SEQUENCE LISTING

<110> Biogen Idec MA Inc.
Biogen Idec International Neuroscience GmbH
Weinreb, Paul H.
Chen, Feng
Garber, Ellen A.
Grimm, Jan
Montrasio, Fabio

<120> HUMAN ANTI-TAU ANTIBODIES

<130> 2159.404PC01

<140> To be assigned
<141> Herewith

<150> 61/745,410
<151> 2012-12-21

<160> 224

<170> PatentIn version 3.5

<210> 1
<211> 352
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<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
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Ala Thr Leu Ala Asp Glu Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
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340 345 350

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<213> Homo sapiens

<220>
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<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)

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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 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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<212> PRT
<213> Homo sapiens

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<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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            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
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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
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Ser Ile Asp Met Val Asp Ser Pro Gln Leu Ala Thr Leu Ala Asp Glu
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Val Ser Ala Ser Leu Ala Lys Gln Gly Leu
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<213>  Homo sapiens


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

<300>
<301>  Goedert M., Spillantini M.G., Potier M.-C., Ulrich J., Crowther
       R.A.
<302>  Cloning and sequencing of the cDNA encoding an isoform of
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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

Lys His Gln Pro Gly Gly Gly Lys Val Gln Ile Ile Asn Lys Lys Leu
    210                 215                 220
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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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<212>  PRT
<213>  Homo sapiens


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<222>  (1)..(412)
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<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
<313>  (1)..(412)
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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 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
            260                 265                 270
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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
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<213> Homo sapiens

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<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> P10636-8
<309> 2010-10-05
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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

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        435                 440
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<210> 7
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<213> Homo sapiens

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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
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<210> 9
<211> 121
<212> PRT
<213> Homo sapiens

<400> 9

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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
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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>
<221>  CDS
<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

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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>
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<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
Ser Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
65                  70                  75                  80
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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
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<212>  DNA
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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> (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
<213>  Homo sapiens
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<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>
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<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

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> 121
<212> PRT
<213> Artificial sequence

<220>
<223> VH antibody

<400> 43

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

<210> 44
<211> 120
<212> PRT
<213> Homo sapiens

<400> 44

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

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

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

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

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

Leu Gln Trp Gly His Leu Lys Ala Ser Asp Ser Ala Met Tyr Phe Cys
                85   90   95

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 45
<211> 120
<212> PRT
<213> Homo sapiens

<400> 45

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

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

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

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

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

Leu Gln Trp Gly His Leu Lys Ala Ser Asp Ser Ala Met Tyr Phe Cys
                85   90   95

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

Gly Thr Gln Val Thr Val Ser Ser
        115   120

<210> 46
<211> 111
<212> PRT
<213> Homo sapiens

<400> 46

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

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

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

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

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

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

Lys Tyr Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 47
<211> 125
<212> PRT
<213> Homo sapiens

<400> 47

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

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

Asp 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 Glu Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
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 Leu Gly Ala Ser Val Thr Thr Ser Asn Ala Glu Asn Phe
            100                 105                 110

His His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
```

<210> 48
<211> 125
<212> PRT
<213> Homo sapiens

<400> 48

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

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

Asp 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 Glu Phe Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
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 Leu Gly Ala Ser Val Thr Thr Ser Asn Ala Glu Asn Phe
100 105 110

His His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 49
<211> 108
<212> PRT
<213> Homo sapiens

<400> 49

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 Arg Tyr Val
20 25 30

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

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

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

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

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

<210> 50
<211> 121
<212> PRT
<213> Homo sapiens

<400> 50

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

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

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

Ser Tyr Ile Ser Gly Thr Tyr Val Ser Gly Gly Thr Gly Thr Met Tyr
50 55 60

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

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

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

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 51
<211> 113
<212> PRT
<213> Homo sapiens

<400> 51

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

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

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

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

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

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

Tyr Tyr Gly Thr Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys

<210> 52
<211> 124
<212> PRT
<213> Homo sapiens

<400> 52

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 Gly Thr Arg Phe Thr Phe Ser Thr Tyr
20 25 30

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

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

Lys Gly Arg Phe Thr Ile 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 Lys Gly Val Tyr Asp Tyr Leu Trp Gly Ser Tyr Arg Leu Phe Asp
100 105 110

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

<210> 53
<211> 108
<212> PRT
<213> Homo sapiens

<400> 53

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

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

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

Asp Asp Ser Asp Arg Pro Ser Arg Ile Pro Glu Arg Phe Ser Gly Ser

```
    50                  55                  60

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

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

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

<210> 54
<211> 114
<212> PRT
<213> Homo sapiens

<400> 54

```
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 Pro Asn Tyr
            20                  25                  30

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

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

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

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

Ala Lys Gly Ser Gly Gly Ile Arg Gly Gln Gly Thr Met Val Thr Val
            100                 105                 110

Ser Ser
```

<210> 55
<211> 110
<212> PRT
<213> Homo sapiens

<400> 55

```
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 Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30
```

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

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

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

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

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

<210> 56
<211> 118
<212> PRT
<213> Homo sapiens

<400> 56

```
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 Thr Phe Ser Gly Ser
            20                  25                  30

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

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

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

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

Tyr Cys Thr Ser Pro Thr Val Thr Thr Glu Val Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 57
<211> 113
<212> PRT
<213> Homo sapiens

<400> 57

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

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

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

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

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

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

Tyr Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
            100                 105                 110

Lys
```

<210> 58
<211> 122
<212> PRT
<213> Homo sapiens

<400> 58

```
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 Ile Gly Ser Ser Gly Met Thr Phe Ser Ser
            20                  25                  30

Tyr Ala Phe Asn Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

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

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

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

Cys Val Arg Ser Thr Ala Ser Gly Ser Arg Ser Pro Gly Ile Ile Trp
            100                 105                 110

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

<210> 59

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

<400> 59

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

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

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

Tyr Ala Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Lys Phe Ser Gly
50 55 60

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

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

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

<210> 60
<211> 126
<212> PRT
<213> Homo sapiens

<400> 60

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

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

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

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

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Gly Met Tyr Tyr Cys
85 90 95

Ala Arg Val Ala Gly Asp Ile Gly Tyr Glu Asn Tyr Tyr Tyr Tyr Gly
100 105 110

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


<210>  61
<211>  113
<212>  PRT
<213>  Homo sapiens

<400>  61

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


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


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


Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg Glu Ser Gly Val
    50                  55                  60


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


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


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


Lys



<210>  62
<211>  118
<212>  PRT
<213>  Homo sapiens

<400>  62

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 Thr Arg Tyr
            20                  25                  30


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


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


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

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


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


Leu Val Thr Val Ser Ser
        115


<210>  63
<211>  113
<212>  PRT
<213>  Homo sapiens

<400>  63

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


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


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


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


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


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


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


Lys



<210>  64
<211>  113
<212>  PRT
<213>  Homo sapiens

<400>  64

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


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


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

