SEQUENCE LISTING

<110> INSTITUT PASTEUR
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.)
UNIVERSITE PIERRE ET MARIE CURIE - PARIS 6

<120> HIGH MAST2-AFFINITY POLYPEPTIDES AND USES THEREOF

<130> B09627A - AD/LV/KN

<140> PCT/EP XXXXXX
<141> 2012-11-07

<150> EP 11306454.7
<151> 2011-11-08

<160> 288

<170> PatentIn version 3.5

<210> 1
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Neurovita1

<400> 1

Ser Trp Glu Ser His Lys Ser Gly Gly Gln Thr Arg Leu
1 5 10

<210> 2
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Cytoplasmic domain

<400> 2

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

Gly Arg Glu Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser
20 25 30

<210> 3
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Signal peptide

<400> 3

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

Cys Phe Gly

<210> 4
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Transmembrane domain

<400> 4

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

Phe Leu Met Thr Cys Cys
20

<210> 5
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Cytoplasmic domain variant

<400> 5

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

Gly Arg Glu Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser
20 25 30

<210> 6
<211> 1798
<212> PRT
<213> Homo sapiens - Microtubule-associated serine/threonine-protein kinase 2 (MAST2)

<400> 6

Met Lys Arg Ser Arg Cys Arg Asp Arg Pro Gln Pro Pro Pro Pro Asp
1 5 10 15

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Arg Arg Glu Asp Gly Val Gln Arg Ala Ala Glu Leu Ser Gln Ser Leu
            20                  25                  30

Pro Pro Arg Arg Arg Ala Pro Pro Gly Arg Gln Arg Leu Glu Glu Arg
        35                  40                  45

Thr Gly Pro Ala Gly Pro Glu Gly Lys Glu Gln Asp Val Val Thr Gly
    50                  55                  60

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

Ser Thr Gly Lys Val Lys Leu Gln Arg Gln Leu Ser Gln Asp Asp Cys
                85                  90                  95

Lys Leu Trp Arg Gly Asn Leu Ala Ser Ser Leu Ser Gly Lys Gln Leu
            100                 105                 110

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

Gln Ser Ser Gly Glu Ala Ser Asn Leu Val Arg Met Arg Asn Gln Ser
    130                 135                 140

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

Leu Pro Arg Arg Gly Ser Phe Cys Arg Thr Ser Asn Arg Lys Ser Leu
                165                 170                 175

Ile Val Thr Ser Ser Thr Ser Pro Thr Leu Pro Arg Pro His Ser Pro
            180                 185                 190

Leu His Gly His Thr Gly Asn Ser Pro Leu Asp Ser Pro Arg Asn Phe
        195                 200                 205

Ser Pro Asn Ala Pro Ala His Phe Ser Phe Val Pro Ala Arg Arg Thr
    210                 215                 220

Asp Gly Arg Arg Trp Ser Leu Ala Ser Leu Pro Ser Ser Gly Tyr Gly
225                 230                 235                 240
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```
Thr Asn Thr Pro Ser Ser Thr Val Ser Ser Ser Cys Ser Ser Gln Glu
                245                 250                 255

Lys Leu His Gln Leu Pro Phe Gln Pro Thr Ala Asp Glu Leu His Phe
            260                 265                 270

Leu Thr Lys His Phe Ser Thr Glu Ser Val Pro Asp Glu Glu Gly Arg
        275                 280                 285

Gln Ser Pro Ala Met Arg Pro Arg Ser Arg Ser Leu Ser Pro Gly Arg
    290                 295                 300

Ser Pro Val Ser Phe Asp Ser Glu Ile Ile Met Met Asn His Val Tyr
305                 310                 315                 320

Lys Glu Arg Phe Pro Lys Ala Thr Ala Gln Met Glu Glu Arg Leu Ala
                325                 330                 335

Glu Phe Ile Ser Ser Asn Thr Pro Asp Ser Val Leu Pro Leu Ala Asp
            340                 345                 350

Gly Ala Leu Ser Phe Ile His His Gln Val Ile Glu Met Ala Arg Asp
        355                 360                 365

Cys Leu Asp Lys Ser Arg Ser Gly Leu Ile Thr Ser Gln Tyr Phe Tyr
    370                 375                 380

Glu Leu Gln Asp Asn Leu Glu Lys Leu Leu Gln Asp Ala His Glu Arg
385                 390                 395                 400

Ser Glu Ser Ser Glu Val Ala Phe Val Met Gln Leu Val Lys Lys Leu
                405                 410                 415

Met Ile Ile Ile Ala Arg Pro Ala Arg Leu Leu Glu Cys Leu Glu Phe
            420                 425                 430

Asp Pro Glu Glu Phe Tyr His Leu Leu Glu Ala Ala Glu Gly His Ala
        435                 440                 445

Lys Glu Gly Gln Gly Ile Lys Cys Asp Ile Pro Arg Tyr Ile Val Ser
    450                 455                 460

Gln Leu Gly Leu Thr Arg Asp Pro Leu Glu Glu Met Ala Gln Leu Ser
465                 470                 475                 480
```

```
Ser Cys Asp Ser Pro Asp Thr Pro Glu Thr Asp Asp Ser Ile Glu Gly
                485                 490                 495

His Gly Ala Ser Leu Pro Ser Lys Lys Thr Pro Ser Glu Glu Asp Phe
            500                 505                 510

Glu Thr Ile Lys Leu Ile Ser Asn Gly Ala Tyr Gly Ala Val Phe Leu
        515                 520                 525

Val Arg His Lys Ser Thr Arg Gln Arg Phe Ala Met Lys Lys Ile Asn
    530                 535                 540

Lys Gln Asn Leu Ile Leu Arg Asn Gln Ile Gln Gln Ala Phe Val Glu
545                 550                 555                 560

Arg Asp Ile Leu Thr Phe Ala Glu Asn Pro Phe Val Val Ser Met Phe
                565                 570                 575

Cys Ser Phe Asp Thr Lys Arg His Leu Cys Met Val Met Glu Tyr Val
            580                 585                 590

Glu Gly Gly Asp Cys Ala Thr Leu Leu Lys Asn Ile Gly Ala Leu Pro
        595                 600                 605

Val Asp Met Val Arg Leu Tyr Phe Ala Glu Thr Val Leu Ala Leu Glu
    610                 615                 620

Tyr Leu His Asn Tyr Gly Ile Val His Arg Asp Leu Lys Pro Asp Asn
625                 630                 635                 640

Leu Leu Ile Thr Ser Met Gly His Ile Lys Leu Thr Asp Phe Gly Leu
                645                 650                 655

Ser Lys Ile Gly Leu Met Ser Leu Thr Thr Asn Leu Tyr Glu Gly His
            660                 665                 670

Ile Glu Lys Asp Ala Arg Glu Phe Leu Asp Lys Gln Val Cys Gly Thr
        675                 680                 685

Pro Glu Tyr Ile Ala Pro Glu Val Ile Leu Arg Gln Gly Tyr Gly Lys
    690                 695                 700
```

```
Pro Val Asp Trp Trp Ala Met Gly Ile Ile Leu Tyr Glu Phe Leu Val
705                 710                 715                 720

Gly Cys Val Pro Phe Phe Gly Asp Thr Pro Glu Glu Leu Phe Gly Gln
                725                 730                 735

Val Ile Ser Asp Glu Ile Val Trp Pro Glu Gly Asp Glu Ala Leu Pro
            740                 745                 750

Pro Asp Ala Gln Asp Leu Thr Ser Lys Leu Leu His Gln Asn Pro Leu
        755                 760                 765

Glu Arg Leu Gly Thr Gly Ser Ala Tyr Glu Val Lys Gln His Pro Phe
    770                 775                 780

Phe Thr Gly Leu Asp Trp Thr Gly Leu Leu Arg Gln Lys Ala Glu Phe
785                 790                 795                 800

Ile Pro Gln Leu Glu Ser Glu Asp Asp Thr Ser Tyr Phe Asp Thr Arg
                805                 810                 815

Ser Glu Arg Tyr His His Met Asp Ser Glu Asp Glu Glu Glu Val Ser
            820                 825                 830

Glu Asp Gly Cys Leu Glu Ile Arg Gln Phe Ser Ser Cys Ser Pro Arg
        835                 840                 845

Phe Asn Lys Val Tyr Ser Ser Met Glu Arg Leu Ser Leu Leu Glu Glu
    850                 855                 860

Arg Arg Thr Pro Pro Pro Thr Lys Arg Ser Leu Ser Glu Glu Lys Glu
865                 870                 875                 880

