SEQUENCE LISTING

<110> Regeneron Pharmaceuticals, Inc.

<120> NON-HUMAN ANIMALS COMPRISING A HUMANIZED TRKB LOCUS

<130> 57766-523380

<150> US 62/592,905
<151> 2017-11-30

<150> US 62/661,373
<151> 2018-04-23

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<170> PatentIn version 3.5

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Met Ser Pro Trp Leu Lys Trp His Gly Pro Ala Met Ala Arg Leu Trp
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Gly Leu Cys Leu Leu Val Leu Gly Phe Trp Arg Ala Ser Leu Ala Cys
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Pro Thr Ser Cys Lys Cys Ser Ser Ala Arg Ile Trp Cys Thr Glu Pro

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        35                  40                  45

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

Pro Glu Asn Ile Thr Glu Ile Leu Ile Ala Asn Gln Lys Arg Leu Glu
65                  70                  75                  80

Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
                85                  90                  95

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

Lys Asn Ser Asn Leu Arg His Ile Asn Phe Thr Arg Asn Lys Leu Thr
        115                 120                 125

Ser Leu Ser Arg Arg His Phe Arg His Leu Asp Leu Ser Asp Leu Ile
    130                 135                 140

Leu Thr Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Leu Lys
145                 150                 155                 160

Thr Leu Gln Glu Thr Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
                165                 170                 175

Leu Asn Glu Ser Ser Lys Asn Met Pro Leu Ala Asn Leu Gln Ile Pro
            180                 185                 190

Asn Cys Gly Leu Pro Ser Ala Arg Leu Ala Ala Pro Asn Leu Thr Val
        195                 200                 205

Glu Glu Gly Lys Ser Val Thr Leu Ser Cys Ser Val Gly Gly Asp Pro
    210                 215                 220

Leu Pro Thr Leu Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
225                 230                 235                 240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
                245                 250                 255
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```
Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
            260                 265                 270

Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
        275                 280                 285

Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
    290                 295                 300

Phe Thr Val Arg Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
305                 310                 315                 320

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

Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
            340                 345                 350

His Met Asn Asn Gly Asp Tyr Thr Leu Met Ala Lys Asn Glu Tyr Gly
        355                 360                 365

Lys Asp Glu Arg Gln Ile Ser Ala His Phe Met Gly Arg Pro Gly Val
    370                 375                 380

Asp Tyr Glu Thr Asn Pro Asn Tyr Pro Glu Val Leu Tyr Glu Asp Trp
385                 390                 395                 400

Thr Thr Pro Thr Asp Ile Gly Asp Thr Thr Asn Lys Ser Asn Glu Ile
                405                 410                 415

Pro Ser Thr Asp Val Ala Asp Gln Ser Asn Arg Glu His Leu Ser Val
            420                 425                 430

Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val
        435                 440                 445

Met Leu Leu Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys
    450                 455                 460

Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro Leu
465                 470                 475                 480
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His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly Gly
                485                 490                 495

Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu Asn
            500                 505                 510

Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr Phe
        515                 520                 525

Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu Leu Gly
    530                 535                 540

Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu Cys
545                 550                 555                 560

Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp Ala
                565                 570                 575

Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu Thr
            580                 585                 590

Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val Glu
        595                 600                 605

Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp Leu
    610                 615                 620

Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met Ala Glu
625                 630                 635                 640

Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala
                645                 650                 655

Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val
            660                 665                 670

His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu
        675                 680                 685

Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp
    690                 695                 700
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Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met Pro
705                 710                 715                 720


Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp
                725                 730                 735


Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro
            740                 745                 750


Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln Gly
        755                 760                 765


Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu Leu
    770                 775                 780


Met Leu Gly Cys Trp Gln Arg Glu Pro His Thr Arg Lys Asn Ile Lys
785                 790                 795                 800


Ser Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro Val Tyr
                805                 810                 815


Leu Asp Ile Leu Gly
            820


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<223>  Transmembrane Domain
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1               5                  10                  15


Gly Leu Cys Leu Leu Val Leu Gly Phe Trp Arg Ala Ser Leu Ala Cys
            20                  25                  30


Pro Met Ser Cys Lys Cys Ser Thr Thr Arg Ile Trp Cys Thr Glu Pro
        35                  40                  45


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


Pro Glu Asn Ile Thr Glu Ile Leu Ile Ala Asn Gln Lys Arg Leu Glu
65                  70                  75                  80


Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Lys Asn Leu
                85                  90                  95


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


Lys Asn Gly Asn Leu Arg His Ile Asn Phe Thr Arg Asn Lys Leu Thr
        115                 120                 125


Ser Leu Ser Arg Arg His Phe Arg His Leu Asp Leu Ser Asp Leu Ile
    130                 135                 140


Leu Thr Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Leu Lys
145                 150                 155                 160


Thr Leu Gln Glu Thr Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
                165                 170                 175


Leu Asn Glu Ser Ser Lys Asn Thr Pro Leu Ala Asn Leu Gln Ile Pro
            180                 185                 190
```

```
Asn Cys Gly Leu Pro Ser Ala Arg Leu Ala Ala Pro Asn Leu Thr Val
        195                 200                 205

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

Leu Pro Thr Leu Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
225                 230                 235                 240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
                245                 250                 255

Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
            260                 265                 270

Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
        275                 280                 285

Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
    290                 295                 300

Phe Thr Val Arg Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
305                 310                 315                 320

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

Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
            340                 345                 350

His Met Asn Asn Gly Asp Tyr Thr Leu Met Ala Lys Asn Glu Tyr Gly
        355                 360                 365

