI-105.24B2-VL (variable light chain sequence VL) CDR1

<400> 32

Ser Gly Asp Ala Leu Pro Lys Gln Phe Val Tyr
1   5   10

<210> 33
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.24B2-VL (variable light chain sequence VL) CDR2

<400> 33

Lys Asp Thr Glu Arg Pro Ser
1 5

<210> 34
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.24B2-VL (variable light chain sequence VL) CDR3

<400> 34

Gln Ser Ala Asp Arg Ser Gly Ala Leu Trp Val
1 5 10

<210> 35
<211> 5
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4A3-VH (variable heavy chain sequence VH) CDR1

<400> 35

Asp Tyr Ala Met His
1 5

<210> 36
<211> 17
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4A3-VH (variable heavy chain sequence VH) CDR2

<400> 36

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

Gly

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

<220>
<223> NI-105.4A3-VH (variable heavy chain sequence VH) CDR3

<400> 37

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

Tyr

<210> 38
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4A3-VL (variable light chain sequence VL) CDR1

<400> 38

Ser Gly Asp Ala Leu Pro Lys Lys Tyr Ala Tyr
1 5 10

<210> 39
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4A3-VL (variable light chain sequence VL) CDR2

<400> 39

Glu Asp Asn Lys Arg Pro Ser
1 5

<210> 40
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> NI-105.4A3-VL (variable light chain sequence VL) CDR3

<400> 40

Tyr Ser Thr Asp Ile Ser Gly Asp Leu Arg Val
1 5 10

<210> 41
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide

<400> 41

Asp His Gly Ala Glu Ile Val Tyr Lys Ser Pro
1 5 10

<210> 42
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Peptide

<400> 42

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

<210> 43
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 43

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

<210> 44
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 44

Ala Gln Val Glu Val Lys Ser Glu Lys Leu Asp Phe Lys Asp Arg
1   5   10   15

<210> 45
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 45

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

<210> 46
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 46

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

<210> 47
<211> 15
<212> PRT

<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 47

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

<210> 48
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 48

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

<210> 49
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 49

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

<210> 50
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 50

Gly Gln Val Glu Val Lys Ala Glu Lys Leu Asp Phe Lys Asp Arg
1 5 10 15

<210> 51
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 51

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

<210> 52
<211> 15

<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 52

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

<210> 53
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 53

Gly Gln Val Glu Val Lys Ser Glu Lys Ala Asp Phe Lys Asp Arg
1 5 10 15

<210> 54
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Alanine mutagenesis 4E4 epitope

<400> 54

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

<210> 55
<211> 15
<212> PRT
<213> Artificial sequence

<220>
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<400> 59

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<400> 65

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<400> 76

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<400> 79

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<400> 81

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<400> 82

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<400> 84

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<400> 85

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

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<400> 86

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

<210> 87
<211> 15
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<400> 87

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

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<400> 88

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

<210> 89
<211> 15
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<220>
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<400> 89

Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ala Pro Leu Gln
1 5 10 15

<210> 90
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<220>
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<400> 90

Gln Glu Gly Asp Thr Asp Ala Gly Leu Lys Glu Ser Ala Leu Gln
1 5 10 15

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<220>
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<400> 91

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

<210> 92
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<220>
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<400> 92

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

<210> 93
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<212> PRT
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<220>
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<400> 93

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe Gln Ile Ser
20 25 30

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

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

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

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

Tyr Cys Thr Val Leu Ser Ala Asn Tyr Asp Thr Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120