Asp His Ser Asp Gly Leu Ala Gly Leu Lys Gly Arg Asp Arg Ser Trp
                885                 890                 895

Val Ile Gly Ser Pro Glu Ile Leu Arg Lys Arg Leu Ser Val Ser Glu
            900                 905                 910

Ser Ser His Thr Glu Ser Asp Ser Ser Pro Pro Met Thr Val Arg Arg
        915                 920                 925

Arg Cys Ser Gly Leu Leu Asp Ala Pro Arg Phe Pro Glu Gly Pro Glu
    930                 935                 940
```

```
Glu Ala Ser Ser Thr Leu Arg Arg Gln Pro Gln Glu Gly Ile Trp Val
945                 950                 955                 960

Leu Thr Pro Pro Ser Gly Glu Gly Val Ser Gly Pro Val Thr Glu His
                965                 970                 975

Ser Gly Glu Gln Arg Pro Lys Leu Asp Glu Glu Ala Val Gly Arg Ser
            980                 985                 990

Ser Gly Ser Ser Pro Ala Met Glu  Thr Arg Gly Arg Gly  Thr Ser Gln
        995                 1000                1005

Leu Ala  Glu Gly Ala Thr Ala  Lys Ala Ile Ser Asp  Leu Ala Val
    1010                1015                1020

Arg Arg  Ala Arg His Arg Leu  Leu Ser Gly Asp Ser  Thr Glu Lys
    1025                1030                1035

Arg Thr  Ala Arg Pro Val Asn  Lys Val Ile Lys Ser  Ala Ser Ala
    1040                1045                1050

Thr Ala  Leu Ser Leu Leu Ile  Pro Ser Glu His His  Thr Cys Ser
    1055                1060                1065

Pro Leu  Ala Ser Pro Met Ser  Pro His Ser Gln Ser  Ser Asn Pro
    1070                1075                1080

Ser Ser  Arg Asp Ser Ser Pro  Ser Arg Asp Phe Leu  Pro Ala Leu
    1085                1090                1095

Gly Ser  Met Arg Pro Pro Ile  Ile Ile His Arg Ala  Gly Lys Lys
    1100                1105                1110

Tyr Gly  Phe Thr Leu Arg Ala  Ile Arg Val Tyr Met  Gly Asp Ser
    1115                1120                1125

Asp Val  Tyr Thr Val His His  Met Val Trp His Val  Glu Asp Gly
    1130                1135                1140

Gly Pro  Ala Ser Glu Ala Gly  Leu Arg Gln Gly Asp  Leu Ile Thr
    1145                1150                1155
```

```
His Val  Asn Gly Glu Pro Val  His Gly Leu Val His  Thr Glu Val
    1160                1165                1170

Val Glu  Leu Ile Leu Lys Ser  Gly Asn Lys Val Ala  Ile Ser Thr
    1175                1180                1185

Thr Pro  Leu Glu Asn Thr Ser  Ile Lys Val Gly Pro  Ala Arg Lys
    1190                1195                1200

Gly Ser  Tyr Lys Ala Lys Met  Ala Arg Arg Ser Lys  Arg Ser Arg
    1205                1210                1215

Gly Lys  Asp Gly Gln Glu Ser  Arg Lys Arg Ser Ser  Leu Phe Arg
    1220                1225                1230

Lys Ile  Thr Lys Gln Ala Ser  Leu Leu His Thr Ser  Arg Ser Leu
    1235                1240                1245

Ser Ser  Leu Asn Arg Ser Leu  Ser Ser Gly Glu Ser  Gly Pro Gly
    1250                1255                1260

Ser Pro  Thr His Ser His Ser  Leu Ser Pro Arg Ser  Pro Thr Gln
    1265                1270                1275

Gly Tyr  Arg Val Thr Pro Asp  Ala Val His Ser Val  Gly Gly Asn
    1280                1285                1290

Ser Ser  Gln Ser Ser Ser Pro  Ser Ser Ser Val Pro  Ser Ser Pro
    1295                1300                1305

Ala Gly  Ser Gly His Thr Arg  Pro Ser Ser Leu His  Gly Leu Ala
    1310                1315                1320

Pro Lys  Leu Gln Arg Gln Tyr  Arg Ser Pro Arg Arg  Lys Ser Ala
    1325                1330                1335

Gly Ser  Ile Pro Leu Ser Pro  Leu Ala His Thr Pro  Ser Pro Pro
    1340                1345                1350

Pro Pro  Thr Ala Ser Pro Gln  Arg Ser Pro Ser Pro  Leu Ser Gly
    1355                1360                1365

His Val  Ala Gln Ala Phe Pro  Thr Lys Leu His Leu  Ser Pro Pro
    1370                1375                1380
```

```
Leu Gly  Arg Gln Leu Ser Arg  Pro Lys Ser Ala Glu  Pro Pro Arg
    1385                 1390                 1395

Ser Pro  Leu Leu Lys Arg Val  Gln Ser Ala Glu Lys  Leu Ala Ala
    1400                 1405                 1410

Ala Leu  Ala Ala Ser Glu Lys  Lys Leu Ala Thr Ser  Arg Lys His
    1415                 1420                 1425

Ser Leu  Asp Leu Pro His Ser  Glu Leu Lys Lys Glu  Leu Pro Pro
    1430                 1435                 1440

Arg Glu  Val Ser Pro Leu Glu  Val Val Gly Ala Arg  Ser Val Leu
    1445                 1450                 1455

Ser Gly  Lys Gly Ala Leu Pro  Gly Lys Gly Val Leu  Gln Pro Ala
    1460                 1465                 1470

Pro Ser  Arg Ala Leu Gly Thr  Leu Arg Gln Asp Arg  Ala Glu Arg
    1475                 1480                 1485

Arg Glu  Ser Leu Gln Lys Gln  Glu Ala Ile Arg Glu  Val Asp Ser
    1490                 1495                 1500

Ser Glu  Asp Asp Thr Glu Glu  Gly Pro Glu Asn Ser  Gln Gly Ala
    1505                 1510                 1515

Gln Glu  Leu Ser Leu Ala Pro  His Pro Glu Val Ser  Gln Ser Val
    1520                 1525                 1530

Ala Pro  Lys Gly Ala Gly Glu  Ser Gly Glu Glu Asp  Pro Phe Pro
    1535                 1540                 1545

Ser Arg  Asp Pro Arg Ser Leu  Gly Pro Met Val Pro  Ser Leu Leu
    1550                 1555                 1560

Thr Gly  Ile Thr Leu Gly Pro  Pro Arg Met Glu Ser  Pro Ser Gly
    1565                 1570                 1575