Lys Asp Glu Arg Gln Ile Ser Ala His Phe Met Gly Arg Pro Gly Val
    370                 375                 380

Asp Tyr Glu Thr Asn Pro Asn Tyr Pro Glu Val Leu Tyr Glu Asp Trp
385                 390                 395                 400

Thr Thr Pro Thr Asp Ile Gly Asp Thr Thr Asn Lys Ser Asn Glu Ile
                405                 410                 415
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```
Pro Ser Thr Asp Val Ala Asp Gln Thr Asn Arg Glu His Leu Ser Val
            420                 425                 430

Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val
        435                 440                 445

Met Leu Leu Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys
    450                 455                 460

Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro Leu
465                 470                 475                 480

His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly Gly
                485                 490                 495

Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu Asn
            500                 505                 510

Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr Phe
        515                 520                 525

Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu Leu Gly
    530                 535                 540

Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu Cys
545                 550                 555                 560

Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp Ala
                565                 570                 575

Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu Thr
            580                 585                 590

Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val Glu
        595                 600                 605

Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp Leu
    610                 615                 620

Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met Ala Glu
625                 630                 635                 640
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Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala
                645                 650                 655

Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val
            660                 665                 670

His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu
        675                 680                 685

Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp
    690                 695                 700

Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met Pro
705                 710                 715                 720

Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp
                725                 730                 735

Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro
            740                 745                 750

Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln Gly
        755                 760                 765

Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu Leu
    770                 775                 780

Met Leu Gly Cys Trp Gln Arg Glu Pro His Thr Arg Lys Asn Ile Lys
785                 790                 795                 800

Asn Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro Val Tyr
                805                 810                 815

Leu Asp Ile Leu Gly
            820
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<213> Homo sapiens

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1               5                  10                  15


Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe Ala Cys
            20                  25                  30


Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
        35                  40                  45


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


Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu
65                  70                  75                  80


Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
                85                  90                  95


Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
            100                 105                 110


Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
        115                 120                 125
```

```
Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
    130                 135                 140

Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
145                 150                 155                 160

Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
                165                 170                 175

Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
            180                 185                 190

Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val
        195                 200                 205

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

Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
225                 230                 235                 240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
                245                 250                 255

Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
            260                 265                 270

Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
        275                 280                 285

Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
    290                 295                 300

Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
305                 310                 315                 320

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

Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
            340                 345                 350
```

```
His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
        355                 360                 365

Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
    370                 375                 380

Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
385                 390                 395                 400

Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu
                405                 410                 415

Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser
            420                 425                 430

Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu
        435                 440                 445

Val Met Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
    450                 455                 460

Lys Asp Phe Ser Trp Phe Gly Phe Gly Lys Val Lys Ser Arg Gln Gly
465                 470                 475                 480

Val Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
                485                 490                 495

Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly
            500                 505                 510

Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu
        515                 520                 525

Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr
    530                 535                 540

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

Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu
                565                 570                 575
```

```
Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp
            580                 585                 590

Ala Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu
        595                 600                 605

Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val
    610                 615                 620

Glu Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
625                 630                 635                 640

Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met Ala
                645                 650                 655

Glu Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile
            660                 665                 670

Ala Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe
        675                 680                 685

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu
    690                 695                 700

Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr
705                 710                 715                 720

Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met
                725                 730                 735

Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val
            740                 745                 750

Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln
        755                 760                 765

Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln
    770                 775                 780

Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu
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785 790 795 800

Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His Met Arg Lys Asn Ile
805 810 815

Lys Gly Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro Val
820 825 830

Tyr Leu Asp Ile Leu Gly
835

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<223> Human Sequence

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<223> Transmembrane Domain

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<223> Mouse Sequence

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Met Ser Pro Trp Leu Lys Trp His Gly Pro Ala Met Ala Arg Leu Trp
1               5                  10                  15


Gly Leu Cys Leu Leu Val Leu Gly Phe Trp Arg Ala Ser Leu Ala Cys
            20                  25                  30


Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
        35                  40                  45


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


Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu
65                  70                  75                  80


Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
                85                  90                  95


Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
            100                 105                 110


Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
        115                 120                 125


Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
    130                 135                 140


Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
145                 150                 155                 160


Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
                165                 170                 175


Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
            180                 185                 190


Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val
```

```
        195                 200                 205

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

Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
225                 230                 235                 240

Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
                245                 250                 255

Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
            260                 265                 270

Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
        275                 280                 285

Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
    290                 295                 300

Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
305                 310                 315                 320

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

Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
            340                 345                 350

His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
        355                 360                 365

Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
    370                 375                 380

Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
385                 390                 395                 400

Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu
                405                 410                 415
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```
Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser
            420                 425                 430

Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu
        435                 440                 445

Val Met Leu Leu Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
    450                 455                 460

Lys Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
465                 470                 475                 480

Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly
                485                 490                 495

Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu
            500                 505                 510

Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr
        515                 520                 525

Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu Leu
    530                 535                 540

Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu
545                 550                 555                 560

Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp
                565                 570                 575

Ala Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu
            580                 585                 590

Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val
        595                 600                 605

Glu Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
    610                 615                 620

Leu Asn Lys Phe Leu Arg Ala His Gly Pro Asp Ala Val Leu Met Ala
625                 630                 635                 640
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```
Glu Gly Asn Pro Pro Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile
                645                 650                 655

Ala Gln Gln Ile Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe
            660                 665                 670

Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu
        675                 680                 685

Leu Val Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr
    690                 695                 700

Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met
705                 710                 715                 720

Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val
                725                 730                 735

Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln
            740                 745                 750

Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln
        755                 760                 765

Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu
    770                 775                 780

Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His Thr Arg Lys Asn Ile
785                 790                 795                 800