```
Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
    50                  55                  60

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

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

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

Lys
```

<210> 65
<211> 120
<212> PRT
<213> Homo sapiens

<400> 65

```
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 Ser Phe Ser Asp Ser
            20                  25                  30

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

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

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

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

Tyr Cys Thr Arg Gln Gly Pro Ser Tyr Gly Gly Ile Asn Trp Gly Leu
            100                 105                 110

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

<210> 66
<211> 113
<212> PRT
<213> Homo sapiens

<400> 66

```
Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
```

1 5 10 15

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

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

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

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

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

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

Lys

<210> 67
<211> 115
<212> PRT
<213> Homo sapiens

<400> 67

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

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

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

Gly His Ile Lys Thr Arg Ile Glu Gly Ala Thr Thr Asp Tyr Ala Ala
50 55 60

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

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

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

Val Ser Ser
115

<210> 68
<211> 113
<212> PRT
<213> Homo sapiens

<400> 68

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

Gln Pro Ala Ser Ile Ser Cys Thr Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30

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

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

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

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

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

Lys

<210> 69
<211> 121
<212> PRT
<213> Homo sapiens

<400> 69

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

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

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

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

Gln Gly His Val Thr Ile Ser Ser Asp Lys Ser Ile Thr Thr Ala Tyr
65 70 75 80

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

```
Ala Arg Val Glu Arg Pro Asp Lys Gly Gly Trp Phe Gly Pro Trp Gly
            100                 105                 110

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

<210> 70
<211> 113
<212> PRT
<213> Homo sapiens

<400> 70

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

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

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

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

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

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

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

Lys
```

<210> 71
<211> 114
<212> PRT
<213> Homo sapiens

<400> 71

```
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 Ala Tyr
            20                  25                  30

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

Ala His Ile Thr Gly Ser Gly Thr Pro Ile Phe Tyr Ala Asp Ser Val
```

```
    50                  55                  60

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

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

Val Arg Gly Thr Val Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
            100                 105                 110

Ser Ser
```

<210> 72
<211> 110
<212> PRT
<213> Homo sapiens

<400> 72

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

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

Gly Ala Ala Trp Leu Gln Gln Phe Pro Gly His Pro Pro Lys Leu Leu
        35                  40                  45

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

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

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

Asn Ala Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110
```

<210> 73
<211> 124
<212> PRT
<213> Homo sapiens

<400> 73

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

Ser Leu Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ile Ser Tyr
            20                  25                  30
```

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

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

Glu Gly Gln Val Ser Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Thr Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

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

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

<210> 74
<211> 113
<212> PRT
<213> Homo sapiens

<400> 74

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

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

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

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

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

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

Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
            100                 105                 110

Lys
```

<210> 75
<211> 117
<212> PRT
<213> Homo sapiens

<400> 75

```
Glu Val Gln Leu Val Glu 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 Ile Phe Thr Ala Phe
            20                  25                  30

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

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

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

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

Ala Thr Gly Met Ala Val Thr Gly Asn Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
        115
```

<210> 76
<211> 117
<212> PRT
<213> Homo sapiens

<400> 76

```
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 Ile Phe Thr Ala Phe
            20                  25                  30

