SEQUENCE LISTING

<110> ARBOR BIOTECHNOLOGIES, INC.

<120> NOVEL CRISPR DNA TARGETING ENZYMES AND SYSTEMS

<130> A2186-7028WO

<140>
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<150> 62/897,859
<151> 2019-09-09

<160> 290

<170> PatentIn version 3.5

<210> 1
<211> 775
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
gut metagenome sequence

<400> 1
Met Gly Asn Thr Thr Lys Lys Gly Asn Leu Thr Lys Thr Tyr Leu Phe
1 5 10 15

Lys Ala Asn Leu Ser Glu Gln Asp Phe Lys Leu Trp Arg Ser Ile Val
20 25 30

Glu Glu Tyr Gln Arg Tyr Lys Glu Val Leu Ser Lys Trp Val Cys Asp
35 40 45

His Leu Thr Thr Met Lys Ile Gly Asp Ile Leu Pro Tyr Ile Asp Arg
50 55 60

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

Tyr Tyr Ser Leu Cys Glu Glu His Lys Asp Glu Pro Leu Tyr Lys Ile
85 90 95

Phe Gln Phe Asp Ser Asn Cys Arg Asn Asn Ala Leu Tyr Glu Val Ile
100 105 110

```
Arg Lys Ile Asn Cys Asp Leu Tyr Thr Gly Asn Ile Leu Asn Leu Gly
        115                 120                 125

Glu Thr Tyr Tyr Arg Arg Asn Gly Phe Val Lys Arg Val Leu Ala Asn
    130                 135                 140

Tyr Ala Thr Lys Ile Ser Gly Met Lys Pro Ser Val Arg Lys Arg Lys
145                 150                 155                 160

Val Thr Ser Asp Ser Thr Glu Glu Glu Ile Arg Asn Gln Val Val Tyr
                165                 170                 175

Glu Ile Phe Asn Asn Asn Ile Lys Asn Glu Lys Asp Phe Lys Gly Val
            180                 185                 190

Leu Glu Tyr Ala Glu Ser Lys Cys Lys Thr Asn Glu Ala Tyr Val Glu
        195                 200                 205

Arg Ile Arg Leu Leu Tyr Asp Phe Tyr Ile Lys His Thr Asp Glu Ile
    210                 215                 220

Lys Glu Tyr Val Glu Tyr Ile Cys Val Glu Gln Leu Lys Glu Phe Cys
225                 230                 235                 240

Gly Val Lys Val Asn Arg Ser Lys Ser Ser Met Asn Ile Asn Ile Gln
                245                 250                 255

Asn Phe Ser Ile Thr Arg Val Asp Gly Lys Cys Thr Tyr Ile Leu His
            260                 265                 270

Leu Pro Ile Gly Lys Lys Val Tyr Asp Ile Lys Leu Trp Gly Asn Arg
        275                 280                 285

Gln Val Val Leu Asn Val Asp Gly Thr Pro Val Asp Ile Ile Asp Ile
    290                 295                 300

Ile Asn Arg His Gly Glu Ser Ile Asp Ile Ile Phe Lys Asn Gly Asp
305                 310                 315                 320
```

```
Ile Tyr Phe Ser Phe Val Val Ser Glu Asp Phe Lys Lys Asp Asp Phe
                325                 330                 335

Glu Ile Gly Asn Val Val Gly Val Asp Val Asn Thr Lys His Met Leu
            340                 345                 350

Ile Gln Thr Asn Ile Val Asp Asn Gly Asn Val Asp Gly Phe Phe Asn
        355                 360                 365

Ile Tyr Lys Glu Leu Val Asn Asp Lys Glu Phe Ser Glu Cys Val Ser
    370                 375                 380

Lys Glu Asp Leu Glu Leu Phe Lys Glu Leu Ser Lys Tyr Val Ser Phe
385                 390                 395                 400

Cys Pro Ile Glu Cys Gln Phe Leu Phe Thr Arg Tyr Ala Glu Gln Lys
                405                 410                 415

Gly Ile Leu Val Tyr Glu Lys Leu Arg Leu Ala Glu Lys Ile Leu Thr
            420                 425                 430

Ser Val Leu Asp Arg Ser Phe Glu Lys Tyr Asn Gly Ile Asp Cys Asn