Lys Ser Ile His Thr Leu Leu Gln Asn Leu Ala Lys Ala Ser Pro Val
                805                 810                 815

Tyr Leu Asp Ile Leu Gly
            820
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<223> Rat Sequence

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<223> Cytoplasmic Domain

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Met Ser Pro Trp Pro Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
1 5 10 15

Gly Leu Cys Leu Leu Val Leu Gly Phe Trp Arg Ala Ser Leu Ala Cys
20 25 30

Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp Pro
35 40 45

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

```
Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu Glu
65                  70                  75                  80

Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
                85                  90                  95

Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
            100                 105                 110

Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
        115                 120                 125

Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
    130                 135                 140

Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
145                 150                 155                 160

Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
                165                 170                 175

Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro
            180                 185                 190

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Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
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Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
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Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
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Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
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Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His Val
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Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
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His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
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Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
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Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
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Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu
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Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser
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Val Met Leu Leu Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
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Lys Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
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Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly
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Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu
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Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp
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Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His Thr Arg Lys Asn Ile
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tctgaactga tcctggtggg caatccattt acatgctcct gtgacattat gtggatcaag 480

actctccaag aggctaaatc cagtccagac actcaggatt tgtactgcct gaatgaaagc 540

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gcaggtgatc cggttcctaa tatgtattgg gatgttggta acctggtttc caaacatatg 720

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<213> Mus musculus

<400> 51

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Gly Leu Cys Leu Leu Val Leu Gly Phe Trp Arg Ala Ser Leu Ala
20 25 30

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<400> 52

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1 5 10 15

Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val
20 25 30

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Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn
    50                  55                  60

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

Leu Lys Asn Ser Asn Leu Arg His Ile Asn Phe Thr Arg Asn Lys Leu
                85                  90                  95

Thr Ser Leu Ser Arg Arg His Phe Arg His Leu Asp Leu Ser Asp Leu
            100                 105                 110

Ile Leu Thr Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Leu
        115                 120                 125

Lys Thr Leu Gln Glu Thr Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr
    130                 135                 140

Cys Leu Asn Glu Ser Ser Lys Asn Met Pro Leu Ala Asn Leu Gln Ile
145                 150                 155                 160

Pro Asn Cys Gly Leu Pro Ser Ala Arg Leu Ala Ala Pro Asn Leu Thr
                165                 170                 175

Val Glu Glu Gly Lys Ser Val Thr Leu Ser Cys Ser Val Gly Gly Asp
            180                 185                 190

Pro Leu Pro Thr Leu Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His
        195                 200                 205

Met Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile
    210                 215                 220

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

Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro
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                245                 250                 255

Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile
            260                 265                 270

Pro Phe Thr Val Arg Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr
        275                 280                 285

Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His
    290                 295                 300

Val Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro
305                 310                 315                 320

Thr His Met Asn Asn Gly Asp Tyr Thr Leu Met Ala Lys Asn Glu Tyr
                325                 330                 335

Gly Lys Asp Glu Arg Gln Ile Ser Ala His Phe Met Gly Arg Pro Gly
            340                 345                 350

Val Asp Tyr Glu Thr Asn Pro Asn Tyr Pro Glu Val Leu Tyr Glu Asp
        355                 360                 365

Trp Thr Thr Pro Thr Asp Ile Gly Asp Thr Thr Asn Lys Ser Asn Glu
    370                 375                 380

Ile Pro Ser Thr Asp Val Ala Asp Gln Ser Asn Arg Glu His
385                 390                 395


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1               5                   10                  15

Leu Leu Val Met Leu Leu Leu Leu
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<211> 368