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

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

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

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

Ala Thr Gly Met Ala Val Thr Gly Asn Phe Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser
```

115

<210> 77
<211> 108
<212> PRT
<213> Homo sapiens

<400> 77

Leu Pro 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 Asp Val Leu Ala Glu Thr Tyr Ala
20 25 30

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

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

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

Asp Glu Ala Val Tyr His Cys His Ser Val Ala Asp Asn Asn Leu Asp
85 90 95

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

<210> 78
<211> 108
<212> PRT
<213> Homo sapiens

<400> 78

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 Val Leu Ala Glu Thr Tyr Ala
20 25 30

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

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

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

Asp Glu Ala Val Tyr His Cys His Ser Val Ala Asp Asn Asn Leu Asp
85 90 95

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

<210> 79
<211> 10
<212> PRT
<213> Homo sapiens

<400> 79

Gly Tyr Ser Phe Thr Asn Phe Trp Ile Gly
1 5 10

<210> 80
<211> 9
<212> PRT
<213> Homo sapiens

<400> 80

Ile Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

<210> 81
<211> 11
<212> PRT
<213> Homo sapiens

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Arg Gly Phe Trp Thr Gly Ser Gln Ile Glu Tyr
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<400> 82

Thr Gly Thr Ser Ser Asp Val Gly Asn Tyr Ser Phe Val Ser
1 5 10

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<400> 83

Asp Val Ser Lys Arg Ser Ser
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<400> 84

Ser Ser Tyr Gly Gly Ser Lys Tyr Pro Trp Val
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Gly Phe Thr Phe Ser Ser Tyr Asp Met His
1 5 10

<210> 86
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<400> 86

Val Ile Trp Phe Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 87
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<400> 87

Asp Leu Gly Ala Ser Val Thr Thr Ser Asn Ala Glu Asn Phe His His
1 5 10 15

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

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Glu Asp Ser Lys Arg Pro Ser
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Tyr Ser Thr Asp Ser Asn Gly His His Trp Val
1 5 10

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Gly Phe Asp Phe Ser Gly Tyr Ser Met Ala
1 5 10

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Tyr Ile Ser Gly Thr Tyr Val Ser Gly Gly Thr Gly Thr Met Tyr Tyr
1 5 10 15

Leu Asp Ser Val Lys Gly
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Val Tyr Asp Tyr Gly Glu Asp
1 5

<210> 94
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<400> 94

Lys Ser Ser Arg Ser Val Leu Tyr Ser Ser Asn Ser Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 95
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Trp Ala Ser Thr Arg Glu Ser
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Gln Gln Tyr Tyr Gly Thr Pro Arg Thr
1 5

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<400> 97

Arg Phe Thr Phe Ser Thr Tyr Ala Met Gly
1 5 10

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<211> 17
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<400> 98

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

Gly

<210> 99
<211> 15
<212> PRT
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<400> 99

Gly Val Tyr Asp Tyr Leu Trp Gly Ser Tyr Arg Leu Phe Asp Tyr
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Gly Gly Asn Asn Ile Ala Ser Lys Ser Val His
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Asp Asp Ser Asp Arg Pro Ser
1 5

<210> 102
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<400> 102

Gln Val Trp Asp Ser Thr Ser Asp His Val Val
1 5 10

<210> 103
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<400> 103

Gly Phe Thr Phe Pro Asn Tyr Val Met Thr
1 5 10

<210> 104
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<400> 104

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

Lys Gly

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<400> 105

Gly Ser Gly Gly Ile
1 5

<210> 106
<211> 14
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<400> 106

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

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<400> 107

Asp Val Thr Lys Arg Pro Ser
1 5

<210> 108
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<212> PRT
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<400> 108

His Ser Tyr Val Gly Ser Tyr Thr Leu Val
1 5 10

<210> 109
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<400> 109

Gly Phe Thr Phe Ser Gly Ser Ala Met His
1 5 10

<210> 110
<211> 19
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<400> 110

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

Val Lys Gly

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<400> 111

Thr Ser Pro Thr Val Thr Thr Glu Val
1 5

<210> 112
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<400> 112

Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asp Tyr Leu
1 5 10 15

Ala

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Trp Ala Ser Thr Arg Glu Ser

1 5

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Gln Gln Tyr Tyr Ser Thr Pro Ile Thr
1 5

<210> 115
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<400> 115

Ser Gly Met Thr Phe Ser Ser Tyr Ala Phe Asn
1 5 10

<210> 116
<211> 17
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<400> 116

Ser Ile Ser Arg Phe Gly Ser Thr Val Asp Tyr Thr Asp Ser Val Arg
1 5 10 15

Gly

<210> 117
<211> 14
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<400> 117

Val Arg Ser Thr Ala Ser Gly Ser Arg Ser Pro Gly Ile Ile
1 5 10

<210> 118
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<400> 118

Arg Ala Ser Gln Gly Ile Val Asn Asn Leu Ala
1 5 10

<210> 119
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<400> 119

Ala Ala Ser Ser Leu Gln Gly
1 5

<210> 120
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<400> 120

Gln Gln Tyr Asn Ser Tyr Pro Trp Thr
1 5

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<400> 121

Gly Tyr Arg Phe Thr Thr Tyr Trp Ile Gly
1 5 10

<210> 122
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<400> 122

Ile Ile Tyr Pro Gly Asp Ser Asp Thr
1 5

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<400> 123

Val Ala Gly Asp Ile Gly Tyr Glu Asn Tyr Tyr Tyr Tyr Gly Met Asp
1 5 10 15

Val

<210> 124
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<400> 124

Lys Ser Ser Gln Ser Val Leu Tyr Gly Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 125
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<212> PRT
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<400> 125

Trp Ala Ser Ala Arg Glu Ser
1 5

<210> 126
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<400> 126

Gln Gln Tyr Tyr Ser Thr Pro Trp Thr
1 5

<210> 127
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<400> 127

Gly Phe Thr Phe Thr Arg Tyr Gly Met His
1 5 10

<210> 128