        435                 440                 445

Ile Ala Asn Tyr Ile Ser Asn Val Arg Met Leu Arg Ser Lys Cys Lys
    450                 455                 460

Ser Tyr Phe Thr Leu Lys Met Lys Tyr Lys Glu Leu Gln His Lys Tyr
465                 470                 475                 480

Asp Asn Glu Met Gly Tyr Val Asp Thr Phe Ser Asp Ser Cys Val Glu
                485                 490                 495

Met Asp Ser Arg Arg Lys Glu Asn Pro Phe Val Gln Thr Asn Glu Ala
            500                 505                 510

Met Glu Leu Ile Gly Lys Met Glu Ser Val Ala Gln Asp Ile Ile Gly
        515                 520                 525

Cys Arg Asp Asn Ile Ile Thr Tyr Ala Tyr Asn Val Phe Arg Arg Asn
    530                 535                 540
```

```
Gly Tyr Asp Thr Val Gly Leu Glu Asn Leu Glu Ser Ser Gln Phe Glu
545                 550                 555                 560

Arg Phe Ser Ser Val Arg Ser Pro Lys Ser Leu Leu Asn Tyr His His
                565                 570                 575

Leu Lys Gly Lys His Ile Asp Phe Ile Asp Ser Asp Glu Cys Ser Val
            580                 585                 590

Lys Val Asn Lys Asp Leu Tyr Asn Phe Thr Leu Glu Asp Asp Gly Thr
        595                 600                 605

Ile Ser Asp Ile Thr Leu Ser Asp Lys Gly Lys Tyr Arg Asn Asp Leu
    610                 615                 620

Ser Met Phe Tyr Asn Gln Ile Ile Lys Thr Ile His Phe Ala Asp Ile
625                 630                 635                 640

Lys Asp Lys Phe Ile Gln Leu Gly Asn Asn Gly Asn Val Gln Thr Val
                645                 650                 655

Leu Val Pro Ser Tyr Phe Thr Ser Gln Met Asn Ser Lys Thr His Lys
            660                 665                 670

Ile Tyr Val Val Asn Val Lys Asn Glu Arg Thr Gly Lys Thr Glu Gln
        675                 680                 685

Lys Leu Ala Asn Lys Asn Met Val Arg Leu Gly Gln Glu Arg His Ile
    690                 695                 700

Asn Gly Leu Asn Ala Asp Val Asn Ala Ser Met Asn Ile Ala Tyr Ile
705                 710                 715                 720

Val Glu Asn Lys Glu Met Arg Asn Ala Met Cys Thr Asn Pro Lys Ser
                725                 730                 735

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

Asn Ile Met Val Val Glu Leu Lys Lys Met Gly Met Val Glu Val Leu
        755   760   765

Asn Glu Lys Ser Thr Glu Ile
    770   775

<210> 2
<211> 786
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      bovine gut metagenome sequence

<400> 2
Met Ala Gln His Lys Ser Asn Asn Glu Glu Ser Ala Ile Asn Lys Thr
1   5   10   15

Phe Ile Phe Lys Ala Lys Cys Asp Lys Asn Asp Val Ile Ser Leu Trp
            20   25   30

Glu Pro Ala Ala Lys Glu Tyr Cys Asp Tyr Tyr Asn Lys Val Ser Lys
        35   40   45

Trp Ile Ala Asp Asn Leu Ile Thr Met Lys Ile Gly Asp Leu Ala Gln
    50   55   60

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

Lys Lys Lys Asp Leu Pro Leu Tyr Arg Ile Phe Gln Lys Gly Phe Ser
                85   90   95

Ser Gln Cys Ala Asp Asn Ala Leu Tyr Cys Ala Ile Lys Ser Ile Asn
            100   105   110

Pro Glu Asn Tyr Lys Gly Asn Ser Leu Gly Ile Gly Glu Ser Asp Tyr
        115   120   125

Arg Arg Phe Gly Tyr Ile Gln Ser Val Val Ser Asn Phe Arg Thr Lys
    130   135   140