Pro His  Arg Arg Leu Gly Ser  Pro Gln Ala Ile Glu  Glu Ala Ala
    1580                 1585                 1590
```

Ser Ser Ser Ser Ala Gly Pro Asn Leu Gly Gln Ser Gly Ala Thr
1595 1600 1605

Asp Pro Ile Pro Pro Glu Gly Cys Trp Lys Ala Gln His Leu His
1610 1615 1620

Thr Gln Ala Leu Thr Ala Leu Ser Pro Ser Thr Ser Gly Leu Thr
1625 1630 1635

Pro Thr Ser Ser Cys Ser Pro Pro Ser Ser Thr Ser Gly Lys Leu
1640 1645 1650

Ser Met Trp Ser Trp Lys Ser Leu Ile Glu Gly Pro Asp Arg Ala
1655 1660 1665

Ser Pro Ser Arg Lys Ala Thr Met Ala Gly Gly Leu Ala Asn Leu
1670 1675 1680

Gln Asp Leu Glu Asn Thr Thr Pro Ala Gln Pro Lys Asn Leu Ser
1685 1690 1695

Pro Arg Glu Gln Gly Lys Thr Gln Pro Pro Ser Ala Pro Arg Leu
1700 1705 1710

Ala His Pro Ser Tyr Glu Asp Pro Ser Gln Gly Trp Leu Trp Glu
1715 1720 1725

Ser Glu Cys Ala Gln Ala Val Lys Glu Asp Pro Ala Leu Ser Ile
1730 1735 1740

Thr Gln Val Pro Asp Ala Ser Gly Asp Arg Arg Gln Asp Val Pro
1745 1750 1755

Cys Arg Gly Cys Pro Leu Thr Gln Lys Ser Glu Pro Ser Leu Arg
1760 1765 1770

Arg Gly Gln Glu Pro Gly Gly His Gln Lys His Arg Asp Leu Ala
1775 1780 1785

Leu Val Pro Asp Glu Leu Leu Lys Gln Thr
1790 1795

<210> 7
<211> 93

<212> PRT
<213> Homo sapiens - PDZ domain of the human MAST2 protein

<400> 7

Met Arg Pro Pro Ile Ile Ile His Arg Ala Gly Lys Lys Tyr Gly Phe
1 5 10 15

Thr Leu Arg Ala Ile Arg Val Tyr Met Gly Asp Ser Asp Val Tyr Thr
20 25 30

Val His His Met Val Trp His Val Glu Asp Gly Gly Pro Ala Ser Glu
35 40 45

Ala Gly Leu Arg Gln Gly Asp Leu Ile Thr His Val Asn Gly Glu Pro
50 55 60

Val His Gly Leu Val His Thr Glu Val Val Glu Leu Ile Leu Lys Ser
65 70 75 80

Gly Asn Lys Val Ala Ile Ser Thr Thr Pro Leu Glu Asn
85 90

<210> 8
<211> 264
<212> DNA
<213> Artificial Sequence

<220>
<223> Neurovita 1

<220>
<221> CDS
<222> (1)..(264)

<400> 8
atg gtt cct cag gct ctc ctg ttt gta ccc ctt ctg gtt ttt cca ttg
48
Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

tgt ttt ggg ggg aag tat gta tta ctg agt gca ggg gcc ctg act gcc
96
Cys Phe Gly Gly Lys Tyr Val Leu Leu Ser Ala Gly Ala Leu Thr Ala
20 25 30

ttg atg ttg ata att ttc ctg atg aca tgt tgt aga aga gtc aat cga
144
Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
35 40 45

tca gaa cct acg caa cac aat ctc aga ggg aca ggg agg gag gtg tca
192
Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser
    50   55   60

gtc act ccc caa agc ggg aag atc ata tct tca tgg gaa tca cac aag
240
Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys
65   70   75   80

agt ggg ggt cag acc aga ctg tga
264
Ser Gly Gly Gln Thr Arg Leu
                85

<210> 9
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 9

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1   5   10   15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35   40   45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys
65   70   75   80

Ser Gly Gly Gln Thr Arg Leu
                85

<210> 10
<211> 252
<212> DNA
<213> Artificial Sequence

<220>
<223> Neurovita1 delta MAST-2 binding domain

<220>
<221> CDS
<222> (1)..(252)

<400> 10
atg gtt cct cag gct ctc ctg ttt gta ccc ctt ctg gtt ttt cca ttg
48
Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1   5   10   15

tgt ttt ggg ggg aag tat gta tta ctg agt gca ggg gcc ctg act gcc
96
Cys Phe Gly Gly Lys Tyr Val Leu Leu Ser Ala Gly Ala Leu Thr Ala
            20   25   30

ttg atg ttg ata att ttc ctg atg aca tgt tgt aga aga gtc aat cga
144
Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35   40   45

tca gaa cct acg caa cac aat ctc aga ggg aca ggg agg gag gtg tca
192
Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser
    50   55   60

gtc act ccc caa agc ggg aag atc ata tct tca tgg gaa tca cac aag
240
Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys
65   70   75   80

agt ggg ggt tga
252
Ser Gly Gly

<210> 11
<211> 83
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Construct

<400> 11

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1   5   10   15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35   40   45

```
Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser
    50                  55                  60

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys
65                  70                  75                  80

Ser Gly Gly
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<210> 12
<211> 524
<212> PRT
<213> Rabies virus - G protein of CVS - NIV

<400> 12

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                   10                  15

Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Pro Asp Lys Leu Gly Pro
            20                  25                  30

Trp Ser Pro Ile Asp Ile His His Leu Ser Cys Pro Asn Asn Leu Val
        35                  40                  45

Val Glu Asp Glu Gly Cys Thr Asn Leu Ser Gly Phe Ser Tyr Met Glu
    50                  55                  60

Leu Lys Val Gly Tyr Ile Leu Ala Ile Lys Met Asn Gly Phe Thr Cys
65                  70                  75                  80

Thr Gly Val Val Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr
                85                  90                  95

Val Thr Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
            100                 105                 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg Tyr Glu
        115                 120                 125

Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr His Trp Leu Arg Thr Val
    130                 135                 140

Lys Thr Thr Lys Glu Ser Leu Val Ile Ile Ser Pro Ser Val Ala Asp
145                 150                 155                 160
```

```
Leu Asp Pro Tyr Asp Arg Ser Leu His Ser Arg Val Phe Pro Ser Gly
                165                 170                 175

Lys Cys Pro Gly Val Ala Val Ser Ser Thr Tyr Cys Ser Thr Asn His
            180                 185                 190

Asp Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys
        195                 200                 205

Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu
    210                 215                 220

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu Lys Gly
225                 230                 235                 240

Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu Arg Leu Met Asp
                245                 250                 255

Gly Thr Trp Val Ala Met Gln Thr Ser Asn Glu Thr Lys Trp Cys Pro
            260                 265                 270

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

His Leu Val Val Glu Glu Leu Val Arg Lys Arg Glu Glu Cys Leu Asp
    290                 295                 300

Ala Leu Glu Ser Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu
305                 310                 315                 320

Ser His Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
                325                 330                 335

Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser Val Arg
            340                 345                 350

Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu Arg Val Gly Gly
        355                 360                 365

Arg Cys His Pro His Val Asn Gly Val Phe Phe Asn Gly Ile Ile Leu
    370                 375                 380
```

```
Gly Pro Asp Gly Asn Val Leu Ile Pro Glu Met Gln Ser Ser Leu Leu
385                 390                 395                 400

Gln Gln His Met Glu Leu Leu Glu Ser Ser Val Ile Pro Leu Val His
                405                 410                 415

Pro Leu Ala Asp Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu
            420                 425                 430

Asp Phe Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly
        435                 440                 445

Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu Ser Ala
    450                 455                 460

Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys
465                 470                 475                 480

Arg Arg Val Asn Arg Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr
                485                 490                 495

Gly Arg Glu Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser
            500                 505                 510