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<400> 128

Val Ile Trp Tyr Asp Gly Thr Asn Lys Tyr Tyr Ala Asp Ser Leu Gln
1 5 10 15

Gly

<210> 129
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<400> 129

Glu Gly Phe Gln Gly Ala Ile Asp Tyr
1 5

<210> 130
<211> 17
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<400> 130

Lys Ser Ser Gln Asn Ile Leu Tyr Ser Ser Asp Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 131
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<400> 131

Trp Ala Ser Thr Arg Glu Ser
1 5

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<400> 132

Gln Gln Tyr Tyr Ser Ile Pro Arg Thr
1 5

<210> 133
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<400> 133

Ser Gly Phe Ser Phe Ser Asp Ser Ala Phe His
1 5 10

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<400> 134

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

Val Lys Gly

<210> 135
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<400> 135

Thr Arg Gln Gly Pro Ser Tyr Gly Gly Ile Asn
1 5 10

<210> 136
<211> 17
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Lys Ser Ser Gln Thr Ile Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 137
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Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 138
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Gln Gln Tyr Tyr Ser Ser Pro Gln Thr
1 5

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<400> 139

Ser Gly Phe Thr Phe Thr Lys Ala Trp Met Thr
1 5 10

<210> 140
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<400> 140

His Ile Lys Thr Arg Ile Glu Gly Ala Thr Thr Asp Tyr Ala Ala Pro
1 5 10 15

Val Glu Gly

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<400> 141

Ser Thr Asp Phe Asp Tyr
1 5

<210> 142
<211> 16

<212> PRT
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<400> 142

Thr Ser Ser Gln Ser Leu Leu Tyr Ser Asp Gly Asn Thr Tyr Leu Asn
1   5   10   15

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<400> 143

Lys Val Ser Lys Arg Asp Pro
1   5

<210> 144
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<400> 144

Met Gln Gly Ser Leu Trp Pro Arg Tyr Thr
1   5   10

<210> 145
<211> 10
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<400> 145

Gly Tyr Asn Phe Pro Asn Tyr Trp Ile Gly
1   5   10

<210> 146
<211> 24
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<400> 146

Ile Ile Tyr Pro Gly Asp Ser Asp Ile Arg Tyr Ser Pro Ser Phe Gln
1   5   10   15

Gly His Val Thr Ile Ser Ser Asp
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<400> 147

Ala Arg Val Glu Arg Pro Asp Lys Gly Gly Trp Phe Gly Pro
1   5   10

<210> 148

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

<400> 148

Lys Ser Ser Gln Thr Leu Leu Tyr Thr Ser Asn Asn Gln Asn Tyr Leu
1 5 10 15

Ala

<210> 149
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<400> 149

Trp Ala Ser Thr Arg Glu Tyr
1 5

<210> 150
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<400> 150

Gln Gln Tyr Tyr Asn Ser Pro Tyr Thr
1 5

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<400> 151

Gly Phe Thr Phe Ser Ala Tyr Gly Met Asn
1 5 10

<210> 152
<211> 17
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<400> 152

His Ile Thr Gly Ser Gly Thr Pro Ile Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

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<211> 7
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<400> 153

Val Arg Gly Thr Val Asp Tyr
1   5

<210> 154
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<400> 154

Ser Gly Asn Ser Asn Asn Val Gly Asn Gln Gly Ala Ala
1   5   10

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Glu Asn Ile Asn Arg Pro Ser
1   5

<210> 156
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<400> 156

Ser Ala Trp Asp Gly His Leu Asn Ala Trp Val
1   5   10

<210> 157
<211> 10
<212> PRT
<213> Homo sapiens

<400> 157

Gly Tyr Ser Phe Ile Ser Tyr Trp Val Gly
1   5   10

<210> 158
<211> 24
<212> PRT
<213> Homo sapiens

<400> 158

Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Glu
1   5   10   15

Gly Gln Val Ser Ile Ser Ala Asp
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<400> 159

His Trp Gly Pro Ala Ala Val Thr Asp Ser Pro Trp Phe Gly Pro
1 5 10 15

<210> 160
<211> 17
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<400> 160

Lys Ser Ser Gln Thr Val Leu Tyr Thr Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 161
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<400> 161

Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 162
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<212> PRT
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<400> 162

Gln His Tyr Tyr Ser Thr Pro Phe Thr
1 5

<210> 163
<211> 10
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<400> 163

Gly Tyr Ile Phe Thr Ala Phe Phe Met His
1 5 10

<210> 164
<211> 17
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<400> 164

Trp Ile Asn Pro Asp Ser Gly Ala Thr Lys Tyr Ala His Asn Phe Gln
1 5 10 15

Gly

<210> 165
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<212> PRT
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<400> 165

Gly Met Ala Val Thr Gly Asn Phe
1 5

<210> 166
<211> 11
<212> PRT
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<400> 166

Ser Gly Asp Val Leu Ala Glu Thr Tyr Ala Arg
1 5 10

<210> 167
<211> 7
<212> PRT
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<400> 167

Arg Asp Arg Glu Arg Pro Ala
1 5

<210> 168
<211> 11
<212> PRT
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<400> 168

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

<210> 169
<211> 360
<212> DNA
<213> Homo sapiens

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tcctgcaagg catttggata cagttttacc aacttctgga tcggctgggt gcgccaggtg 120

cccgggaaag gcctggagtg ggtgggaatc atctatcctg gtgactctga caccagatac 180

agtccgtcct tccaaggcca ggtcaccatt tcagccgaca agtccattga caccgcctac 240

ctacagtggg gccacctgaa ggcctcggac agcgccatgt atttctgtgc cagacggggt 300

ttttggactg gaagtcaaat tgaatactgg ggccagggca ccctggtcac cgtctcctcg 360

<210> 170
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<212> DNA
<213> Homo sapiens

<400> 170
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tcctgcaagg catttggata cagttttacc aacttctgga tcggctgggt gcgccaggtg 120

cccgggaaag gcctggagtg ggtgggaatc atctatcctg gtgactctga caccagatac 180

agtccgtcct tccaaggcca ggtcaccatt tcagccgaca agtccattga caccgcctac 240

ctacagtggg gccacctgaa ggcctcggac agcgccatgt atttctgtgc cagacggggt 300

ttttggactg gaagtcaaat tgaatactgg ggccagggca cccaggtcac cgtctcctcg 360

<210> 171
<211> 333
<212> DNA
<213> Homo sapiens

<400> 171
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tcctgcactg gaactagtag tgacgttggt aattatagtt ttgtctcctg gtatcaacag 120

tatcccggca aagcccccaa agtcatcatt tatgacgtca gtaagcggtc ctcaggggtc 180

cctgatcgct tctttggctc caagtctgcc aacacggcct ccctgaccgt ctctggggtc 240

caggaagagg atgaggctga ctatttttgc agctcatacg gaggcagcaa atatccgtgg 300

gtgtttggcg gagggaccaa gctgaccgtc ctt 333

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

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tcctgtgcag cgtctggatt caccttcagt agttatgaca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcggtt atatggtttg atggaagtaa tgaattctat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaccta 300