```
Met Ser Ser Leu Lys Ala Thr Val Lys Trp Lys Lys Phe Asp Val Asn
145                 150                 155                 160

Asn Val Asp Asp Glu Thr Leu Lys Ile Gln Thr Ile Tyr Asp Val Asp
                165                 170                 175

Lys Tyr Gly Ile Glu Thr Ala Lys Glu Phe Lys Glu Leu Ile Glu Thr
            180                 185                 190

Leu Lys Thr Arg Val Glu Thr Pro Gln Leu Asn Asp Thr Ile Ala Arg
        195                 200                 205

Leu Glu Cys Leu Cys Asp Tyr Tyr Ser Lys Asn Glu Lys Ala Ile Asn
    210                 215                 220

Asn Glu Ile Glu Thr Met Ala Ile Ala Asp Leu Gln Lys Phe Gly Gly
225                 230                 235                 240

Cys Gln Arg Lys Ser Leu Asn Ala Phe Thr Ile His Lys Gln Asp Ser
                245                 250                 255

Leu Met Glu Lys Val Gly Asn Thr Ser Phe Arg Leu Gln Leu Pro Phe
            260                 265                 270

Arg Lys Lys Thr Tyr Val Ile Asn Leu Leu Gly Asn Arg Gln Val Val
        275                 280                 285

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

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

His Leu Thr Ser Pro Ile Val Phe Asp Lys Asp Val Arg Asp Ile Arg
                325                 330                 335

Asn Val Val Gly Ile Asp Val Asn Ile Lys His Ser Met Leu Ala Thr
            340                 345                 350