Trp Glu Ser His Lys Ser Gly Gly Gln Thr Arg Leu
        515                 520
```

<210> 13
<211> 524
<212> PRT
<213> Rabies virus - G protein of ERA - NIV

<400> 13

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                   10                  15

Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Pro Asp Lys Leu Gly Pro
            20                  25                  30

Trp Ser Pro Ile Asp Ile His His Leu Ser Cys Pro Asn Asn Leu Ile
        35                  40                  45

Val Glu Asp Glu Gly Cys Thr Asn Leu Ser Gly Phe Ser Tyr Met Glu
    50                  55                  60
```

```
Leu Lys Val Gly Tyr Ile Leu Ala Ile Lys Met Asn Gly Phe Thr Cys
65                  70                  75                  80

Thr Gly Val Val Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr
                85                  90                  95

Val Thr Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
            100                 105                 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg Tyr Glu
        115                 120                 125

Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp Leu Arg Thr Val
    130                 135                 140

Lys Thr Thr Lys Glu Ser Leu Val Ile Ile Ser Pro Ser Val Ala Asp
145                 150                 155                 160

Leu Asp Pro Tyr Asp Arg Ser Leu His Ser Arg Val Phe Pro Ser Gly
                165                 170                 175

Lys Cys Ser Gly Val Ala Val Ser Ser Thr Tyr Cys Ser Thr Asn His
            180                 185                 190

Asp Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys
        195                 200                 205

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

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu Lys Gly
225                 230                 235                 240

Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu Arg Leu Met Asp
                245                 250                 255

Gly Thr Trp Val Ala Met Gln Thr Ser Asn Glu Thr Lys Trp Cys Pro
            260                 265                 270

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

His Leu Val Val Glu Glu Leu Val Arg Lys Arg Glu Glu Cys Leu Asp
```

```
    290                 295                 300

Ala Leu Glu Ser Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu
305                 310                 315                 320

Ser His Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
                325                 330                 335

Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser Val Arg
            340                 345                 350

Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu Arg Val Gly Gly
        355                 360                 365

Arg Cys His Pro His Val Asn Gly Val Phe Phe Asn Gly Ile Ile Leu
    370                 375                 380

Gly Pro Asp Gly Asn Val Leu Ile Pro Glu Met Gln Ser Ser Leu Leu
385                 390                 395                 400

Gln Gln His Met Glu Leu Leu Glu Ser Ser Val Ile Pro Leu Val His
                405                 410                 415

Pro Leu Ala Asp Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu
            420                 425                 430

Asp Phe Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly
        435                 440                 445

Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu Ser Ala
    450                 455                 460

Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys
465                 470                 475                 480

Arg Arg Val Asn Arg Ser Glu Pro Thr Gln Leu Asn Leu Arg Gly Thr
                485                 490                 495

Gly Arg Glu Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser
            500                 505                 510

Trp Glu Ser His Lys Ser Gly Gly Glu Thr Arg Leu
        515                 520
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<210> 14
<211> 522
<212> PRT
<213> Rabies virus G protein NCBI CAI43218

<400> 14

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

Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Pro Asp Glu Leu Gly Pro
20 25 30

Trp Ser Pro Ile Asp Ile His His Leu Ser Cys Pro Asn Asn Leu Val
35 40 45

Val Glu Asp Glu Gly Cys Thr Asn Leu Ser Glu Phe Ser Tyr Met Glu
50 55 60

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

Thr Gly Val Val Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr
85 90 95

Val Thr Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
100 105 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg Tyr Glu
115 120 125

Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr His Trp Leu Arg Thr Val
130 135 140

Arg Thr Thr Lys Glu Ser Leu Ile Ile Ile Ser Pro Ser Val Thr Asp
145 150 155 160

Leu Asp Pro Tyr Asp Lys Ser Leu His Ser Arg Val Phe Pro Gly Gly
165 170 175

Lys Cys Ser Gly Ile Thr Val Ser Ser Thr Tyr Cys Ser Thr Asn His
180 185 190

Asp Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Arg Thr Pro Cys
195 200 205

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Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Asn Lys
    210                 215                 220

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu Lys Gly
225                 230                 235                 240

Ala Cys Arg Leu Lys Leu Cys Gly Val Leu Gly Leu Arg Leu Met Asp
                245                 250                 255

Gly Thr Trp Val Ala Met Gln Thr Ser Asp Glu Thr Lys Trp Cys Pro
            260                 265                 270

Asp Gln Leu Val Asn Leu His Asp Phe Arg Ser Asp Glu Ile Glu His
        275                 280                 285

Leu Val Val Glu Glu Leu Val Lys Lys Arg Glu Glu Cys Leu Asp Ala
    290                 295                 300

Leu Glu Ser Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser
305                 310                 315                 320

His Leu Arg Lys Leu Val Pro Gly Gly Lys Ala Tyr Thr Ile Phe Asn
                325                 330                 335

Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser Val Arg Thr Trp
            340                 345                 350

Asn Glu Ile Ile Pro Ser Lys Gly Cys Leu Lys Val Gly Gly Arg Cys
        355                 360                 365

His Pro His Val Asn Gly Val Phe Phe Asn Gly Ile Ile Leu Gly Pro
    370                 375                 380

Asp Gly His Val Leu Ile Pro Glu Met Gln Ser Ser Leu Leu Gln Gln
385                 390                 395                 400

His Met Glu Leu Leu Lys Ser Ser Val Ile Pro Leu Met His Pro Leu
                405                 410                 415

Ala Asp Pro Ser Thr Val Phe Lys Glu Gly Asp Glu Ala Glu Asp Phe
            420                 425                 430
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Val Glu Val His Leu Pro Asp Val Tyr Lys Gln Ile Ser Gly Val Asp
435 440 445

Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Met Thr Ala Gly Ala
450 455 460

Met Ile Gly Leu Val Leu Ile Phe Ser Leu Met Thr Trp Cys Arg Arg
465 470 475 480

Ala Asn Arg Pro Glu Ser Lys Gln Arg Ser Phe Gly Gly Thr Gly Arg
485 490 495

Asn Val Ser Val Thr Ser Gln Ser Gly Lys Val Ile Pro Ser Trp Glu
500 505 510

Ser Tyr Lys Ser Gly Gly Gln Thr Arg Leu
515 520

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

Cys Phe Gly Gly Lys Tyr Val Leu Met Thr Ala Gly Ala Met Ile Gly
20 25 30

Leu Val Leu Ile Phe Ser Leu Met Thr Trp Cys Arg Arg Ala Asn Arg
35 40 45

Pro Glu Ser Lys Gln Arg Ser Phe Gly Gly Thr Gly Arg Asn Val Ser
50 55 60

Val Thr Ser Gln Ser Gly Lys Val Ile Pro Ser Trp Glu Ser Tyr Lys
65 70 75 80

Ser Gly Gly Gln Thr Arg Leu
85

<210> 16
<211> 13
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<213> Rabies virus - MAST-2 binding domain

<400> 16

Ser Trp Glu Ser Tyr Lys Ser Gly Gly Gln Thr Arg Leu
1 5 10

<210> 17
<211> 74
<212> PRT
<213> Artificial Sequence

<220>
<223> Part of polypeptide

<400> 17

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
35 40 45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser
65 70

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<220>
<223> Part of polypeptide

<400> 18

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
35 40 45

Ser Glu Pro Thr Gln Leu Asn Leu Arg Gly Thr Gly Arg Glu Val Ser
50 55 60

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser
65 70

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<400> 19

Ser Trp Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
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1   5   10

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<220>
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<222> (5)..(7)
<223> Xaa can be any naturally occurring amino acid

<400> 22

Ser Trp Xaa Val Xaa Xaa Xaa Gln Thr Arg Leu
1   5   10

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1 5 10

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<223> Xaa can be any naturally occurring amino acid

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1 5 10

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<223> Xaa can be any naturally occurring amino acid

<400> 26

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<223> Xaa can be any naturally occurring amino acid

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Ser Trp Xaa Xaa Tyr Xaa Xaa Gln Thr Arg Leu
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<400> 28

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1 5 10

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<400> 29

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1 5 10

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<220>
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<400> 30

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1 5 10

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<400> 31

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1 5 10

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<400> 33

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1 5 10

<210> 34
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<400> 34

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1 5 10

<210> 35
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1 5 10

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<400> 36

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1   5   10

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<400> 37

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1   5   10

<210> 38
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<222> (7)..(7)
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<400> 38

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1 5 10

<210> 39
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<400> 39

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1 5 10

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1 5 10

<210> 41
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<400> 41

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1   5   10

<210> 42
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<400> 42

Ser Trp Glu Val His Xaa Xaa Gln Thr Arg Leu
1   5   10

<210> 43
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<400> 43

Ser Trp Glu Val Ala Xaa Xaa Gln Thr Arg Leu
1   5   10

<210> 44
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1 5 10

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1 5 10

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1 5 10

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1 5 10

<210> 48
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<400> 48

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1 5 10

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1 5 10

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1 5 10

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1 5 10

<210> 52
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1 5 10

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<400> 53

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1 5 10

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1 5 10

<210> 55
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<400> 55

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1   5   10

<210> 56
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<400> 56

Ser Trp Glu Val His Xaa Gln Gln Thr Arg Leu
1   5   10

<210> 57
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<400> 57

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1   5   10

<210> 58
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<400> 58

Ser Trp Glu Val Ala Xaa Gln Gln Thr Arg Leu
1 5 10

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<400> 59

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1 5 10

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1 5 10

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<222> (5)..(5)
<223> Xaa is H, A or Y

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<222> (6)..(6)
<223> Xaa is G or T

<220>
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<222> (7)..(7)
<223> Xaa is G or Q

<400> 61

Ser Trp Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

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Ser Trp Glu Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

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Ser Trp Glu Val Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 64
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<400> 64

Ser Trp Glu Val His Gly Gly Gln Thr Arg Leu

1 5 10

<210> 65
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<400> 65

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1 5 10

<210> 66
<211> 11
<212> PRT
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<220>
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<400> 66

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1 5 10

<210> 67
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<400> 67

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1 5 10

<210> 68
<211> 11
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<400> 68

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1 5 10

<210> 69
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<400> 69

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1 5 10

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<400> 70

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1 5 10

<210> 71
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<400> 71

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1 5 10

<210> 72
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<400> 72

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1 5 10

<210> 73

<211> 11
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<400> 73

Ser Trp Glu Val Tyr Gly Gln Gln Thr Arg Leu
1 5 10

<210> 74
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<400> 75

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<400> 82

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1 5 10

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<400> 83

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1   5   10

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1   5   10

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<400> 85

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1 5 10

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<400> 101

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1 5 10

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1   5   10

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<223> Xaa is G, T or Q

<400> 191

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<223> Xaa can be any naturally occurring amino acid

<400> 196

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 197
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is H, A or Y

<220>
<221> misc_feature
<222> (6)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 197

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 198
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is selected from non polar residues with small volume, polar neutral residues and positively charged residues

<220>
<221> misc_feature
<222> (7)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 198

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 199
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(5)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is K, A or Q

<220>
<221> misc_feature
<222> (7)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 199

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 200
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
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<222> (3)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is selected from polar neutral residues and positively charged residues

<220>
<221> misc_feature
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 200

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 201
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is S or H

<220>
<221> misc_feature
<222> (8)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 201

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 202
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
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<222> (3)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa is selected from non polar residues with small volume, preferably flexible, and polar neutral residues

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 202

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 203
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa is G or T

<220>

<221> misc_feature
<222> (9)..(9)
<223> Xaa can be any naturally occurring amino acid

<400> 203

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 204
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is selected from non polar residues with small volume, preferably flexible, and polar neutral residues

<400> 204

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 205
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is G or Q

<400> 205

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu

1 5 10

<210> 206
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa is E or A

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa is S, V or E

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is H, A or Y

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is K, A or Q

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is S or H

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa is G or T

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is G or Q

<400> 206

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1 5 10

<210> 207
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 13 residue MAST-2 binding domain

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa is E or A

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa is V or E

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is H, A or Y

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is K, A or Q

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is S or H

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa is G or T

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is G or Q

<400> 207

Ser Trp Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Thr Arg Leu
1   5   10

<210> 208
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 443 MAST-2 binding domain

<400> 208

Ser Trp Ala Glu Ala Gln His Thr Gln Gln Thr Arg Leu
1   5   10

<210> 209
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> 442 MAST-2 binding domain

<400> 209

Ser Trp Glu Val His Ala Ser Gly Gly Gln Thr Arg Leu
1 5 10

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

<220>
<223> Neurovita2 (441) polypeptide

<400> 210

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
35 40 45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val His Gly
65 70 75 80

Gly Gln Thr Arg Leu
85

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

<220>
<223> Neurovita3 (454) polypeptide

<400> 211

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                  10                  15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35                  40                  45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val His Gly
65                  70                  75                  80

Gln Gln Thr Arg Leu
                85
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<210> 212
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> 461 polypeptide

<400> 212

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                  10                  15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35                  40                  45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val Ala Thr
65                  70                  75                  80

Gln Gln Thr Arg Leu
                85
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<210> 213
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> 453 polypeptide

<400> 213

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                  10                  15


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


Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35                  40                  45


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


Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val Tyr Thr
65                  70                  75                  80


Gly Gln Thr Arg Leu
                85
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<210> 214
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> 455 polypeptide

<400> 214

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                  10                  15


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


Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35                  40                  45


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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val His Thr
65 70 75 80

Gly Gln Thr Arg Leu
85

<210> 215
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> 439 polypeptide

<400> 215

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
35 40 45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val His Thr
65 70 75 80

Gln Gln Thr Arg Leu
85

<210> 216
<211> 85
<212> PRT
<213> Artificial Sequence

<220>
<223> 460 polypeptide

<400> 216

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35                  40                  45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val Ala Gly
65                  70                  75                  80

Gly Gln Thr Arg Leu
                85
```

