SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> rat NogoA_342-357

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Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
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Glu Ala

<210> 2

<211> 221

<212> PRT

<213> Mus musculus

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<221> CHAIN

<222> (1)..(221)

<223> Variable part of Heavy Chain of 3A6 with leader sequence

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Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
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Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
20 25 30

Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val

130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
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<210> 3

<211> 238

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<222> (1)..(238)

<223> Light Chain of 3A6 with leader sequence

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Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
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Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
20 25 30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu

115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 4

<211> 3919

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(3579)

<223> Human NogoA

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

ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag      96
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
            20                  25                  30

gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac     144
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
        35                  40                  45

ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc     192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
    50                  55                  60

gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac     240
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65                  70                  75                  80

ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc     288
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
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85 90 95

gct ccc ccc gtc gcc ccg gag cgg cag ccg tct tgg gac ccg agc ccg 336
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc 384
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
115 120 125

tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc cgg cct ccc 432
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc 480
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

ccg cca gcc ccg gct ccc gcc gcg ccc ccc tcc acc ccg gcc gcg ccc 528
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt 576
Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
180 185 190

cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac 624
Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp
195 200 205

ttg aag gag cag cca ggt aac act att tcg gct ggt caa gag gat ttc 672
Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
210 215 220

cca tct gtc ctg ctt gaa act gct gct tct ctt cct tct ctg tct cct 720
Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
225 230 235 240

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ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt ggt aat ttg tca      768
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
                245                 250                 255

aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct      816
Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
            260                 265                 270

tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat      864
Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
        275                 280                 285

tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc      912
Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
    290                 295                 300

agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg      960
Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
305                 310                 315                 320

gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt     1008
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
                325                 330                 335

aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa     1056
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
            340                 345                 350

ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt     1104
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
        355                 360                 365

ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat     1152
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
    370                 375                 380
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gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag     1200
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385                 390                 395                 400

gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg     1248
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu
                405                 410                 415

gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act     1296
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
            420                 425                 430

aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc     1344
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
        435                 440                 445

agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt     1392
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys
    450                 455                 460

gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt     1440
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe
465                 470                 475                 480

cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa     1488
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
                485                 490                 495

ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc     1536
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr
            500                 505                 510

aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat     1584
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp
        515                 520                 525

tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca     1632
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Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala
    530                 535                 540

aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa    1680
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
545                 550                 555                 560

agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa    1728
Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
                565                 570                 575

atg gac ttg gtt caa aca tca gaa gtt atg caa gag tca ctc tat cct    1776
Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
            580                 585                 590

gca gca cag ctt tgc cca tca ttt gaa gag tca gaa gct act cct tca    1824
Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
        595                 600                 605

cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt    1872
Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
    610                 615                 620

cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa    1920
Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625                 630                 635                 640

gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc    1968
Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
                645                 650                 655

cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga    2016
Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
            660                 665                 670

ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa    2064
Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
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675 680 685

gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa 2112
Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
690 695 700

aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa 2160
Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
705 710 715 720

atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa 2208
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
725 730 735

gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca 2256
Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
740 745 750

ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa 2304
Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
755 760 765

gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat 2352
Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
770 775 780

aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg 2400
Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785 790 795 800

gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct 2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg 2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

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gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct     2544
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
        835                 840                 845

aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca     2592
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
    850                 855                 860

att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat     2640
Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865                 870                 875                 880

tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac     2688
Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
                885                 890                 895

aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc     2736
Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
            900                 905                 910

aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt     2784
Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
        915                 920                 925

gaa gag aaa atc agt ttc tca gat gac ttt tct aaa aat ggg tct gct     2832
Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
    930                 935                 940

aca tca aag gtg ctc tta ttg cct cca gat gtt tct gct ttg gcc act     2880
Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945                 950                 955                 960

caa gca gag ata gag agc ata gtt aaa ccc aaa gtt ctt gtg aaa gaa     2928
Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
                965                 970                 975
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gct gag aaa aaa ctt cct tcc gat aca gaa aaa gag gac aga tca cca      2976
Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
            980                 985                 990

tct gct ata ttt tca gca gag ctg  agt aaa act tca gtt  gtt gac ctc   3024
Ser Ala Ile Phe Ser Ala Glu Leu  Ser Lys Thr Ser Val  Val Asp Leu
        995                 1000                1005

ctg tac  tgg aga gac att aag  aag act gga gtg gtg  ttt ggt gcc      3069
Leu Tyr  Trp Arg Asp Ile Lys  Lys Thr Gly Val Val  Phe Gly Ala
    1010                1015                1020