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<213> Mus musculus

<400> 54

Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys Gly Pro Ala Ser Val
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Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro Leu His His Ile Ser Asn
20 25 30

Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly Gly Pro Asp Ala Val Ile
35 40 45

Ile Gly Met Thr Lys Ile Pro Val Ile Glu Asn Pro Gln Tyr Phe Gly
50 55 60

Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr Phe Val Gln His Ile Lys
65 70 75 80

Arg His Asn Ile Val Leu Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly
85 90 95

Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys
100 105 110

Ile Leu Val Ala Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg
115 120 125

Lys Asp Phe His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu
130 135 140

His Ile Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile
145 150 155 160

Met Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg
165 170 175

Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro Thr
180 185 190

Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile Ala Ala

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        195                 200                 205

Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg Asp Leu Ala
    210                 215                 220

Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val Lys Ile Gly Asp
225                 230                 235                 240

Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp Tyr Tyr Arg Val Gly
                245                 250                 255

Gly His Thr Met Leu Pro Ile Arg Trp Met Pro Pro Glu Ser Ile Met
            260                 265                 270

Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp Ser Leu Gly Val Val
        275                 280                 285

Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro Trp Tyr Gln Leu Ser
    290                 295                 300

Asn Asn Glu Val Ile Glu Cys Ile Thr Gln Gly Arg Val Leu Gln Arg
305                 310                 315                 320

Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu Leu Met Leu Gly Cys Trp
                325                 330                 335

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

Leu Gln Asn Leu Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly
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<210>  55
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<212>  PRT
<213>  Rattus norvegicus

<400>  55

Met Ser Pro Trp Pro Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
1               5                   10                  15

Gly Leu Cys Leu Leu Val Leu Gly Phe Trp Arg Ala Ser Leu Ala
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            20                  25                  30


<210>  56
<211>  398
<212>  PRT
<213>  Rattus norvegicus

<400>  56

Cys Pro Met Ser Cys Lys Cys Ser Thr Thr Arg Ile Trp Cys Thr Glu
1               5                   10                  15


Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Ile
            20                  25                  30


Asp Pro Glu Asn Ile Thr Glu Ile Leu Ile Ala Asn Gln Lys Arg Leu
        35                  40                  45


Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Lys Asn
    50                  55                  60


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


Leu Lys Asn Gly Asn Leu Arg His Ile Asn Phe Thr Arg Asn Lys Leu
                85                  90                  95


Thr Ser Leu Ser Arg Arg His Phe Arg His Leu Asp Leu Ser Asp Leu
            100                 105                 110


Ile Leu Thr Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Leu
        115                 120                 125


Lys Thr Leu Gln Glu Thr Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr
    130                 135                 140


Cys Leu Asn Glu Ser Ser Lys Asn Thr Pro Leu Ala Asn Leu Gln Ile
145                 150                 155                 160


Pro Asn Cys Gly Leu Pro Ser Ala Arg Leu Ala Ala Pro Asn Leu Thr
                165                 170                 175


Val Glu Glu Gly Lys Ser Val Thr Ile Ser Cys Ser Val Gly Gly Asp
```

```
            180                 185                 190

Pro Leu Pro Thr Leu Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His
        195                 200                 205

Met Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile
    210                 215                 220

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

Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro
                245                 250                 255

Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile
            260                 265                 270

Pro Phe Thr Val Arg Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr
        275                 280                 285

Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His
    290                 295                 300

Val Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro
305                 310                 315                 320

Thr His Met Asn Asn Gly Asp Tyr Thr Leu Met Ala Lys Asn Glu Tyr
                325                 330                 335

Gly Lys Asp Glu Arg Gln Ile Ser Ala His Phe Met Gly Arg Pro Gly
            340                 345                 350

Val Asp Tyr Glu Thr Asn Pro Asn Tyr Pro Glu Val Leu Tyr Glu Asp
        355                 360                 365

Trp Thr Thr Pro Thr Asp Ile Gly Asp Thr Thr Asn Lys Ser Asn Glu
    370                 375                 380

Ile Pro Ser Thr Asp Val Ala Asp Gln Thr Asn Arg Glu His
385                 390                 395
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<210> 57
<211> 24
<212> PRT
<213> Rattus norvegicus

<400> 57

Leu Ser Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys
1 5 10 15

Leu Leu Val Met Leu Leu Leu Leu
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<210> 58
<211> 368
<212> PRT
<213> Rattus norvegicus

<400> 58

Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys Gly Pro Ala Ser Val
1 5 10 15

Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro Leu His His Ile Ser Asn
20 25 30

Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly Gly Pro Asp Ala Val Ile
35 40 45

Ile Gly Met Thr Lys Ile Pro Val Ile Glu Asn Pro Gln Tyr Phe Gly
50 55 60

Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr Phe Val Gln His Ile Lys
65 70 75 80

Arg His Asn Ile Val Leu Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly
85 90 95

Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys
100 105 110

Ile Leu Val Ala Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg
115 120 125

Lys Asp Phe His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu

```
    130                 135                 140

His Ile Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile
145                 150                 155                 160

Met Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg
                165                 170                 175

Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro Thr
            180                 185                 190

Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile Ala Ala
        195                 200                 205

Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg Asp Leu Ala
    210                 215                 220

Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val Lys Ile Gly Asp
225                 230                 235                 240

Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp Tyr Tyr Arg Val Gly
                245                 250                 255

Gly His Thr Met Leu Pro Ile Arg Trp Met Pro Pro Glu Ser Ile Met
            260                 265                 270

Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp Ser Leu Gly Val Val
        275                 280                 285

Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro Trp Tyr Gln Leu Ser
    290                 295                 300

Asn Asn Glu Val Ile Glu Cys Ile Thr Gln Gly Arg Val Leu Gln Arg
305                 310                 315                 320

Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu Leu Met Leu Gly Cys Trp
                325                 330                 335

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

```
Leu Gln Asn Leu Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly
        355                 360                 365


<210>  59
<211>  31
<212>  PRT
<213>  Homo sapiens

<400>  59

Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu Trp
1               5                   10                  15


Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe Ala
            20                  25                  30


<210>  60
<211>  399
<212>  PRT
<213>  Homo sapiens

<400>  60

Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys Ser Asp
1               5                   10                  15


Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro Asn Ser Val
            20                  25                  30


Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn Gln Lys Arg Leu
        35                  40                  45


Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn
    50                  55                  60


Leu Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe
65                  70                  75                  80


Leu Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu
                85                  90                  95


Thr Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu
            100                 105                 110


Ile Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile
```

```
        115                 120                 125

Lys Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr
    130                 135                 140

Cys Leu Asn Glu Ser Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile
145                 150                 155                 160

Pro Asn Cys Gly Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr
                165                 170                 175

Val Glu Glu Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp
            180                 185                 190

Pro Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His
        195                 200                 205

Met Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile
    210                 215                 220

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

Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro
                245                 250                 255

Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile
            260                 265                 270

Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr
        275                 280                 285

Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile Cys Thr Lys Ile His
    290                 295                 300

Val Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro
305                 310                 315                 320

Thr His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr
                325                 330                 335
```

```
Gly Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly
            340                 345                 350


Ile Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp
        355                 360                 365


Tyr Gly Thr Ala Ala Asn Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn
    370                 375                 380


Glu Ile Pro Ser Thr Asp Val Thr Asp Lys Thr Gly Arg Glu His
385                 390                 395


<210>  61
<211>  24
<212>  PRT
<213>  Homo sapiens

<400>  61

Leu Ser Val Tyr Ala Val Val Val Ile Ala Ser Val Val Gly Phe Cys
1               5                   10                  15


Leu Leu Val Met Leu Phe Leu Leu
            20


<210>  62
<211>  384
<212>  PRT
<213>  Homo sapiens

<400>  62

Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys Asp Phe Ser Trp Phe
1               5                   10                  15


Gly Phe Gly Lys Val Lys Ser Arg Gln Gly Val Gly Pro Ala Ser Val
            20                  25                  30


Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro Leu His His Ile Ser Asn
        35                  40                  45


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


Ile Gly Met Thr Lys Ile Pro Val Ile Glu Asn Pro Gln Tyr Phe Gly
```

```
65                  70                  75                  80

Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr Phe Val Gln His Ile Lys
                85                  90                  95

Arg His Asn Ile Val Leu Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly
            100                 105                 110

Lys Val Phe Leu Ala Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys
        115                 120                 125

Ile Leu Val Ala Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg
    130                 135                 140

Lys Asp Phe His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu
145                 150                 155                 160

His Ile Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile
                165                 170                 175

Met Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg
            180                 185                 190

Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro Thr
        195                 200                 205

Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile Ala Ala
    210                 215                 220

Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg Asp Leu Ala
225                 230                 235                 240

Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val Lys Ile Gly Asp
                245                 250                 255

Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp Tyr Tyr Arg Val Gly
            260                 265                 270

Gly His Thr Met Leu Pro Ile Arg Trp Met Pro Pro Glu Ser Ile Met