<210> 217
<211> 87
<212> PRT
<213> Artificial Sequence

<220>
<223> 443 polypeptide

<400> 217

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Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1               5                   10                  15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
        35                  40                  45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Ala Glu Ala Gln
65                  70                  75                  80

His Thr Gln Gln Thr Arg Leu
                85
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<210> 218
<211> 87
<212> PRT

<213> Artificial Sequence

<220>
<223> 442 polypeptide

<400> 218

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu
1 5 10 15

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

Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val Asn Arg
35 40 45

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

Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Val His Ala
65 70 75 80

Ser Gly Gly Gln Thr Arg Leu
85

<210> 219
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Neurovita2 (441) polynucleotide

<400> 219
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtacacggg
240

ggtcagacca gactgtga
258

<210> 220
<211> 258

<212> DNA
<213> Artificial Sequence

<220>
<223> Neurovita3 (454) polynucleotide

<400> 220
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtacacggg
240

cagcagacca gactgtga
258

<210> 221
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide encoding the polypeptide of SEQ ID NO:212

<400> 221
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtagccacg
240

cagcagacca gactgtga
258

<210> 222
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide encoding the polypeptide of SEQ ID NO:213

<400> 222

atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtatacacg
240

gggcagacca gactgtga
258

<210> 223
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide encoding the polypeptide of SEQ ID NO:214

<400> 223
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtacacacg
240

gggcagacca gactgtga
258

<210> 224
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide encoding the polypeptide of SEQ ID NO:215

<400> 224
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtacacacg
240

cagcagacca gactgtga
258

<210> 225
<211> 258
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial/ polynucleotide encoding the polypeptide of SEQ ID
       NO:216

<400> 225
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtagccggg
240

gggcagacca gactgtga
258

<210> 226
<211> 264
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide encoding the polypeptide of SEQ ID NO:217

<400> 226
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatgggc cgaagcccag
240

cacacgcagc agaccagact gtga
264

<210> 227
<211> 264
<212> DNA
<213> Artificial Sequence

<220>
<223> Polynucleotide encoding the polypeptide of SEQ ID NO:218

<400> 227
atggttcctc aggctctcct gtttgtaccc cttctggttt ttccattgtg ttttgggggg
60

aagtatgtat tactgagtgc aggggccctg actgccttga tgttgataat tttcctgatg
120

acatgttgta gaagagtcaa tcgatcagaa cctacgcaac acaatctcag agggacaggg
180

agggaggtgt cagtcactcc ccaaagcggg aagatcatat cttcatggga agtacacgcc
240

tctgggggc agaccagact gtga
264

<210> 228
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> CAEV FLAP

<400> 228
gttccagcca caatttgtcg ctgtagaatc agccatagca gcagccctag tcgccataaa
60

tataaaaaga aagggtgggc tggggacaag ccctatggat atttttatat ataataaaga
120

acagaaaaga ataaataata aatataataa aaattctcaa aaaattcaat tctgttatta
180

cagaataagg aaaagaggac
200

<210> 229
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> EIAV FLAP

<400> 229

cttgtaacaa agggagggaa agtatgggag gacagacacc atgggaagta tttatcacta
60

atcaagcaca agtaatacat gagaaacttt tactacagca agcacaatcc tccaaaaaat
120

tttgttttta caaaatccct ggtgaacatg attggaaggg acctactagg gtgctgtgga
180

agggtgatgg tgcagtagta
200

<210> 230
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> VISNA FLAP

<400> 230
ggaccctcat tactctaaat ataaaaagaa agggtgggct agggacaagc cctatggata
60

tatttatatt taataaggaa caacaaagaa tacagcaaca aagtaaatca aaacaagaaa
120

aaattcgatt ttgttattac agaacaagaa aaagagggca tccaggagag tggcaaggac
180

caacacaggt actttggggc
200

<210> 231
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> SIV AGM FLAP

<400> 231
tactgatggc ttgcatactt cacaatttta aaagaaaggg aggaataggg ggacagactt
60

cagcagagag actaattaat ataataacaa cacaattaga aatacaacat ttacaaacca
120

aaattcaaaa aattttaaat tttagagtct actacagaga agggagagac cctgtgtgga
180

aaggaccggc acaattaatc
200

<210> 232

<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-2 RID FLAP

<400> 232
tgcatgaatt ttaaaagaag ggggggaata ggggatatga ctccatcaga aagattaatc
60

aatatgatca ccacagaaca agagatacaa ttcctccaag ccaaaaattc aaaattaaaa
120

gattttcggg tctatttcag agaaggcaga gatcagttgt ggaaaggacc tggggaacta
180

ctgtggaaag gagaaggagc
200

<210> 233
<211> 200
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 LAI FLAP

<400> 233
cagtattcat ccacaatttt aaaagaaaag gggggattgg ggggtacagt gcaggggaaa
60

gaatagtaga cataatagca acagacatac aaactaaaga attacaaaaa caaattacaa
120

aaattcaaaa ttttcgggtt tattacaggg acagcagaga tccactttgg aaaggaccag
180

caaagctcct ctggaaaggt
200

<210> 234
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 FLAP

<400> 234
ttttaaaaga aaaggggga ttgggggta cagtgcaggg gaaagaatag tagacataat
60

agcaacagac atacaaacta aagaattaca aaaacaaatt acaaaaattc aaaattttc
119

<210> 235
<211> 13
<212> PRT
<213> Rabies virus - MAST-2 binding domain of the G protein of an attenuated strain

<400> 235

Ser Trp Glu Ser His Lys Ser Gly Gly Glu Thr Arg Leu
1 5 10

<210> 236
<211> 7385
<212> DNA
<213> Homo sapiens - roundabout, axon guidance receptor, homolog 1 (ROBO1)