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

```
Glu Leu Leu Asn Asp Asp Glu Phe Val Ser Thr Cys Asn Glu Ser Glu
    370                 375                 380

Leu Ala Leu Tyr Arg Gln Met Ser Glu Asn Val Asn Phe Gly Ile Leu
385                 390                 395                 400

Glu Thr Asp Ser Leu Phe Glu Arg Ile Val Asn Gln Ser Lys Gly Gly
                405                 410                 415

Cys Leu Lys Asn Lys Leu Ile Arg Arg Glu Leu Ala Met Gln Lys Val
            420                 425                 430

Phe Glu Arg Ile Thr Lys Thr Asn Lys Asp Gln Asn Ile Val Asp Tyr
        435                 440                 445

Val Asn Tyr Val Lys Met Met Arg Ala Lys Cys Lys Ala Ser Tyr Ile
    450                 455                 460

Leu Lys Glu Lys Tyr Asp Glu Lys Gln Lys Glu Tyr Tyr Val Lys Met
465                 470                 475                 480

Gly Phe Thr Asp Glu Ser Thr Glu Ser Lys Glu Thr Met Asp Lys Arg
                485                 490                 495

Arg Glu Glu Phe Pro Phe Val Asn Thr Asp Thr Ala Lys Glu Leu Leu
            500                 505                 510

Val Lys Gln Asn Asn Ile Arg Gln Asp Ile Ile Gly Cys Arg Asp Asn
        515                 520                 525

Ile Val Thr Tyr Ala Phe Asn Val Phe Lys Asn Asn Glu Tyr Asp Thr
    530                 535                 540

Leu Ser Val Glu Tyr Leu Asp Ser Ser Gln Phe Asp Lys Arg Arg Ile
545                 550                 555                 560

Ala Thr Pro Lys Ser Leu Leu Lys Tyr His Lys Phe Glu Gly Lys Thr
                565                 570                 575
```

```
Lys Asp Glu Val Glu Asn Met Met Lys Ser Glu Lys Leu Ser Asn Ala
            580                 585                 590

Tyr Tyr Thr Phe Lys Tyr Glu Asn Asp Val Val Ser Asp Ile Asp Tyr
        595                 600                 605

Ser Asp Glu Gly Asn Leu Arg Arg Ser Lys Leu Asn Phe Gly Asn Trp
    610                 615                 620

Ile Ile Lys Ser Ile His Phe Ala Asp Ile Lys Asp Lys Phe Val Gln
625                 630                 635                 640

Leu Ser Asn Asn Asn Lys Met Asn Ile Val Phe Cys Pro Ser Ala Phe
                645                 650                 655

Ser Ser Gln Met Asp Ser Ile Thr His Thr Leu Tyr Tyr Val Glu Lys
            660                 665                 670

Ile Thr Lys Asn Lys Lys Gly Lys Glu Lys Lys Lys Tyr Val Leu Ala
        675                 680                 685

Asn Lys Lys Met Val Arg Thr Gln Gln Glu Lys His Ile Asn Gly Leu
    690                 695                 700

Asn Ala Asp Tyr Asn Ser Ala Cys Asn Leu Lys Tyr Ile Ala Leu Asn
705                 710                 715                 720

Asp Glu Leu Arg Asp Lys Met Thr Asp Arg Phe Lys Ala Ser Lys Lys
                725                 730                 735

Ile Lys Thr Met Tyr Asn Ile Pro Ala Tyr Asn Ile Lys Ser Asn Phe
            740                 745                 750

Lys Lys Asn Leu Ser Ala Lys Thr Ile Gln Thr Phe Arg Glu Leu Gly
        755                 760                 765

His Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Met Phe Val Glu Asn
    770                 775                 780

Leu Glu
785
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<210> 3
<211> 774
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
gut metagenome sequence

<400> 3
Met Leu Asn Ile Lys Asn Asn Gly Glu Ser Val Asp Met Asn Thr Ile
1 5 10 15

Glu Leu Ala Met Lys Glu Tyr Asn Arg Tyr Tyr Asn Ile Cys Ser Asp
20 25 30

Trp Ile Cys Asn Asn Leu Met Thr Pro Ile Gly Ser Leu Tyr Gln Tyr
35 40 45

Ile Asp Asp Lys Cys Lys Asn Asn Ala Tyr Ala Gln Asn Leu Ile Ala
50 55 60

Glu Glu Trp Lys Asp Lys Pro Leu Tyr Tyr Met Phe Tyr Lys Gly Tyr
65 70 75 80

Asn Ala Asn Asn Cys Ala Asn Ala Ile Cys Cys Ala Ile Arg Ser Gln
85 90 95

Val Pro Glu Val Asn Lys Ala Glu Asn Ile Leu Asn Leu Ser Tyr Thr
100 105 110

Tyr Tyr Phe Arg Asn Gly Val Ile Lys Ser Val Ile Ser Asn Tyr Ala
115 120 125

Ser Lys Met Arg Ile Leu Ser Asp Lys Gln Ile Lys Tyr Cys Ile Val
130 135 140

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

Leu Lys Arg Arg His Glu Asp Leu Lys Asp Trp Glu Glu Asn Leu Lys
165 170 175

```
Tyr Leu Ile Leu Lys Gly Asn Glu Ser Ala Ile Thr Arg Phe Thr Ile
            180                 185                 190

Leu Lys Asp Phe Tyr Ser Lys Asn Ile Glu Arg Val Lys Glu Glu Arg
        195                 200                 205

Glu Ile Met Ala Ile Ala Glu Leu Lys Asp Phe Gly Gly Cys Arg Arg
    210                 215                 220

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

Asp Ile Lys Val Ser Arg Val Lys Thr Thr His Asn Tyr Thr Glu Leu
                245                 250                 255

Val Asp Asp Tyr Thr Glu Asn Phe Asn Ile Lys Phe Ser Ala Leu Asp
            260                 265                 270

Phe Asn Val Met Gly Arg Arg Asp Val Val Lys Thr Lys Leu Asn Lys
        275                 280                 285

Thr Glu Asp Asp Ser Asn Thr Trp Gly Gly Thr Glu Leu Leu Val Asp
    290                 295                 300

Ile Ile Asn Asn His Gly Cys Ser Leu Thr Phe Lys Leu Val Asp Asp
305                 310                 315                 320