ggggcctcag tgactacttc caacgctgaa aacttccacc actggggcca gggcaccctg 360

gtcaccgtct cctcg 375

<210> 173
<211> 375
<212> DNA
<213> Homo sapiens

<400> 173
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tcctgtgcag cgtctggatt caccttcagt agttatgaca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcggtt atatggtttg atggaagtaa tgaattctat 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgttt 240

ctgcaaatga acagcctgag agccgaggac acggctgtgt attactgtgc gagagaccta 300

ggggcctcag tgactacttc caacgctgaa aacttccacc actggggcca gggcaccctg 360

gtcaccgtct cctcg 375

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

<400> 174
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acctgctctg gagatgcatt gccaaaaaga tatgtttatt ggtaccagca gaagtcaggc 120

caggcccctg tgctggtcat ctatgaggac agcaaacgac cctccgggat ccctgagaca 180

ttctctggct ccagctcagg gacaatggcc accttgacta tcagtggggc ccaggtagag 240

gatgaagctg actactactg ttactcaaca gacagcaatg gtcatcattg ggtgttcggc 300

ggagggacca agctgaccgt ccta 324

<210> 175
<211> 363
<212> DNA
<213> Homo sapiens

<400> 175
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tcctgtgcag cctctggatt cgacttcagc ggctatagca tggcctgggt ccgccaggct 120

ccagggaagg ggctggagtg ggtttcgtat attagcggca cttatgttag tggtggtaca 180

ggcacgatgt attatttaga ctctgtgaag ggccgattct tcatctccag agacgatgcc 240

accagttcac tgtatctgca aatggacagc ctgagggacg aggacacggc tgtgtattac 300

tgtgcgagag tttatgacta cggtgaagac tggggccagg gaaccctggt caccgtctcc 360

tcg 363

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

<400> 176
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atcaactgca agtccagccg gagtgtctta tacagctcca acagtaagaa ctacttagct 120

tggtatcagc agaaacccgg acagcctcct aagttgctca tttactgggc atctacgcgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagaatt cactctcacc 240

atcagcagcc tgcaggctga agatgtggcg gtttattact gtcagcaata ttatggtact 300

cctcgcacgt tcggccaagg gaccaaggtg gaaatcaaa 339

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

<400> 177
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tcctgtgcag gcactagatt cacctttagc acctatgcca tgggctgggt ccgccaggct 120

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gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agccgaggac acggccgtat attattgtgc gaaaggggtt 300

tatgattacc tttgggggag ttatcggctc tttgactact ggggccaggg aaccctggtc 360

accgtctcct cg 372

<210> 178
<211> 324
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<400> 178
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acctgtgggg gaaacaacat tgcaagtaaa agtgtgcact ggtaccagca gaagccaggc 120

caggcccctg tgctggtcgt ctatgatgat agcgaccggc cctcacggat ccctgagcga 180

ttctctggct ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg 240

gatgaggccg actattactg tcaggtgtgg gatagtacta gtgatcatgt ggtattcggc 300

ggagggacca agctgaccgt ccta 324

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<212> DNA
<213> Homo sapiens

<400> 179
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ccagggaagg ggctggagtg ggtctcaggt attagtggta gtggtggtag cacagactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgttgtat 240

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ggtggtatcc ggggccaagg gacaatggtc accgtctctt cg 342

<210> 180
<211> 330
<212> DNA
<213> Homo sapiens

<400> 180
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tcctgcactg gaaccagcag tgatgttggt ggttataact atgtctcctg gcaccagcag 120

cacccaggca aagcccccaa actcctgatt tatgatgtca ctaagcggcc ctcaggggtc 180

cctgatcgct tctctggctc caagtctggc aacacggccg ccctgaccat ctctgggctc 240

caggctgagg atgaggctga ttattactgc cactcatatg taggcagcta cactttggta 300

ttcggcggag ggaccaagct gaccgtcctc 330

<210> 181
<211> 354
<212> DNA
<213> Homo sapiens

<400> 181
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tcctgtgcag cctctgggtt cacattcagt ggctctgcta tgcactgggt ccgccaggct 120

tccgggaaag ggctggagtg ggttggccgt attagaagca aagctaatag ttatgcgaca 180

gcatatgctg cgtcggtgaa aggcaggttc accatctcca gagatgattc aaagaacacg 240

gcgtatctac aaatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtactagc 300

cctacggtga ctaccgaggt ctggggccag ggaaccctgg tcaccgtctc ctcg 354

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

<400> 182
gatattgtga tgactcaatc accagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tacagctcca acaataagga ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aagctgctca tttactgggc atctacccgg 180

gaatccgggg tctctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtgtattact gtcagcaata ttatagtacc 300

ccgatcacct tcggccaagg gacacgactg gagattaaa 339

<210> 183
<211> 366
<212> DNA
<213> Homo sapiens

<400> 183
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc cgggggggtc cctgagactg 60

tcctgtatag gctcctctgg aatgaccttc agtagttatg ccttcaactg ggtccgccag 120

actccaggga aggggctgga gtgggtttca tccatcagtc gtttcggttc gaccgtggac 180

tacacagact cggtgcgggg ccgatttacc atctccagag acgatggcca gaggtcactg 240

tatctgcaaa tgaacagcct gagagtcgaa gacacggctg tttattattg tgtcagatcg 300

acggcttctg gttcgcggtc ccccggaatt atctggggcc aggggaccac ggtcaccgtc 360

tcctcg 366

<210> 184
<211> 321
<212> DNA
<213> Homo sapiens

<400> 184
gacatccaga tgacccagtc tccatcctca ctgtctgctt ctgtaggaga cagagtcacc 60

atcacttgtc gggcgagtca gggcattgtc aataatttag cctggtttca gcagaagcca 120

gggaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaggtgg ggtcccatca 180

aaattcagcg gcagtgcgtc tgggacagat ttcagtctca ccatcagcaa cctgcagcct 240

gaagactttg caacttattt ctgccaacag tataatagtt acccttggac gttcggccaa 300

gggaccaagg tggagatcaa a 321

<210> 185
<211> 378
<212> DNA
<213> Homo sapiens

<400> 185
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg gttctggata caggtttacc acctactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatggggatc atctatcctg gtgactctga taccagatac 180

agcccgtcct accaaggcca ggtcaccatt tcagccgaca agtccatcag taccgcctac 240

ctgcagtgga gcagcctgaa ggcctcggac accggcatgt attactgtgc gagagtggca 300

ggggatattg gctacgagaa ctactactac tacggtatgg acgtctgggg ccaagggacc 360

acggtcaccg tctcctcg 378

<210> 186
<211> 339
<212> DNA
<213> Homo sapiens

<400> 186
gatattgtga tgactcaatc accagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gagtgtttta tatggctcca acaataagaa ctacttagct 120

tggtaccagc agaaactagg acagtctcct aaactgctca tttactgggc atctgcccgg 180

gaatccgggg tccctgaccg attcggtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtctattact gtcagcaata ttacagtact 300

ccgtggacgt tcggccaggg gaccaaggtg gaaatcaaa 339

<210> 187
<211> 354
<212> DNA
<213> Homo sapiens

<400> 187
caggtgcagc tggtggagtc tgggggaggc gtggtccagc ctgggaggtc cctgagactc 60

tcctgtgcag cgtctggatt cacgttcact agatatggca tgcactgggt ccgccaggct 120

ccaggcaagg ggctggagtg ggtggcagtt atatggtatg atggaactaa taaatattat 180

gcagactcac tgcagggccg attcaccatc tccagagaca cttccacgaa cacgctgtat 240

ctgcaaatga acggcctgag agtcgaggac agggctgtat attactgtgc gagagagggg 300

tttcagggag cgatcgacta ctggggccag ggcaccctgg tcaccgtctc ctcg 354

<210> 188
<211> 339
<212> DNA
<213> Homo sapiens

<400> 188
gaaattgtga tgactcagtc tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtcaagcca gaatatttta tacagctccg acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcct aaactactca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtatt 300