agc cta  ttc ctg ctg ctt tca  ttg aca gta ttc agc  att gtg agc      3114
Ser Leu  Phe Leu Leu Leu Ser  Leu Thr Val Phe Ser  Ile Val Ser
    1025                1030                1035

gta aca  gcc tac att gcc ttg  gcc ctg ctc tct gtg  acc atc agc      3159
Val Thr  Ala Tyr Ile Ala Leu  Ala Leu Leu Ser Val  Thr Ile Ser
    1040                1045                1050

ttt agg  ata tac aag ggt gtg  atc caa gct atc cag  aaa tca gat      3204
Phe Arg  Ile Tyr Lys Gly Val  Ile Gln Ala Ile Gln  Lys Ser Asp
    1055                1060                1065

gaa ggc  cac cca ttc agg gca  tat ctg gaa tct gaa  gtt gct ata      3249
Glu Gly  His Pro Phe Arg Ala  Tyr Leu Glu Ser Glu  Val Ala Ile
    1070                1075                1080

tct gag  gag ttg gtt cag aag  tac agt aat tct gct  ctt ggt cat      3294
Ser Glu  Glu Leu Val Gln Lys  Tyr Ser Asn Ser Ala  Leu Gly His
    1085                1090                1095

gtg aac  tgc acg ata aag gaa  ctc agg cgc ctc ttc  tta gtt gat      3339
Val Asn  Cys Thr Ile Lys Glu  Leu Arg Arg Leu Phe  Leu Val Asp
    1100                1105                1110

gat tta  gtt gat tct ctg aag  ttt gca gtg ttg atg  tgg gta ttt      3384
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Asp Leu  Val Asp Ser Leu Lys  Phe Ala Val Leu Met  Trp Val Phe
    1115                 1120                 1125

acc tat  gtt ggt gcc ttg ttt  aat ggt ctg aca cta  ctg att ttg      3429
Thr Tyr  Val Gly Ala Leu Phe  Asn Gly Leu Thr Leu  Leu Ile Leu
    1130                 1135                 1140

gct ctc  att tca ctc ttc agt  gtt cct gtt att tat  gaa cgg cat      3474
Ala Leu  Ile Ser Leu Phe Ser  Val Pro Val Ile Tyr  Glu Arg His
    1145                 1150                 1155

cag gca  cag ata gat cat tat  cta gga ctt gca aat  aag aat gtt      3519
Gln Ala  Gln Ile Asp His Tyr  Leu Gly Leu Ala Asn  Lys Asn Val
    1160                 1165                 1170

aaa gat  gct atg gct aaa atc  caa gca aaa atc cct  gga ttg aag      3564
Lys Asp  Ala Met Ala Lys Ile  Gln Ala Lys Ile Pro  Gly Leu Lys
    1175                 1180                 1185

cgc aaa  gct gaa tga aaacgcccaa aataattagt aggagttcat ctttaaaggg   3619
Arg Lys  Ala Glu
    1190

gatattcatt tgattatacg ggggagggtc agggaagaac gaaccttgac gttgcagtgc   3679

agtttcacag atcgttgtta gatctttatt tttagccatg cactgttgtg aggaaaaatt   3739

acctgtcttg actgccatgt gttcatcatc ttaagtattg taagctgcta tgtatggatt   3799

taaaccgtaa tcatatcttt ttcctatctg aggcactggt ggaataaaaa acctgtatat   3859

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<213> Homo sapiens

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Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

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

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

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

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
180 185 190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp
195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
210 215 220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
275 280 285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
290 295 300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
305 310 315 320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
325 330 335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
340 345 350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
355 360 365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385 390 395 400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu

405 410 415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr
420 425 430

Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro
435 440 445

Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys
450 455 460

Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe
465 470 475 480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys
485 490 495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr
500 505 510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp
515 520 525

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala
530 535 540

Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu
545 550 555 560

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
645 650 655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
725 730 735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
755 760 765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu

995 1000 1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala
1010 1015 1020

Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
1025 1030 1035

Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
1040 1045 1050

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp
1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe
1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu
1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
1160 1165 1170

Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
1175 1180 1185

Arg Lys Ala Glu
1190

<210> 6

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> Human NogoA_342-357

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15

Glu Ala

<210> 7

<211> 819

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(819)

<223> human Nig

<400> 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg
1 5 10 15

Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile
20 25 30

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

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
100 105 110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

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

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val

305 310 315 320

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

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
355 360 365

Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
370 375 380

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

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
405 410 415

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

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
435 440 445

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
450 455 460

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn
610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
805 810 815