        275                 280                 285
```

```
Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val Trp Ser Leu Gly Val Val
    290                 295                 300

Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln Pro Trp Tyr Gln Leu Ser
305                 310                 315                 320

Asn Asn Glu Val Ile Glu Cys Ile Thr Gln Gly Arg Val Leu Gln Arg
                325                 330                 335

Pro Arg Thr Cys Pro Gln Glu Val Tyr Glu Leu Met Leu Gly Cys Trp
            340                 345                 350

Gln Arg Glu Pro His Met Arg Lys Asn Ile Lys Gly Ile His Thr Leu
        355                 360                 365

Leu Gln Asn Leu Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly
    370                 375                 380
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<210> 63
<211> 93
<212> DNA
<213> Mus musculus

<400> 63
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ctggtcttgg gcttctggag ggcctctctc gcc 93

<210> 64
<211> 1194
<212> DNA
<213> Mus musculus

<400> 64
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atcgtggcat tcccgaggtt ggaacctaac agcgttgacc cggagaacat cacggaaatt 120

ctcattgcaa accagaaaag gctagaaatc atcaatgaag atgacgttga agcttacgtg 180

gggctgagaa accttacaat tgtggattcc ggcttaaagt ttgtggctta caaagcgttt 240

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tgctcctgcg acatcatgtg gctcaagact ctccaggaga ctaaatccag ccccgacact 420

caggatttgt actgcctcaa tgagagcagc aagaacatgc ccctggcgaa cctgcagata 480

cccaattgtg gtctgccatc tgcacgtctg gctgctccta acctcaccgt ggaggaagga 540

aagtctgtga ccctttcctg cagtgtgggg ggtgacccac tccccacctt gtactgggac 600

gttgggaatt tggtttccaa gcacatgaat gaaacaagcc acacacaggg ctccttaagg 660

ataacgaaca tttcatctga tgacagtgga aagcaaatct cttgtgtggc agaaaacctt 720

gtaggagaag atcaagattc tgtgaacctc actgtgcatt ttgcgccaac tatcacgttt 780

ctcgagtctc caacctcaga tcaccactgg tgcattccat tcactgtgag aggcaacccc 840

aagcctgcgc ttcagtggtt ctacaatggg gccatactga atgagtccaa gtacatctgt 900

actaagatcc acgtcaccaa tcacacggag taccatggct gcctccagct ggataacccc 960

actcatatga ataacggaga ctacaccctg atggccaaga acgagtatgg gaaggatgag 1020

agacagatct ccgctcactt catgggccgg cctggagtcg actacgagac aaacccaaat 1080

taccctgaag tcctctatga agactggacc acgccaactg acattgggga tactacgaac 1140

aaaagtaatg aaatcccctc cacggatgtt gctgaccaaa gcaatcggga gcat 1194

<210> 65
<211> 72
<212> DNA
<213> Mus musculus

<400> 65
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ttgctcctgc tc 72

<210> 66
<211> 1104
<212> DNA
<213> Mus musculus

<400> 66
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gatgactctg ccagcccccc ccaccacatc tccaatggga gtaacactcc atcttcttcg 120

gagggcggtc ccgacgctgt cattattgga atgaccaaga ttcctgttat tgaaaacccc 180

cagtactttg gcatcaccaa cagtcagctc aagccagaca catttgttca gcatatcaag 240

agacacaaca tcgttctgaa gagggaactt ggggaaggag ccttcgggaa agttttcctt 300

gccgagtgct acaacctctg cccagagcag gataagatcc tggtggctgt gaagacgctg 360

aaggacgcca gcgacaatgc acgcaaggac tttcatcggg aagctgagct gctgaccaac 420

ctccagcacg agcacattgt caagttctac ggtgtctgtg tggagggcga cccactcatc 480

atggtctttg agtacatgaa gcacggggac ctcaacaagt tccttagggc acacgggccc 540

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cacatcgctc agcaaatcgc agcaggtatg gtctacctgg cgtcccaaca ctttgtgcac 660

cgtgacctgg ccacccggaa ctgcctggtg ggagagaacc tgctggtgaa aattggggac 720

tttgggatgt cccgagatgt gtacagcacc gactactatc gggtcggtgg ccacacaatg 780

ttgcccatcc gatggatgcc tccagagagc atcatgtaca ggaaattcac caccgagagc 840

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cctcgaacgt gtccccagga ggtgtatgag ctcatgcttg gatgctggca gcgggaacca 1020

cacacccgga agaacatcaa gagcatccac accctccttc agaacttggc caaggcatct 1080

cccgtctacc tggatatcct aggc 1104

<210> 67
<211> 93
<212> DNA
<213> Rattus norvegicus

<400> 67
atgtcgccct ggccgaggtg gcatggaccc gccatggcgc ggctctgggg cttatgcttg 60

ctggtcttgg gcttctggag ggcttctctt gcc 93

<210> 68
<211> 1194
<212> DNA
<213> Rattus norvegicus

<400> 68
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atcgtggcat ttccgaggtt ggaacctaac agcattgacc cagagaacat caccgaaatt 120

ctcattgcaa accagaaaag gttagaaatc atcaatgaag atgatgtcga agcttacgtg 180

gggctgaaaa accttacaat tgtggattcc ggcttaaagt ttgtggctta caaggcgttt 240

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caggatttgt attgcctcaa tgagagcagc aagaataccc ctctggcgaa cctgcagatt 480

cccaattgtg gtctgccgtc tgcacgtctg gccgctccta acctcacggt ggaggaaggg 540

aagtctgtga ccatttcctg cagcgtcggg ggtgacccgc tccccacctt gtactgggac 600

gttgggaatt tggtttccaa acacatgaat gaaacaagcc acacacaggg ctccttaagg 660

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actcatatga ataatggaga ctacacccta atggccaaga atgaatatgg gaaggacgag 1020

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aaaagtaatg agatcccctc cacggatgtt gctgaccaaa ccaatcggga gcat 1194

<210> 69
<211> 72
<212> DNA
<213> Rattus norvegicus

<400> 69
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ctgcttctgc tc 72

<210> 70
<211> 1104
<212> DNA
<213> Rattus norvegicus

<400> 70
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gatgactctg ccagccctct ccaccacatc tccaacggga gcaacactcc gtcttcttcg 120

gagggcgggc ccgatgctgt catcattggg atgaccaaga tccctgtcat tgaaaacccc 180

cagtacttcg gtatcaccaa cagccagctc aagccggaca catttgttca gcacatcaag 240

agacacaaca tcgttctgaa gagggagctt ggagaaggag cctttgggaa agttttccta 300

gcggagtgct ataacctctg ccccgagcag gataagatcc tggtggccgt gaagacgctg 360

aaggacgcca gcgacaatgc tcgcaaggac tttcatcgcg aagccgagct gctgaccaac 420

ctccagcacg agcacattgt caagttctac ggtgtctgtg tggagggcga cccactcatc 480

atggtctttg agtacatgaa gcacggggac ctcaacaagt tccttagggc acacgggcca 540

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cgagacctgg ccacccggaa ctgcttggta ggagagaacc tgctggtgaa aattggggac 720

ttcgggatgt cccgggatgt atacagcacc gactactacc gggttggtgg ccacacaatg 780

ttgcccatcc gatggatgcc tccagagagc atcatgtaca ggaaattcac caccgagagt 840

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cacacaagga agaacatcaa gaacatccac acactccttc agaacttggc gaaggcgtcg 1080

cccgtctacc tggacatcct aggc 1104

<210> 71
<211> 93
<212> DNA
<213> Homo sapiens

<400> 71
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ctggttgtgg gcttctggag ggccgctttc gcc 93

<210> 72
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 72
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atcgtggcat ttccgagatt ggagcctaac agtgtagatc ctgagaacat caccgaaatt 120

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tgctcctgtg acattatgtg gatcaagact ctccaagagg ctaaatccag tccagacact 420

caggatttgt actgcctgaa tgaaagcagc aagaatattc ccctggcaaa cctgcagata 480

cccaattgtg gtttgccatc tgcaaatctg gccgcaccta acctcactgt ggaggaagga 540

aagtctatca cattatcctg tagtgtggca ggtgatccgg ttcctaatat gtattgggat 600

gttggtaacc tggtttccaa acatatgaat gaaacaagcc acacacaggg ctccttaagg 660

ataactaaca tttcatccga tgacagtggg aagcagatct cttgtgtggc ggaaaatctt 720

gtaggagaag atcaagattc tgtcaacctc actgtgcatt ttgcaccaac tatcacattt 780

ctcgaatctc caacctcaga ccaccactgg tgcattccat tcactgtgaa aggcaacccc 840

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aacagaagta atgaaatccc ttccacagac gtcactgata aaaccggtcg ggaacat 1197

<210> 73
<211> 72
<212> DNA
<213> Homo sapiens

<400> 73
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ctgtttctgc tt 72

<210> 74
<211> 1152
<212> DNA
<213> Homo sapiens

<400> 74
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gtaaaatcaa gacaaggtgt tggcccagcc tccgttatca gcaatgatga tgactctgcc 120

agcccactcc atcacatctc caatgggagt aacactccat cttcttcgga aggtggccca 180