cctcggacgt tcggccaagg gaccaaggtg gagatcaaa 339

<210> 189
<211> 360
<212> DNA
<213> Homo sapiens

<400> 189
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggGtc cctgaaactc 60

tcctgtgcag cctctgggtt cagtttcagt gactctgctt tccactgggc ccgccaggct 120

tccgggaaag ggctggagtg ggttggccgt attagaagta aaggtaataa ttacgcgaca 180

gcatatgctg cgtcggtgaa aggcaggttc accgtctcca gagatgattc aaagaacacg 240

acgtatctac agatgaacag cctgaaaacc gacgacacgg ccatatatta ctgtactaga 300

cagggcccct cctacggtgg tattaattgg ggcctgggca ccctggtcac cgtctcctcg 360

<210> 190
<211> 339
<212> DNA
<213> Homo sapiens

<400> 190
gatattgtga tgactcaatc accagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gactatttta tacagttcca acaataagaa ctacttagct 120

tggtaccagc agaaaccagg acagcctcca aagctgctca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcgggctga agatgtggca gtttattact gtcagcaata ttatagttct 300

cctcaaacgt tcggccaggg gaccaaggtg gaaatcaaa 339

<210> 191
<211> 345
<212> DNA
<213> Homo sapiens

<400> 191
gaggtgcagc tggtggagtc tgggggaggc ttcgtgaggc cgggggggtc cattacactg 60

tcctgtgcaa cctctggatt tactttcact aaagcctgga tgacctgggt ccgccaggct 120

ccagtgaagg ggctggagtg gattggccat attaaaacca gaattgaagg tgcgacaaca 180

gactacgctg cgcccgtgga aggccgattc accatttcaa gagacgattc aaaaaatatg 240

gtatatcttc aaatgaacag cctgaagacc gaagactcag gcatttatta ctgttccaca 300

gactttgact attggggcca gggaaccctg gtcaccgtct cctcg 345

<210> 192
<211> 339
<212> DNA
<213> Homo sapiens

<400> 192
gatgttgtga tgactcagtc tccactctcc ctgcccgtca cccttggaca gccggcctcc 60

atctcctgca cgtctagtca aagcctccta tacagtgatg gaaacaccta cttgaattgg 120

tttcagcaga ggccaggcca atctccaagg cgcctaatgt ataaggtttc taagcgggac 180

cctggggtcc cagacagatt cagcggcagt gggtcaggca ctgatttcac actgagcatc 240

agcagggtgg aggctgagga tgttggcgtt tattactgca tgcaaggttc actctggcct 300

cggtacactt ttggccaggg gaccaaggtg gagatcaaa 339

<210> 193
<211> 363
<212> DNA
<213> Homo sapiens

<400> 193
gaggtgcagc tggtgcagtc tggagcagaa gtgaaaaagc ccggggactc tctgaggatc 60

tcctgtaagg cttctggata caactttccc aactactgga tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatgggaatc atctaccctg gtgactctga tatcagatac 180

agcccgtcct tccagggaca cgtcaccatc tccagtgaca agtccatcac caccgcctat 240

ctccagtgga ccagtctgaa ggtcgcggac agcgccatgt attattgtgc gagagtggaa 300

aggcctgaca agggggctg gttcggcccc tggggccagg gaaccctggt caccgtctcc 360

tcg 363

<210> 194
<211> 339
<212> DNA
<213> Homo sapiens

<400> 194
gatattgtga tgactcaatc accagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gactcttttg tacacgtcca ataatcagaa ctatttagct 120

tggtaccaac acaaaccggg acagcctcct aaggtgctca tatactgggc atctacccgg 180

gaatatgggg tccctgaccg attcagtggc agcgggtctg gaacagattt cactctcacc 240

atcagcagcc tgcagcctga agatgtggct gtttattact gtcagcaata ttataatagt 300

ccctacactt ttggccaggg gaccaagctg gagatcaaa 339

<210> 195
<211> 342

<212> DNA
<213> Homo sapiens

<400> 195
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctgggggtc cctgagactc 60

tcctgtgcag cctctggatt caccttcagt gcatatggca tgaactgggt ccgccaggct 120

ccaggaaagg ggctggagtg ggttgcacac attactggta gtggcactcc catcttctac 180

gcagactctg tgaagggccg attcaccatt tccagagaca atgccaagag ttccctatat 240

ctgcaaatga acagcctgag aaacgatgac acggctctat atttctgtgt gagaggtacc 300

gttgactact ggggccaggg caccctggtc accgtctcct cg 342

<210> 196
<211> 330
<212> DNA
<213> Homo sapiens

<400> 196
caggctggtc tgactcagcc accctcggtg tccaaggact tgagacagac cgccacactc 60

acctgcagtg ggaacagcaa caatgtcggc aaccaaggag cagcttggct gcagcagttc 120

ccgggccacc ctcccaaact cctcttctac gaaaatatca accggccctc aggaatttca 180

gagagattct ctgcatccag gtcaggaaac acagcttccc tgaccattac tggactccag 240

cctgaggacg aggctgacta ttactgctca gcgtgggacg gccacctcaa tgcttgggtg 300

ttcggcggag ggaccaagct gaccgtccta 330

<210> 197
<211> 372
<212> DNA
<213> Homo sapiens

<400> 197
gaggtgcagc tggtgcagtc tggagcagag gtgaaaaagc ccggggagtc tctgaagatc 60

tcctgtaagg cttctggata tagttttatc agctactggg tcggctgggt gcgccagatg 120

cccgggaaag gcctggagtg gatgggcatc atctatcccg gtgactctga caccagatac 180

agcccgtcct tcgaaggcca ggtcagcatc tcagccgaca agtccatcag caccgcctac 240

ctccagtgga ccagcctgaa ggcctcggac accgccatgt attactgtgc gagacattgg 300

gggccggcag cagtgacgga ttctccctgg ttcggccct ggggccaggg aaccctggtc 360

accgtctcct cg 372

<210> 198
<211> 339
<212> DNA
<213> Homo sapiens

<400> 198
gatattgtga tgacccagag tccagactcc ctggctgtgt ctctgggcga gagggccacc 60

atcaactgca agtccagcca gactgtttta tatacctcca acaataagaa ctacttagct 120

tggtaccagc agaagccagg acagcctcct aagttactca tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcacta ttatagtact 300

ccattcactt tcggccctgg gaccaaagtg gatatcaaa 339

<210> 199
<211> 351
<212> DNA
<213> Homo sapiens

<400> 199
gaggtgcagc tggtggagtc tggggctgag gtgaagaaac ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata catctttacc gccttcttta tgcactgggt gcgacaggcc 120

cctggacaag gccttgagtg gatgggatgg atcaaccctg acagtggtgc cacaaagtat 180

gcacacaact ttcagggcag ggttaccatg accagggaca cgtccatcag cacagccttc 240

atggagctga gtggactgaa gtctgacgac acgggcgtat attactgtgc gacgggtatg 300

gcagtgactg gtaacttctg gggccaggga accctggtca ccgtctcctc g 351

<210> 200
<211> 351
<212> DNA
<213> Homo sapiens

<400> 200
caggtgcagc tggtgcaatc tggggctgag gtgaagaaac ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata catctttacc gccttcttta tgcactgggt gcgacaggcc 120

cctggacaag gccttgagtg gatgggatgg atcaaccctg acagtggtgc cacaaagtat 180

gcacacaact ttcagggcag ggttaccatg accagggaca cgtccatcag cacagccttc 240

atggagctga gtggactgaa gtctgacgac acgggcgtat attactgtgc gacgggtatg 300

gcagtgactg gtaacttctg gggccagggc accctggtca ccgtctcctc g 351

<210> 201
<211> 324
<212> DNA
<213> Homo sapiens

<400> 201
ctgcctgtgc tgactcagcc accctcagtg tcagtgtctc cgggacagac agccaggatc 60

acctgctcag gagatgtact ggcagaaaca tatgctcggt ggttccagca gaagccaggc 120

caggcccctg tgttggtgat gtatagagac cgtgagcggc ccgcagggat ccctgagcga 180

ttctccggct ccagctcagg gaacacagtc accttgacca tcagcggggc ccaggctgag 240

gatgaggctg tctatcattg tcactctgtg gctgacaaca atctagattg ggtgttcggc 300

ggagggacca aactgaccgt ccta 324

<210> 202
<211> 324
<212> DNA
<213> Homo sapiens

<400> 202
tcctatgagc tgactcagcc accctcagtg tcagtgtctc cgggacagac agccaggatc 60

acctgctcag gagatgtact ggcagaaaca tatgctcggt ggttccagca gaagccaggc 120

caggcccctg tgttggtgat gtatagagac cgtgagcggc ccgcagggat ccctgagcga 180

ttctccggct ccagctcagg gaacacagtc accttgacca tcagcggggc ccaggctgag 240

gatgaggctg tctatcattg tcactctgtg gctgacaaca atctagattg ggtgttcggc 300

ggagggacca aactgaccgt ccta 324

<210> 203
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 203

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

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

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

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

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

Leu Gln Trp Gly His Leu Lys Ala Ser Asp Ser Ala Met Tyr Phe Cys
85 90 95

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

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

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

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

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

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser

```
            180                 185                 190

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Gly Lys
    450
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<210> 204
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 204

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


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


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


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


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


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


Lys Tyr Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110


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


Glu Leu Glu Thr Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp Phe
    130                 135                 140


Tyr Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro Val
145                 150                 155                 160


Thr Gln Gly Met Glu Thr Thr Gln Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175


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


His Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly His Thr Val Glu
        195                 200                 205


Lys Ser Leu Ser Arg Ala Asp Cys Ser
    210                 215
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<210> 205

<211> 455
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 205

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

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

Asp 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 Glu Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
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 Leu Gly Ala Ser Val Thr Thr Ser Asn Ala Glu Asn Phe
            100                 105                 110

His His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr
        115                 120                 125

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

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

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

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
            180                 185                 190

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

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

Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro
225                 230                 235                 240
```

```
Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys
                245                 250                 255

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

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

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

Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp
305                 310                 315                 320

Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu
                325                 330                 335

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

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

Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp
    370                 375                 380

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

Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser
                405                 410                 415

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

Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser
        435                 440                 445

Phe Ser Arg Thr Pro Gly Lys
    450                 455


<210>  206
<211>  213
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimaera

<400>  206

Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr
1               5                   10                  15
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Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Arg Tyr Val Tyr
            20                  25                  30

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

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

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

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

Val Phe Gly Gly Gly Thr Lys Leu 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>  207
<211>  444
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimaera

<400>  207

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 Pro Asn Tyr
            20                  25                  30
```

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

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

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

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

Ala Lys Gly Ser Gly Gly Ile Arg Gly Gln Gly Thr Met Val Thr Val
            100                 105                 110

Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val
        115                 120                 125

Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys
    130                 135                 140

Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu
145                 150                 155                 160

Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr
                165                 170                 175

Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln
            180                 185                 190

Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp
        195                 200                 205

Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys
    210                 215                 220

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

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

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

Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr
        275                 280                 285

His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro
    290                 295                 300
```

```
Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val
305                 310                 315                 320

Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro
                325                 330                 335

Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu
            340                 345                 350

Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp
        355                 360                 365

Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr
    370                 375                 380

Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu
                405                 410                 415

Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
        435                 440
```

<210> 208
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 208

```
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 Pro Asn Tyr
            20                  25                  30

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

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

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

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

```
Ala Lys Gly Ser Gly Gly Ile Trp Gly Gln Gly Thr Met Val Thr Val
            100                 105                 110

Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val
        115                 120                 125

Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys
    130                 135                 140

Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu
145                 150                 155                 160

Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr
                165                 170                 175

Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln
            180                 185                 190

Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp
        195                 200                 205

Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys
    210                 215                 220

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

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

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

Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr
        275                 280                 285

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

Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val
305                 310                 315                 320

Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro
                325                 330                 335

Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu
            340                 345                 350

Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp
        355                 360                 365
```

```
Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr
    370                 375                 380

Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu
                405                 410                 415

Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His
            420                 425                 430

His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
        435                 440
```

<210> 209
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 209

```
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 Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

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

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

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

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

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

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

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

Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro Val Thr
145                 150                 155                 160
```

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

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

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

Ser Leu Ser Arg Ala Asp Cys Ser
    210                 215
```

<210> 210
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 210

```
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 Ile Gly Ser Ser Gly Met Thr Phe Ser Ser
            20                  25                  30

Tyr Ala Phe Asn Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

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

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

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

Cys Val Arg Ser Thr Ala Ser Gly Ser Arg Ser Pro Gly Ile Ile Trp
            100                 105                 110

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

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

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

Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro
```

```
                165                 170                 175

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Thr Pro Gly Lys
    450

<210> 211
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 211

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

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

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

Tyr Ala Ala Ser Ser Leu Gln Gly Gly Val Pro Ser Lys Phe Ser Gly
    50   55   60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Asp Ala Ala
            100   105   110

Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly
        115   120   125

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

Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu
145   150   155   160

Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser
                165   170   175

Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr
            180   185   190

Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser
        195   200   205

Phe Asn Arg Asn Glu Cys

210

<210> 212
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 212

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

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

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

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

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

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

Lys Tyr Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110

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

Glu Leu Glu Thr Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp Phe
    130                 135                 140

Tyr Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro Val
145                 150                 155                 160

Thr Gln Gly Met Glu Thr Thr Gln Pro Ser Lys Gln Ser Asn Asn Lys
                165                 170                 175

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

His Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly His Thr Val Glu
        195                 200                 205

Lys Ser Leu Ser Arg Ala Asp Cys Ser
    210                 215
```