Lys Thr Ser

<210> 8

<211> 10

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(10)

<223> hypervariable part of heavy chain of 3A6

<400> 8

Gly Phe Asp Phe Arg Arg Asn Trp Met Ser
1 5 10

<210> 9

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(17)

<223> hypervariable part of heavy chain of 3A6

<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
1 5 10 15

Asp

<210> 10

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of heavy chain of 3A6

<400> 10

Pro Val Trp Met Tyr Ala Met Asp Tyr
1 5

<210> 11

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(16)

<223> hypervariable part of light chain of 3A6

<400> 11

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

<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(7)

<223> hypervariable part of light chain of 3A6

<400> 12

Leu Val Ser Lys Leu Asp Ser
1 5

<210> 13

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of light chain of 3A6

<400> 13

Trp Gln Gly Thr His Phe Pro Gln Thr
1 5

<210> 14

<211> 30

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(30)

<223> DNA-CDR-H1-3A6

<400> 14
ggattcgatt ttagaagaaa ttggatgagt 30

<210> 15

<211> 51

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(51)

<223> DNA-CDR-H2-3A6

<400> 15
gaaattaatc cagatagcag taagataaac tatacgccat ctctaaagga t 51

<210> 16

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(27)

<223> DNA-CDR-H3-3A6

<400> 16
ccggtctgga tgtatgctat ggactac 27

<210> 17

<211> 48

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(48)

<223> DNA-CDR'1-3A6

<400> 17
aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat 48

<210> 18

<211> 21

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(21)

<223> DNA-CDR'2-3A6

<400> 18
ctggtgtcta aactggactc t 21

<210> 19

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(27)

<223> DNA-CDR'3-3A6

<400> 19
tggcaaggta cacattttcc tcagacg 27

<210> 20

<211> 54

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(54)

<223> leader sequence for heavy chain of 3A6

<400> 20

atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc 48
Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

cag tgt 54
Gln Cys

<210> 21

<211> 18

<212> PRT

<213> Mus musculus

<400> 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

Gln Cys

<210> 22

<211> 57

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(57)

<223> leader sequence for 3A6-light chain

<400> 22

atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa 48
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

acc agc ggt 57
Thr Ser Gly

<210> 23

<211> 19

<212> PRT

<213> Mus musculus

<400> 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

Thr Ser Gly

<210> 24

<211> 181

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(181)

<223> human Nig-D20

<400> 24

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

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
85 90 95

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile
115 120 125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro
130 135 140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro
145 150 155 160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu
165 170 175

Pro Val Asp Leu Phe
180

<210> 25

<211> 3492

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(3492)

<223> rat NogoA

<400> 25

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atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc acg gac agc      48
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
1               5                  10                  15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc      96
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
            20                  25                  30

gag gac gag gag gac gag gag gag gag gag gac gag gag gag gac gac     144
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
        35                  40                  45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg     192
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
    50                  55                  60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac     240
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65                  70                  75                  80

ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc     288
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
                85                  90                  95

gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc     336
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
            100                 105                 110

gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc ctg ccc tcc     384
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
        115                 120                 125
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aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg cct ccg ccg      432
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
    130                 135                 140

cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc cct tcc acg      480
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145                 150                 155                 160

ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat gag acc ctt      528
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
                165                 170                 175

ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa      576
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
            180                 185                 190

aaa att atg gat ttg atg gag cag cca ggt aac act gtt tcg tct ggt      624
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
        195                 200                 205

caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct      672
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
    210                 215                 220

tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat gga tac ctt      720
Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225                 230                 235                 240

ggt aac tta tca gca gtg tca tcc tca gaa gga aca att gaa gaa act      768
Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
                245                 250                 255

tta aat gaa gct tct aaa gag ttg cca gag agg gca aca aat cca ttt      816
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
            260                 265                 270

gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat tca gaa atg      864
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Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
        275                 280                 285

gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc ata tta gta      912
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
    290                 295                 300

gaa aac act aag gaa gaa gta att gtg agg agt aaa gac aaa gag gat      960
Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305                 310                 315                 320

tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca cct gtg ggt     1008
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
                325                 330                 335

aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat     1056
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
            340                 345                 350

gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac     1104
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
        355                 360                 365

ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga     1152
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
    370                 375                 380

agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac     1200
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385                 390                 395                 400

aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat     1248
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
                405                 410                 415

agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct     1296
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
```

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                420                 425                 430

gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc tca    1344
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
        435                 440                 445

gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat    1392
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
    450                 455                 460

act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc    1440
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465                 470                 475                 480

caa att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt    1488
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
                485                 490                 495

gta gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta    1536
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
            500                 505                 510

tca aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg    1584
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
        515                 520                 525

cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca    1632
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
    530                 535                 540

ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca    1680
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545                 550                 555                 560

gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca    1728
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
                565                 570                 575
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ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt   1776
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
            580                 585                 590

atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta   1824
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
        595                 600                 605

gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat   1872
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
    610                 615                 620

gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc   1920
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625                 630                 635                 640

atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag   1968
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
                645                 650                 655

cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata   2016
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
            660                 665                 670

tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca   2064
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
        675                 680                 685

agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg   2112
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
    690                 695                 700

gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa   2160
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705                 710                 715                 720
```

```
cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca      2208
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
                725                 730                 735

caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct      2256
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
            740                 745                 750

gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag      2304
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
        755                 760                 765

gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt      2352
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
    770                 775                 780

aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag      2400
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
785                 790                 795                 800

aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat      2448
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
                805                 810                 815

gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca      2496
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
            820                 825                 830

ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt      2544
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
        835                 840                 845

gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat      2592
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
    850                 855                 860

cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca      2640
```

```
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865                 870                 875                 880

gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat    2688
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
                885                 890                 895

ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat    2736
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
            900                 905                 910

agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct    2784
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
        915                 920                 925

ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt    2832
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
    930                 935                 940

acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac    2880
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945                 950                 955                 960

aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt    2928
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val
                965                 970                 975

gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt    2976
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
            980                 985                 990

ggt gcc agc tta ttc ctg ctg ctg  tct ctg aca gtg ttc  agc att gtc   3024
Gly Ala Ser Leu Phe Leu Leu Leu  Ser Leu Thr Val Phe  Ser Ile Val
        995                 1000                1005

agt gta  acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc.       3069
Ser Val  Thr Ala Tyr Ile Ala  Leu Ala Leu Leu Ser  Val Thr Ile
```

```
    1010                1015                1020

agc ttt  agg ata tat aag ggc  gtg atc cag gct atc  cag aaa tca      3114
Ser Phe  Arg Ile Tyr Lys Gly  Val Ile Gln Ala Ile  Gln Lys Ser
    1025                1030                1035

gat gaa  ggc cac cca ttc agg  gca tat tta gaa tct  gaa gtt gct      3159
Asp Glu  Gly His Pro Phe Arg  Ala Tyr Leu Glu Ser  Glu Val Ala