<400> 236
aattgagctg gagaggaggc agcgtgagag cagaaacttc agacgccgct gatccgggag
60

gagctggggt gagccgcggc ggccgtctct cccacccgca gcagcatcct ctctgccctt
120

ctctgccacc ccggggagag ccgggagctg cctctttaca gcttccacga gccaggggtg
180

caggcagctg cccccaggaa gtttgggctt ctgcgtagtt taggggtgcc tgcgagcgcc
240

ccagagggcg aggggccgag ggcgatgttg ggcgccgcgc ggggctgggg gcgcccagaa
300

gacgtgcgag tgtccgcggt cctgctgctg tctccagtac cctccgcatc ccccaagtga
360

tgggaacaag ggcccgccca ggcagccgct gtcgccgcac cgccccctcg ctcgctctct
420

gcgcgcggag tcacccagtc acactcccgg caccccgagc ccttcctccg gagctgctgc
480

ttctactttg gctgctatcg ccgccgccgc gggtggcccg ctgctgactg ggctcgccgg
540

gagacggaga agcacttttt ggccctccct cagcagctct cacaccccaa ctttgccgcc
600

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(HEY2)

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cggcaccaag ctggtgaagg acctgagccc cggggaccgc gtgctggcgg cggacgacca
840

gggccggctg ctctacagcg acttcctcac tttcctggac cgcgacgacg gcgccaagaa
900

ggtcttctac gtgatcgaga cgcgggagcc gcgcgagcgc ctgctgctca ccgccgcgca
960

cctgctcttt gtggcgccgc acaacgactc ggccaccggg gagcccgagg cgtcctcggg
1020

ctcggggccg ccttccgggg gcgcactggg gcctcgggcg ctgttcgcca gccgcgtgcg
1080

cccgggccag cgcgtgtacg tggtggccga gcgtgacggg gaccgccggc tcctgcccgc
1140

cgctgtgcac agcgtgaccc taagcgagga ggccgcgggc gcctacgcgc cgctcacggc
1200

ccagggcacc attctcatca accgggtgct ggcctcgtgc tacgcggtca tcgaggagca
1260

cagctgggcg caccgggcct tcgcgccctt ccgcctggcg cacgcgctcc tggctgcact
1320

ggcgcccgcg cgcacggacc gcggcgggga cagcggcggc ggggaccgcg ggggcggcgg
1380

cggcagagta gccctaaccg ctccaggtgc tgccgacgct ccgggtgcgg gggccaccgc
1440

gggcatccac tggtactcgc agctgctcta ccaaataggc acctggctcc tggacagcga
1500

ggccctgcac ccgctgggca tggcggtcaa gtccagctga agccgggggg ccgggggagg
1560

ggcgcgggag ggggcg
1576

<210> 251
<211> 2611
<212> DNA
<213> Homo sapiens - Bruton agammaglobulinemia tyrosine kinase (BTK)

<400> 251
aactgagtgg ctgtgaaagg gtggggtttg ctcagactgt ccttcctctc tggactgtaa
60

gaatatgtct ccagggccag tgtctgctgc gatcgagtcc caccttccaa gtcctggcat
120

ctcaatgcat ctgggaagct acctgcatta agtcaggact gagcacacag gtgaactcca
180

gaaagaagaa gctatggccg cagtgattct ggagagcatc tttctgaagc gatcccaaca
240

gaaaaagaaa acatcacctc taaacttcaa gaagcgcctg tttctcttga ccgtgcacaa
300

actctcctac tatgagtatg actttgaacg tgggagaaga ggcagtaaga agggttcaat
360

agatgttgag aagatcactt gtgttgaaac agtggttcct gaaaaaaatc ctcctccaga
420

aagacagatt ccgagaagag gtgaagagtc cagtgaaatg gagcaaattt caatcattga
480

aaggttccct tatcccttcc aggttgtata tgatgaaggg cctctctacg tcttctcccc
540

aactgaagaa ctaaggaagc ggtggattca ccagctcaaa aacgtaatcc ggtacaacag
600

tgatctggtt cagaaatatc acccttgctt ctggatcgat gggcagtatc tctgctgctc
660

tcagacagcc aaaaatgcta tgggctgcca aattttggag aacaggaatg gaagcttaaa
720

acctgggagt tctcaccgga agacaaaaaa gcctcttccc ccaacgcctg aggaggacca
780

gatcttgaaa aagccactac cgcctgagcc agcagcagca ccagtctcca caagtgagct
840

gaaaaaggtt gtggcccttt atgattacat gccaatgaat gcaaatgatc tacagctgcg
900

gaagggtgat gaatatttta tcttggagga aagcaactta ccatggtgga gagcacgaga
960

taaaaatggg caggaaggct acattcctag taactatgtc actgaagcag aagactccat
1020

agaaatgtat gagtggtatt ccaaacacat gactcggagt caggctgagc aactgctaaa
1080

gcaagagggg aaagaaggag gtttcattgt cagagactcc agcaaagctg gcaaatatac
1140

agtgtctgtg tttgctaaat ccacagggga ccctcaaggg gtgatacgtc attatgttgt
1200

gtgttccaca cctcagagcc agtattacct ggctgagaag cacctttca gcaccatccc
1260

tgagctcatt aactaccatc agcacaactc tgcaggactc atatccaggc tcaaatatcc
1320

agtgtctcaa caaaacaaga atgcaccttc cactgcaggc ctgggatacg gatcatggga
1380

aattgatcca aaggacctga ccttcttgaa ggagctgggg actggacaat ttggggtagt
1440

gaagtatggg aaatggagag gccagtacga cgtggccatc aagatgatca aagaaggctc
1500

catgtctgaa gatgaattca ttgaagaagc caaagtcatg atgaatcttt cccatgagaa
1560

gctggtgcag ttgtatggcg tctgcaccaa gcagcgcccc atcttcatca tcactgagta
1620

catggccaat ggctgcctcc tgaactacct gagggagatg cgccaccgct tccagactca
1680

gcagctgcta gagatgtgca aggatgtctg tgaagccatg gaatacctgg agtcaaagca
1740

gttccttcac cgagacctgg cagctcgaaa ctgtttggta aacgatcaag gagttgttaa
1800

agtatctgat ttcggcctgt ccaggtatgt cctggatgat gaatacacaa gctcagtagg
1860

ctccaaattt ccagtccggt ggtccccacc ggaagtcctg atgtatagca agttcagcag
1920

caaatctgac atttgggctt ttggggtttt gatgtgggaa atttactccc tggggaagat
1980

gccatatgag agatttacta acagtgagac tgctgaacac attgcccaag gcctacgtct
2040

ctacaggcct catctggctt cagagaaggt atataccatc atgtacagtt gctggcatga
2100

gaaagcagat gagcgtccca ctttcaaaat tcttctgagc aatattctag atgtcatgga
2160

tgaagaatcc tgagctcgcc aataagcttc ttggttctac ttctcttctc cacaagcccc
2220

aatttcactt tctcagagga aatcccaagc ttaggagccc tggagccttt gtgctcccac
2280

tcaatacaaa aaggcccctc tctacatctg ggaatgcacc tcttctttga ttccctggga
2340

tagtggcttc tgagcaaagg ccaagaaatt attgtgcctg aaatttcccg agagaattaa
2400

gacagactga atttgcgatg aaaatatttt ttaggaggga ggatgtaaat agccgcacaa
2460

aggggtccaa cagctctttg agtaggcatt tggtagagct tgggggtgtg tgtgtggggg
2520

tggaccgaat ttggcaagaa tgaaatggtg tcataaagat gggaggggag ggtgttttga
2580

taaaataaaa ttactagaaa gcttgaaagt c
2611

<210> 252
<211> 2158
<212> DNA
<213> Homo sapiens - FBJ murine osteosarcoma viral oncogene homolog
(FOS)