<210> 213
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 213

```
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 Ala Lys
        115                 120                 125


Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
    130                 135                 140


Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
145                 150                 155                 160


Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
                165                 170                 175


His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
            180                 185                 190


Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
        195                 200                 205


Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
    210                 215                 220


Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val
225                 230                 235                 240
```

```
Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile
                245                 250                 255

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

Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His
        275                 280                 285

Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Gln Ser Thr Phe Arg
    290                 295                 300

Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys
305                 310                 315                 320

Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu
                325                 330                 335

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

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

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

Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile
385                 390                 395                 400

Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln
                405                 410                 415

Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His
            420                 425                 430

Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro
        435                 440                 445

Gly Lys
    450


<210>  214
<211>  445
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimaera

<400>  214

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 Pro Pro Ser
        115                 120                 125

Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val
    130                 135                 140

Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val
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 Pro
            180                 185                 190

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

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

Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys
                245                 250                 255

Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln
            260                 265                 270

Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln
        275                 280                 285
```

```
Pro Arg Glu Glu Gln Phe Gln Ser Thr Phe Arg Ser Val Ser Glu Leu
    290                 295                 300

Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg
305                 310                 315                 320

Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr
        355                 360                 365

Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln
    370                 375                 380

Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly
385                 390                 395                 400

Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu
                405                 410                 415

Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn
            420                 425                 430

His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
        435                 440                 445


<210>  215
<211>  449
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimaera

<400>  215

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

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

Asp 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 Glu Phe Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
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 Leu Gly Ala Ser Val Thr Thr Ser Asn Ala Glu Asn Phe
            100                 105                 110

His His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Lys Thr
        115                 120                 125

Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr
    130                 135                 140

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

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

Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser
            180                 185                 190

Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn
        195                 200                 205

Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro
    210                 215                 220

Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser
225                 230                 235                 240

Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr
                245                 250                 255

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

Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr
        275                 280                 285

Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Gln Ser Thr Phe Arg Ser
    290                 295                 300

Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu
305                 310                 315                 320

Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys
                325                 330                 335

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

```
Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr
        355                 360                 365

Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln
    370                 375                 380

Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met
385                 390                 395                 400

Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys
                405                 410                 415

Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu
            420                 425                 430

Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro Gly
        435                 440                 445

Lys
```

<210> 216
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 216

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

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

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

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

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

Leu Gln Trp Gly His Leu Lys Ala Ser Asp Ser Ala Met Tyr Phe Cys
                85                  90                  95

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

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

```
Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
    130                 135                 140

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

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

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

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

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

Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val
                245                 250                 255

Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe
            260                 265                 270

Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro
        275                 280                 285

Arg Glu Glu Gln Phe Gln Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
    290                 295                 300

Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
305                 310                 315                 320

Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
                325                 330                 335

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

Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
        355                 360                 365

Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
    370                 375                 380

Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
385                 390                 395                 400
```

Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
405 410 415

Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
420 425 430

His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
435 440

<210> 217
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 217

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

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

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

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

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

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

Lys Tyr Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

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

Glu Leu Glu Thr Asn Lys Ala Thr Leu Val Cys Thr Ile Thr Asp Phe
130 135 140

Tyr Pro Gly Val Val Thr Val Asp Trp Lys Val Asp Gly Thr Pro Val
145 150 155 160

Thr Gln Gly Met Glu Thr Thr Gln Pro Ser Lys Gln Ser Asn Asn Lys
165 170 175

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

```
His Ser Ser Tyr Ser Cys Gln Val Thr His Glu Gly His Thr Val Glu
        195                 200                 205

Lys Ser Leu Ser Arg Ala Asp Cys Ser
    210                 215
```

<210> 218
<211> 458
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 218

```
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 Pro Asn Tyr
            20                  25                  30

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

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

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

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

Ala Lys Gly Ser Gly Gly Ile Trp Gly Gln Gly Thr Met Val Thr Val
            100                 105                 110

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

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
    130                 135                 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145                 150                 155                 160

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

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
            180                 185                 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
```

```
        195                 200                 205

Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
    210                 215                 220

Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
225                 230                 235                 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                 250                 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            260                 265                 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        275                 280                 285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
    290                 295                 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                 310                 315                 320

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
                325                 330                 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            340                 345                 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        355                 360                 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
    370                 375                 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                 390                 395                 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
                405                 410                 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            420                 425                 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Gln Ser Ala Leu Thr
        435                 440                 445

Gln Pro Arg Ser Val Ser Gly Ser Pro Gly
    450                 455


<210>  219
<211>  216
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<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 219

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

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

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

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

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

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

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

Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
    130                 135                 140

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145                 150                 155                 160

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

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
            180                 185                 190

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

Thr Val Ala Pro Thr Glu Cys Ser
    210                 215
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<210> 220
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 220

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 Pro Asn Tyr
            20   25   30

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

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

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

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

Ala Lys Gly Ser Gly Gly Ile Trp Gly Gln Gly Thr Met Val Thr Val
            100   105   110

Ser Ser

<210> 221
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimaera

<400> 221

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

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

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

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

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

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

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Lys Tyr Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  222
<211>  111
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Chimaera

<400>  222

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


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


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


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


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


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


Lys Tyr Pro Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
            100                 105                 110


<210>  223
<211>  339
<212>  DNA
<213>  Homo sapiens

<400>  223
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atcaactgca agtcaagcca gaatatttta tacagctccg acaataagaa ctacttagct      120

tggtaccagc agaaaccagg acagcctcct aaactactca tttactgggc atctacccgg      180

gaatccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc      240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatagtatt      300

cctcggacgt tcggccaagg gaccaaggtg gagatcaaa                              339


<210>  224
<211>  14
<212>  PRT
<213>  Homo sapiens

<400>  224
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Thr Gly Thr Ser Ser Asp Val Gly Gln Tyr Ser Phe Val Ser
1               5                   10
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