    1040                1045                1050

ata tca  gag gaa ttg gtt cag  aaa tac agt aat tct  gct ctt ggt      3204
Ile Ser  Glu Glu Leu Val Gln  Lys Tyr Ser Asn Ser  Ala Leu Gly
    1055                1060                1065

cat gtg  aac agc aca ata aaa  gaa ctg agg cgg ctt  ttc tta gtt      3249
His Val  Asn Ser Thr Ile Lys  Glu Leu Arg Arg Leu  Phe Leu Val
    1070                1075                1080

gat gat  tta gtt gat tcc ctg  aag ttt gca gtg ttg  atg tgg gtg      3294
Asp Asp  Leu Val Asp Ser Leu  Lys Phe Ala Val Leu  Met Trp Val
    1085                1090                1095

ttt act  tat gtt ggt gcc ttg  ttc aat ggt ctg aca  cta ctg att      3339
Phe Thr  Tyr Val Gly Ala Leu  Phe Asn Gly Leu Thr  Leu Leu Ile
    1100                1105                1110

tta gct  ctg atc tca ctc ttc  agt att cct gtt att  tat gaa cgg      3384
Leu Ala  Leu Ile Ser Leu Phe  Ser Ile Pro Val Ile  Tyr Glu Arg
    1115                1120                1125

cat cag  gtg cag ata gat cat  tat cta gga ctt gca  aac aag agt      3429
His Gln  Val Gln Ile Asp His  Tyr Leu Gly Leu Ala  Asn Lys Ser
    1130                1135                1140

gtt aag  gat gcc atg gcc aaa  atc caa gca aaa atc  cct gga ttg      3474
Val Lys  Asp Ala Met Ala Lys  Ile Gln Ala Lys Ile  Pro Gly Leu
    1145                1150                1155
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aag cgc aaa gca gat tga 3492
Lys Arg Lys Ala Asp
1160

<210> 26

<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

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

Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
20 25 30

Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65 70 75 80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
130 135 140

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

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
180 185 190

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

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly

370 375 380

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385 390 395 400

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
405 410 415

Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
420 425 430

Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
435 440 445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
450 455 460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465 470 475 480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
485 490 495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
500 505 510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
675 680 685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
690 695 700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705 710 715 720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
725 730 735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
740 745 750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
755 760 765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
770 775 780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
785 790 795 800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
805 810 815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
835 840 845

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965 970 975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser
1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val
1085 1090 1095

Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
1145 1150 1155

Lys Arg Lys Ala Asp
1160

<210> 27

<211> 25

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> rat PEP4

<400> 27

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

Ser Thr Ile Lys Glu Leu Arg Arg Leu
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29
aagcaccatt gaattctgca gttcc 25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer_bind

<222> (1)..(28)

<223>

<400> 30
aactgcagta ctgagctcct ccatctgc 28

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'

<220>

<221> primer_bind

<222> (1)..(33)

<223> forward primer

<400> 31
gtcgcggatc catggagacc ctttttgctc ttc 33

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'

<220>

<221> primer_bind

<222> (1)..(27)

<223> reverse primer

<400> 32
gttctcgagt tatgaagttt tactcag 27

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'-1

<220>

<221> primer_bind

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<400> 33

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<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>

<221> primer_bind

<222> (1)..(28)

<223> primer

<400> 34
gtttctcgag tgaagtttta ttcagctc 28

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer

<220>

<221> primer_bind

<222> (1)..(20)

<223> primer

<400> 35
tccaccccgg ccgcgcccaa 20

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer 2

<220>

<221> primer_bind

<222> (1)..(22)

<223> primer

<400> 36
aatgatgggc aaagctgtgc tg 22

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer_bind

<222> (1)..(24)

<223> primer

<400> 37
ggtacaaaga ttgcttatga aaca 24

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer 2

<220>

<221> primer_bind

<222> (1)..(22)

<223> primer

<400> 38
agcagggcca aggcaatgta gg 22

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VL leader

<220>

<221> primer_bind

<222> (1)..(28)

<223> primer

<400> 39
aatatgagtc ctgcccagtt cctgtttc 28

<210> 40

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-Ck

<220>

<221> primer_bind

<222> (1)..(32)

<223> primer

<400> 40
ttaggaattc ctaacactct cccctgttga ag 32

<210> 41

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VH leader

<220>

<221> primer_bind

<222> (1)..(31)

<223> primer

<400> 41
aatatggatt ttgggctgat ttttttttatt g 31

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-CH hinge

<220>

<221> primer_bind

<222> (1)..(24)

<223> primer

<400> 42
aattgggcaa cgttgcaggt gacg 24

<210> 43

<211> 663

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(663)

<223> DNA variable part of heavy chain 3A6

<400> 43

atggattttg ggctgatttt ttttattgtt ggtcttttaa aaggggtcca gtgtgaggtg 60

aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt 120

gtagtctcag gattcgattt tagaagaaat tggatgagtt gggtccggca ggctcctggg 180

aaagggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgcca 240

tctctaaagg ataaattcat catctccaga gacaatgcca agaatacgct gtacctgcaa 300

gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg 360

tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaacgaca 420

cccccatctg tctatccact ggcccctgga tctgctgccc aaactaactc catggtgacc 480

ctgggatgcc tggtcaaggg ctatttccct gagccagtga cagtgacctg gaactctgga 540

tccctgtcca gcggtgtgca caccttccca gctgtcctgc agtctgacct ctacactctg 600

agcagctcag tgactgtccc ctccagcacc tggcccagcg agaccgtcac ctgcaacgtt 660

gcc 663

<210> 44

<211> 717

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(717)

<223> variable part of light chain of 3A6

<400> 44

atgagtcctg cccagttcct gtttctgtta gtgctctgga ttcgggaaac cagcggtgat 60

gttctgttga cccagactcc tctcactttg tcgataacca ttggacaacc agcctccatc 120

tcttgcaagt caagtcagag cctcttgcat agtgatggaa agacatattt gaattggttg 180

ttacagaggc caggccagtc tccaaagcgc ctaatctatc tggtgtctaa actggactct 240

ggagtccctg acaggttcac tggcagtgga tcagggacgg atttcacact gaaaatcagc 300

agagtggagg ctgaggattt gggactttat tattgctggc aaggtacaca ttttcctcag 360

acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420

atcttcccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg 480

aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540

aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600

agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660

actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag 717