<400> 252
attcataaaa cgcttgttat aaaagcagtg gctgcggcgc ctcgtactcc aaccgcatct
60

gcagcgagca tctgagaagc caagactgag ccggcggccg cggcgcagcg aacgagcagt
120

gaccgtgctc ctacccagct ctgctccaca gcgcccacct gtctccgccc ctcggcccct
180

cgcccggctt tgcctaaccg ccacgatgat gttctcgggc ttcaacgcag actacgaggc
240

gtcatcctcc cgctgcagca gcgcgtcccc ggccggggat agcctctctt actaccactc
300

acccgcagac tccttctcca gcatgggctc gcctgtcaac gcgcaggact tctgcacgga
360

cctggccgtc tccagtgcca acttcattcc cacggtcact gccatctcga ccagtccgga
420

cctgcagtgg ctggtgcagc ccgccctcgt ctcctccgtg gccccatcgc agaccagagc
480

ccctcaccct ttcggagtcc ccgccccctc cgctggggct tactccaggg ctggcgttgt
540

gaagaccatg acaggaggcc gagcgcagag cattggcagg aggggcaagg tggaacagtt
600

atctccagaa gaagaagaga aaaggagaat ccgaagggaa aggaataaga tggctgcagc
660

caaatgccgc aaccggagga gggagctgac tgatacactc caagcggaga cagaccaact
720

agaagatgag aagtctgctt tgcagaccga gattgccaac ctgctgaagg agaaggaaaa
780

actagagttc atcctggcag ctcaccgacc tgcctgcaag atccctgatg acctgggctt
840

cccagaagag atgtctgtgg cttcccttga tctgactggg ggcctgccag aggttgccac
900

cccggagtct gaggaggcct tcaccctgcc tctcctcaat gaccctgagc ccaagccctc
960

agtggaacct gtcaagagca tcagcagcat ggagctgaag accgagccct ttgatgactt
1020

cctgttccca gcatcatcca ggcccagtgg ctctgagaca gcccgctccg tgccagacat
1080

ggacctatct gggtccttct atgcagcaga ctgggagcct ctgcacagtg gctccctggg
1140

gatggggccc atggccacag agctggagcc cctgtgcact ccggtggtca cctgtactcc
1200

cagctgcact gcttacacgt cttccttcgt cttcacctac cccgaggctg actccttccc
1260

cagctgtgca gctgcccacc gcaagggcag cagcagcaat gagccttcct ctgactcgct
1320

cagctcaccc acgctgctgg ccctgtgagg gggcagggaa ggggaggcag ccggcaccca
1380

caagtgccac tgcccgagct ggtgcattac agagaggaga aacacatctt ccctagaggg
1440

ttcctgtaga cctagggagg accttatctg tgcgtgaaac acaccaggct gtgggcctca
1500

aggacttgaa agcatccatg tgtggactca agtccttacc tcttccggag atgtagcaaa
1560

acgcatggag tgtgtattgt tcccagtgac acttcagaga gctggtagtt agtagcatgt
1620

tgagccaggc ctgggtctgt gtctcttttc tctttctcct tagtcttctc atagcattaa
1680

ctaatctatt gggttcatta ttggaattaa cctggtgctg gatattttca aattgtatct
1740

agtgcagctg attttaacaa taactactgt gttcctggca atagtgtgtt ctgattagaa
1800

atgaccaata ttatactaag aaaagatacg actttatttt ctggtagata gaaataaata
1860

gctatatcca tgtactgtag tttttcttca acatcaatgt tcattgtaat gttactgatc
1920

atgcattgtt gaggtggtct gaatgttctg acattaacag ttttccatga aaacgtttta
1980

ttgtgttttt aatttattta ttaagatgga ttctcagata tttatatttt tattttattt
2040

ttttctacct tgaggtcttt tgacatgtgg aaagtgaatt tgaatgaaaa atttaagcat
2100

tgtttgctta ttgttccaag acattgtcaa taaaagcatt taagttgaat gcgaccaa
2158

<210> 253
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> ROBO1 Forward primer

<400> 253
gtgtggtgtg tggcttca
18

<210> 254
<211> 17

<212> DNA
<213> Artificial Sequence

<220>
<223> ROBO1 Backward primer

<400> 254
gtatacagtc tcatgcc
17

<210> 255
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> POU4F1 Forward primer

<400> 255
ccctccctga gcacaag
17

<210> 256
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> POU4F1 Backward primer

<400> 256
gtgggcaggc aggccc
16

<210> 257
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PTN Forward primer

<400> 257
ggcaagaaac aggagaaga
19

<210> 258
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> PTN Backward primer

<400> 258
gtttgctgat gtccttt
17

<210> 259
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PARD6B Forward primer

<400> 259
catatagtca ttagtatg
18

<210> 260
<211> 17
<212> DNA
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<220>
<223> PARD6B Backward primer

<400> 260
ctgggagaat atccacg
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<210> 261
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PAFAH1B1 Forward primer

<400> 261
cggcaagctt ctggcttc
18

<210> 262
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> PAFAH1B1 Backward primer

<400> 262
gcattcaaag ccctg
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<210> 263

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> PIK3CG Forward primer

<400> 263
cgagatctac gacaagtacc
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<210> 264
<211> 20
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<220>
<223> PIK3CG Backward primer

<400> 264
ccggtgcgtg gccttccagt
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<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> BMP2 Forward primer

<400> 265
ccaccatgaa gaatctttg
19

<210> 266
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> BMP2 Backward primer

<400> 266
attaaagaag aatctccgg
19

<210> 267
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> DRD1 Forward primer

<400> 267
gtgtcagagc ccctgatgtg
20

<210> 268
<211> 18
<212> DNA
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<220>
<223> DRD1 Backward primer

<400> 268
gtcccgtcca tggcagag
18

<210> 269
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PAX5 Forward primer

<400> 269
cgtcagttcc atcaacagg
19

<210> 270
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> PAX5 Backward primer

<400> 270
ggaagctggg actggttg
18

<210> 271
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<212> DNA
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<220>
<223> S100A6 Forward primer

<400> 271
caccgaccgc tataagg
17

<210> 272
<211> 19
<212> DNA
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<220>
<223> S100A6 Backward primer

<400> 272
gccaaatgcg acgcgagcg
19

<210> 273
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> DRD2 Forward primer

<400> 273
cattgtcacc ctgctggtc
19

<210> 274
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> DRD2 Backward primer

<400> 274
ggtgttgact cgcttgc
17

<210> 275
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> HDHC7 Forward primer

<400> 275
gtagtagcag cacgcccg
18

<210> 276
<211> 16
<212> DNA
<213> Artificial Sequence

<220>

<223> HDAC7 Backward primer

<400> 276
aggatgggat tggggc
16

<210> 277
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> HEY2 Forward Primer

<400> 277
gcagccctgc tccagccca
19

<210> 278
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> HEY2 Backward Primer

<400> 278
ctgaagttgt ggagagg
17

<210> 279
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> INHBA Forward primer

<400> 279
gggggagagg agtgaactg
19

<210> 280
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> INHBA Backward primer

<400> 280
gaagacatgc caggtgc
17

<210> 281
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> SHH Forward primer

<400> 281
gctggcccgc ctggcggtgg
20

<210> 282
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> SHH Backward primer

<400> 282
gcagtggata tgtgccttgg
20

<210> 283
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> BTK Forward primer

<400> 283
gaatatttta tcttggagga
20

<210> 284
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> BTK Backward primer

<400> 284
agccttcctg cccattttt
19

<210> 285
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> FOS Forward primer

<400> 285
gaggaggcct tcaccctgcc
20

<210> 286
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> FOS Backward primer

<400> 286
tgctcttgac aggttccact
20

<210> 287
<211> 1575
<212> DNA
<213> Rabies virus

<220>
<221> CDS
<222> (1)..(1575)

<400> 287
atg gtt cct cag gtt ctt ttg ttt gta ctc ctt ctg ggt ttt tcg ttg
48
Met Val Pro Gln Val Leu Leu Phe Val Leu Leu Leu Gly Phe Ser Leu
1   5   10   15

tgt ttc ggg aag ttc ccc att tac acg ata cca gac aaa ctt ggt ccc
96
Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Pro Asp Lys Leu Gly Pro
            20   25   30

tgg agc cct att gac ata cac cat ctc cgc tgt cca aat aac ctg gtt
144
Trp Ser Pro Ile Asp Ile His His Leu Arg Cys Pro Asn Asn Leu Val
        35   40   45

gtg gag gat gaa gga tgt atc aac ctg tcc ggg ttc tcc tac atg gaa
192
Val Glu Asp Glu Gly Cys Ile Asn Leu Ser Gly Phe Ser Tyr Met Glu
    50   55   60