gatgctgtca ttattggaat gaccaagatc cctgtcattg aaaatcccca gtactttggc 240

atcaccaaca gtcagctcaa gccagacaca tttgttcagc acatcaagcg acataacatt 300

gttctgaaaa gggagctagg cgaaggagcc tttggaaaag tgttcctagc tgaatgctat 360

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cacatcgtca agttctatgg cgtctgcgtg gagggcgacc ccctcatcat ggtctttgag 540

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atggctgagg gcaacccgcc cacggaactg acgcagtcgc agatgctgca tatagcccag 660

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


Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr Val Gly Leu Arg Asn Leu
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Thr Ile Val Asp Ser Gly Leu Lys Phe Val Ala His Lys Ala Phe Leu
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Lys Asn Ser Asn Leu Gln His Ile Asn Phe Thr Arg Asn Lys Leu Thr
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Ser Leu Ser Arg Lys His Phe Arg His Leu Asp Leu Ser Glu Leu Ile
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Leu Val Gly Asn Pro Phe Thr Cys Ser Cys Asp Ile Met Trp Ile Lys
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Thr Leu Gln Glu Ala Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys
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Val Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met
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Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile Ser
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Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn Leu Val
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Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe Ala Pro Thr
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Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His Trp Cys Ile Pro
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Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu Gln Trp Phe Tyr Asn
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Thr Asn His Thr Glu Tyr His Gly Cys Leu Gln Leu Asp Asn Pro Thr
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His Met Asn Asn Gly Asp Tyr Thr Leu Ile Ala Lys Asn Glu Tyr Gly
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Lys Asp Glu Lys Gln Ile Ser Ala His Phe Met Gly Trp Pro Gly Ile
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Asp Asp Gly Ala Asn Pro Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr
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Val Met Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met
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Lys Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro
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Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu Gly
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Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val Ile Glu
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Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys Pro Asp Thr
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Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu Lys Arg Glu Leu
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Cys Pro Glu Gln Asp Lys Ile Leu Val Ala Val Lys Thr Leu Lys Asp
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Ala Ser Asp Asn Ala Arg Lys Asp Phe His Arg Glu Ala Glu Leu Leu
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Thr Asn Leu Gln His Glu His Ile Val Lys Phe Tyr Gly Val Cys Val
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Glu Gly Asp Pro Leu Ile Met Val Phe Glu Tyr Met Lys His Gly Asp
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Val His Arg Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu
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Asp Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met
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Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp Val
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Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly Lys Gln
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Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys Ile Thr Gln
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ctccatcaca tctccaatgg gagtaacact ccatcttctt cggaaggtgg cccagatgct 1500

gtcattattg gaatgaccaa gatccctgtc attgaaaatc cccagtactt tggcatcacc 1560

aacagtcagc tcaagccaga cacatttgtt cagcacatca agcgacataa cattgttctg 1620

aaaagggagc taggcgaagg agcctttgga aaagtgttcc tagctgaatg ctataacctc 1680

tgtcctgagc aggacaagat cttggtggca gtgaagaccc tgaaggatgc cagtgacaat 1740

gcacgcaagg acttccaccg tgaggccgag ctcctgacca acctccagca tgagcacatc 1800

gtcaagttct atggcgtctg cgtggagggc gacccccтca tcatggtctt tgagtacatg 1860

aagcatgggg acctcaacaa gttcctcagg gcacacggcc ctgatgccgt gctgatggct 1920

gagggcaacc cgcccacgga actgacgcag tcgcagatgc tgcatatagc ccagcagatc 1980

gccgcgggca tggtctacct ggcgtcccag cacttcgtgc accgcgattt ggccaccagg 2040

aactgcctgg tcggggagaa cttgctggtg aaaatcgggg actttgggat gtcccgggac 2100

gtgtacagca ctgactacta cagggtcggt ggccacacaa tgctgcccat tcgctggatg 2160

cctccagaga gcatcatgta caggaaattc acgacggaaa gcgacgtctg gagcctgggg 2220

gtcgtgttgt gggagatttt cacctatggc aaacagccct ggtaccagct gtcaaacaat 2280

gaggtgatag agtgtatcac tcagggccga gtcctgcagc gaccccgcac gtgcccccag 2340

gaggtgtatg agctgatgct ggggtgctgg cagcgagagc cccacatgag gaagaacatc 2400

aagggcatcc ataccctcct tcagaacttg gccaaggcat ctccggtcta cctggacatt 2460

ctaggctag 2469

<210> 78
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 78
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tcctgtgcag cctctggatt cagcttcagt agctttggca tgcactgggt ccgccaggct 120

ccaggcaagg gactggagtg ggtgtcagtt atatcatatg atggaattaa tacatactat 180

acagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acggcctgag agctgaggac acggctcttt attactgtgt gcaagggtca 300

attggaaccg tttttgaata ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 79
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 79

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

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

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


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


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


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


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


Leu Val Thr Val Ser Ser
        115


<210>  80
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  80
ggattcagct tcagtagctt tggc                                              24


<210>  81
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  81

Gly Phe Ser Phe Ser Ser Phe Gly
1               5


<210>  82
<211>  24
<212>  DNA
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<213> Artificial Sequence

<220>
<223> Synthetic

<400> 82
atatcatatg atggaattaa taca 24

<210> 83
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 83

Ile Ser Tyr Asp Gly Ile Asn Thr
1 5

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 84
gtgcaagggt caattggaac cgtttttgaa tac 33

<210> 85
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 85

Val Gln Gly Ser Ile Gly Thr Val Phe Glu Tyr
1 5 10

<210> 86
<211> 321
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic

<400> 86
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcgagtca gggcattagc aattatttag cctggtatca gcagaaacca 120

gggaaagttc ctaaactcct gatctatgct gcatccactt tacaatcagg ggtcccatct 180

cggttcggtg gcagtggatc tgggacagat ttcactctca ccatcagcag cctgcagcct 240