ctc aaa gtg gga tac atc tca gcc atc aaa gtg aac ggg ttc act tgc
240
Leu Lys Val Gly Tyr Ile Ser Ala Ile Lys Val Asn Gly Phe Thr Cys
65   70   75   80

```
aca ggt gtt gtg aca gag gca gag acc tac acc aac ttt gtt ggt tat
288
Thr Gly Val Val Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr
                85                  90                  95

gtc aca acc aca ttc aag aga aag cat ttc cgc ccc acc cca gac gca
336
Val Thr Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
            100                 105                 110

tgt aga gcc gcg tat aac tgg aag atg gcc ggt gac ccc aga tat gaa
384
Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg Tyr Glu
        115                 120                 125

gag tcc cta caa aat cca tac ccc gac tac cac tgg ctt cga act gta
432
Glu Ser Leu Gln Asn Pro Tyr Pro Asp Tyr His Trp Leu Arg Thr Val
    130                 135                 140

aga acc acc aaa gag tcc ctc att atc ata tcc cca agt gtg aca gat
480
Arg Thr Thr Lys Glu Ser Leu Ile Ile Ile Ser Pro Ser Val Thr Asp
145                 150                 155                 160

ttg gac cca tat gac aaa tcc ctt cac tca agg gtc ttc cct ggc gga
528
Leu Asp Pro Tyr Asp Lys Ser Leu His Ser Arg Val Phe Pro Gly Gly
                165                 170                 175

aag tgc tca gga ata acg gtg tcc tct acc tac tgc tca act aac cat
576
Lys Cys Ser Gly Ile Thr Val Ser Ser Thr Tyr Cys Ser Thr Asn His
            180                 185                 190

gat tac acc att tgg atg ccc gag aat ccg aga cca ggg aca cct tgt
624
Asp Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Gly Thr Pro Cys
        195                 200                 205

gac att ttt acc aat agc aga ggg aag aga gca tcc aac ggg aac aag
672
Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Asn Gly Asn Lys
    210                 215                 220

act tgc ggc ttt gtg gat gaa aga ggc ctg tat aag tct cta aaa gga
720
Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu Lys Gly
225                 230                 235                 240

gca tgc agg ctc aag tta tgt gga gtt ctt gga ctt aga ctt atg gat
768
Ala Cys Arg Leu Lys Leu Cys Gly Val Leu Gly Leu Arg Leu Met Asp
                245                 250                 255

gga aca tgg gtc gcg atg caa aca tca gat gag acc aaa tgg tgc tct
816
Gly Thr Trp Val Ala Met Gln Thr Ser Asp Glu Thr Lys Trp Cys Ser
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            260                 265                 270

cca gat cag ttg gtg aat ttg cac gac ttt cgc tca gac gag att gag
864
Pro Asp Gln Leu Val Asn Leu His Asp Phe Arg Ser Asp Glu Ile Glu
        275                 280                 285

cat ctc gtt gtg gag gag tta gtc aag aaa aga gag gaa tgt ctg gat
912
His Leu Val Val Glu Glu Leu Val Lys Lys Arg Glu Glu Cys Leu Asp
    290                 295                 300

aca tta gag tcc atc atg acc acc aag tca gta agt ttc aga cgt ctc
960
Thr Leu Glu Ser Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu
305                 310                 315                 320

agt cac ctg aga aaa ctt gtc cca ggg ttt gga aaa gca tat acc ata
1008
Ser His Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
                325                 330                 335

ttc aac aaa acc ttg atg gag gct gat gct cac tac aag tca gtc cgg
1056
Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser Val Arg
            340                 345                 350

acc tgg aat gag atc atc ccc tca aaa ggg tgt ttg aaa gtt gga gga
1104
Thr Trp Asn Glu Ile Ile Pro Ser Lys Gly Cys Leu Lys Val Gly Gly
        355                 360                 365

agg tgc cat cct cat gtg aac ggg gtg ttt ttc aat ggt ata ata tta
1152
Arg Cys His Pro His Val Asn Gly Val Phe Phe Asn Gly Ile Ile Leu
    370                 375                 380

ggg cct gac gac cgt gtc cta atc cca gag atg caa tca tcc ctc ctc
1200
Gly Pro Asp Asp Arg Val Leu Ile Pro Glu Met Gln Ser Ser Leu Leu
385                 390                 395                 400

cgg caa cat atg gag ttg ttg gaa tct tca gtt atc ccc ctg atg cac
1248
Arg Gln His Met Glu Leu Leu Glu Ser Ser Val Ile Pro Leu Met His
                405                 410                 415

ccc ctg gct gac cct tct aca gtt ttc aaa gaa ggt gat gag gct gag
1296
Pro Leu Ala Asp Pro Ser Thr Val Phe Lys Glu Gly Asp Glu Ala Glu
            420                 425                 430

gat ttt gtt gaa gtt cac ctc ccc gat gtg tac aaa cag atc tca ggg
1344
Asp Phe Val Glu Val His Leu Pro Asp Val Tyr Lys Gln Ile Ser Gly
        435                 440                 445
```

```
gtt gac ctg ggt ctc ccg aac tgg gga aag tat gta ttg atg act gca
1392
Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Met Thr Ala
    450                 455                 460

ggg gcc atg att ggc ctg gtg ttg ata ttt tcc cta atg aca tgg tgc
1440
Gly Ala Met Ile Gly Leu Val Leu Ile Phe Ser Leu Met Thr Trp Cys
465                 470                 475                 480

aga aga gcc aat cga cca gaa tcg aaa caa cgc agt ttt gga ggg aca
1488
Arg Arg Ala Asn Arg Pro Glu Ser Lys Gln Arg Ser Phe Gly Gly Thr
                485                 490                 495

ggg ggg aat gtg tca gtc act tcc caa agc gga aaa gtc ata cct tca
1536
Gly Gly Asn Val Ser Val Thr Ser Gln Ser Gly Lys Val Ile Pro Ser
            500                 505                 510

tgg gaa tca tat aag agt gga ggt gag atc aga ctg tga
1575
Trp Glu Ser Tyr Lys Ser Gly Gly Glu Ile Arg Leu
        515                 520
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<210> 288
<211> 524
<212> PRT
<213> Rabies virus

<400> 288

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Met Val Pro Gln Val Leu Leu Phe Val Leu Leu Leu Gly Phe Ser Leu
1               5                   10                  15

Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Pro Asp Lys Leu Gly Pro
            20                  25                  30

Trp Ser Pro Ile Asp Ile His His Leu Arg Cys Pro Asn Asn Leu Val
        35                  40                  45

Val Glu Asp Glu Gly Cys Ile Asn Leu Ser Gly Phe Ser Tyr Met Glu
    50                  55                  60

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

Thr Gly Val Val Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr
                85                  90                  95

Val Thr Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
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            100                 105                 110

Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg Tyr Glu
        115                 120                 125

Glu Ser Leu Gln Asn Pro Tyr Pro Asp Tyr His Trp Leu Arg Thr Val
    130                 135                 140

Arg Thr Thr Lys Glu Ser Leu Ile Ile Ile Ser Pro Ser Val Thr Asp
145                 150                 155                 160

Leu Asp Pro Tyr Asp Lys Ser Leu His Ser Arg Val Phe Pro Gly Gly
                165                 170                 175

Lys Cys Ser Gly Ile Thr Val Ser Ser Thr Tyr Cys Ser Thr Asn His
            180                 185                 190

Asp Tyr Thr Ile Trp Met Pro Glu Asn Pro Arg Pro Gly Thr Pro Cys
        195                 200                 205

Asp Ile Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Asn Gly Asn Lys
    210                 215                 220

Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu Lys Gly
225                 230                 235                 240

Ala Cys Arg Leu Lys Leu Cys Gly Val Leu Gly Leu Arg Leu Met Asp
                245                 250                 255

Gly Thr Trp Val Ala Met Gln Thr Ser Asp Glu Thr Lys Trp Cys Ser
            260                 265                 270

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

His Leu Val Val Glu Glu Leu Val Lys Lys Arg Glu Glu Cys Leu Asp
    290                 295                 300

Thr Leu Glu Ser Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu
305                 310                 315                 320

Ser His Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
                325                 330                 335
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Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser Val Arg
            340                 345                 350

Thr Trp Asn Glu Ile Ile Pro Ser Lys Gly Cys Leu Lys Val Gly Gly
        355                 360                 365

Arg Cys His Pro His Val Asn Gly Val Phe Phe Asn Gly Ile Ile Leu
    370                 375                 380

Gly Pro Asp Asp Arg Val Leu Ile Pro Glu Met Gln Ser Ser Leu Leu
385                 390                 395                 400

Arg Gln His Met Glu Leu Leu Glu Ser Ser Val Ile Pro Leu Met His
                405                 410                 415

Pro Leu Ala Asp Pro Ser Thr Val Phe Lys Glu Gly Asp Glu Ala Glu
            420                 425                 430

Asp Phe Val Glu Val His Leu Pro Asp Val Tyr Lys Gln Ile Ser Gly
        435                 440                 445

Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Met Thr Ala
    450                 455                 460

Gly Ala Met Ile Gly Leu Val Leu Ile Phe Ser Leu Met Thr Trp Cys
465                 470                 475                 480

Arg Arg Ala Asn Arg Pro Glu Ser Lys Gln Arg Ser Phe Gly Gly Thr
                485                 490                 495

Gly Gly Asn Val Ser Val Thr Ser Gln Ser Gly Lys Val Ile Pro Ser
            500                 505                 510

Trp Glu Ser Tyr Lys Ser Gly Gly Glu Ile Arg Leu
        515                 520
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