gaagatgttg caacttatta ctgtcaaaag tataccagtg ccccattcac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 87
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 87

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

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

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

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

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Lys Tyr Thr Ser Ala Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 88

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

<220>
<223> Synthetic

<400> 88
cagggcatta gcaattat 18

<210> 89
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 89

Gln Gly Ile Ser Asn Tyr
1 5

<210> 90
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 90
gctgcatcc 9

<210> 91
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 91

Ala Ala Ser
1

<210> 92
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 92
caaaagtata ccagtgcccc attcact 27

<210> 93
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 93

Gln Lys Tyr Thr Ser Ala Pro Phe Thr
1 5

<210> 94
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 94
gaggtgcagc tggtggagtc tgggggaggc ttggtccagc ctgggggtc cctaaaactc 60

tcctgtacag cctctgggtt caccttcagt ggctctgtta ttcactgggt ccgccaggct 120

tccgggaaag ggctggagtg gattggccgt attagaaaca aggctaacag ttacgcgaca 180

gcatatggtg cgtcggtgac aggcaggttc accatctcca gagatgattc aaagaacacg 240

gcgtatctgc aaatgaacag cctgaaaacc gaggacacgg ccgtttatta ctgtactttc 300

ccgggtgtag tgggacgagg aggttttgac tactggggcc agggcaccct ggtcaccgtc 360

tcctca 366

<210> 95
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 95

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


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


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


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


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


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


Tyr Cys Thr Phe Pro Gly Val Val Gly Arg Gly Gly Phe Asp Tyr Trp
            100                 105                 110


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


<210>  96
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  96
gggttcacct tcagtggctc tgtt                                              24


<210>  97
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Synthetic

<400>  97
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Gly Phe Thr Phe Ser Gly Ser Val
1 5

<210> 98
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 98
attagaaaca aggctaacag ttacgcgaca 30

<210> 99
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 99

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

<210> 100
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 100
actttcccgg gtgtagtggg acgaggaggt tttgactac 39

<210> 101
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 101

Thr Phe Pro Gly Val Val Gly Arg Gly Gly Phe Asp Tyr
1 5 10

<210> 102
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 102
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atcaactgca tgtccagcca gagtgtttta ttcagctcca acaataagaa ctacttagct 120

tggtaccaac agaaaccagg acagcctcct aagttgctct tttactgggc atctacccgg 180

gaatccgggg tccctgaccg attcggtggc agcgggtctg ggacagattt ctctctcacc 240

atcaacagcc tgcagactga agatgtggca gtttattact gtctccaata ttatagtatt 300

ccgtggacgt tcggccaagg gaccaaggtg gaaatcaaa 339

<210> 103
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 103

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

Glu Gly Ala Thr Ile Asn Cys Met Ser Ser Gln Ser Val Leu Phe Ser
20 25 30

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

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

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

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

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

Lys

<210> 104
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 104
cagagtgttt tattcagctc caacaataag aactac 36

<210> 105
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 105

Gln Ser Val Leu Phe Ser Ser Asn Asn Lys Asn Tyr
1 5 10

<210> 106
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 106
tgggcatct 9

<210> 107
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 107

Trp Ala Ser
1

<210> 108
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 108
ctccaatatt atagtattcc gtggacg 27

<210> 109
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 109

Leu Gln Tyr Tyr Ser Ile Pro Trp Thr
1 5

<210> 110
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 110
gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggagggtc cctgacactc 60

tcctgtgcag cctctggatt caatttccgt gattatgaaa tgatctgggt ccgccagact 120

ccagggaagg ggctggagtg gatttcatac attagtaata gtggttatac catatactac 180

gcagactctg tgaagggccg attcaccatc tccagagaca acgccaggaa ctcaatatat 240

ctgcaagtga acagcctgag agccgaggac acggctgttt attactgttc gagacgtact 300

actatgattc ggggcattag ggcgtactac tattacggtc tggacgtctg gggccaaggg 360

accacggtca ccgtctcctc a 381

<210> 111
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 111

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

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

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

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

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

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

Ser Arg Arg Thr Thr Met Ile Arg Gly Ile Arg Ala Tyr Tyr Tyr Tyr
100 105 110

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

<210> 112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 112
ggattcaatt tccgtgatta tgaa 24

<210> 113
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 113

Gly Phe Asn Phe Arg Asp Tyr Glu
1 5

<210> 114
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 114
attagtaata gtggttatac cata 24

<210> 115
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 115

Ile Ser Asn Ser Gly Tyr Thr Ile
1 5

<210> 116
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 116
tcgagacgta ctactatgat tcggggcatt agggcgtact actattacgg tctggacgtc 60

<210> 117
<211> 20

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 117

Ser Arg Arg Thr Thr Met Ile Arg Gly Ile Arg Ala Tyr Tyr Tyr Tyr
1 5 10 15

Gly Leu Asp Val
20

<210> 118
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 118
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccgtca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctccgat caccttcggc 300

caagggacac gactggagat taaa 324

<210> 119
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 119

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

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

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

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

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

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

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

<210> 120
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 120
cagagcatta gcagctat   18

<210> 121
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 121

Gln Ser Ile Ser Ser Tyr
1   5

<210> 122
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 122
gctgcatcc 9

<210> 123
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 123

Ala Ala Ser
1

<210> 124
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 124
caacagagtt acagtacccc tccgatcacc 30

<210> 125
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 125

Gln Gln Ser Tyr Ser Thr Pro Pro Ile Thr
1 5 10