Lys Leu Tyr Val Asp Ile Pro Ile Asp Thr Glu His Ile Asn Lys Thr
                325                 330                 335

Thr Asp Phe Lys Lys Ser Val Gly Ile Asp Val Asn Leu Lys His Ser
            340                 345                 350

Leu Leu Asn Thr Asp Ile Leu Asp Asn Gly Gly Ile Asn Gly Tyr Ile
        355                 360                 365

Asn Ile Tyr Lys Lys Leu Leu Ala Asp Asp Ala Phe Met Ser Ala Cys
    370                 375                 380
```

```
Thr Lys Ala Asp Leu Val Asn Tyr Ile Asp Ile Ala Lys Thr Val Thr
385                 390                 395                 400

Phe Cys Pro Ile Glu Ala Asp Phe Ile Ile Ser Asn Val Val Glu Lys
                405                 410                 415

Tyr Leu His Met Lys Asp Asn Thr Asn Lys Met Glu Ile Ala Phe Ser
            420                 425                 430

Ser Val Leu Met Asn Ile Arg Lys Glu Leu Glu Ile Lys Leu Leu His
        435                 440                 445

Ser Ser Lys Glu Glu Ser Pro Leu Ile Arg Lys Gln Ile Ile Tyr Ile
    450                 455                 460

Asn Cys Ile Ile Cys Leu Arg Asn Glu Leu Lys Gln Tyr Ala Ile Ala
465                 470                 475                 480

Lys His Arg Tyr Tyr Lys Lys Gln Gln Glu Tyr Asp Thr Leu Cys Asp
                485                 490                 495

Thr Leu His Gly Val Asp Tyr Lys Gln Ile His Pro Tyr Ala Gln Ser
            500                 505                 510

Lys Glu Gly Ala Glu Gln Met Lys Lys Met Lys Thr Ile Glu Asn Asn
        515                 520                 525

Leu Ile Ala Asn Arg Asn Asn Ile Ile Glu Tyr Ala Tyr Thr Val Phe
    530                 535                 540

Glu Leu Asn Asn Phe Asp Leu Ile Ala Leu Glu Asn Ile Thr Lys Asp
545                 550                 555                 560

Ile Met Glu Asp Lys Lys Lys Arg Lys Ser Phe Pro Ser Ile Asn Ser
                565                 570                 575

Leu Leu Lys Tyr His Lys Val Ile Asn Cys Thr Glu Asp Asn Ile Asn
            580                 585                 590

Asp Asn Glu Thr Tyr Gln Lys Phe Ala Lys Tyr Tyr Asn Val Ser Tyr
        595                 600                 605
```

```
Glu Asn Gly Lys Val Thr Gly Ala Thr Leu Ser Gln Glu Gly Asn Lys
    610                 615                 620

Val Lys Leu Lys Asp Asp Phe Tyr Asp Lys Leu Leu Lys Val Leu His
625                 630                 635                 640

Phe Thr Ser Ile Lys Asp Tyr Phe Thr Thr Leu Ser Asn Lys Arg Lys
                645                 650                 655

Ile Ala Val Ala His Val Pro Ala Tyr Tyr Thr Ser Gln Ile Asp Ser
            660                 665                 670

Ile Asp Asn Lys Ile Cys Met Ile Lys Ser Thr Asp Lys Asn Gly Lys
        675                 680                 685

Ser Thr Tyr Lys Ile Ala Asp Lys Thr Ile Val Arg Pro Thr Gln Glu
    690                 695                 700

Lys His Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Arg Asn Ile
705                 710                 715                 720

Asn Phe Ile Val Ala Asp Glu Lys Trp Arg Lys Lys Phe Val Arg Pro
                725                 730                 735

Thr Asn Thr Asn Lys Pro Leu Tyr Asn Ser Pro Val Phe Ser Pro Ala
            740                 745                 750

Val Lys Ser Glu Gly Gly Thr Ile Lys Asn Leu Gln Ile Leu Ser Ala
        755                 760                 765

Thr Lys Thr Ile Ile Leu
    770
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<210> 4
<211> 756
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 4
Met Thr Thr Lys Gln Val Lys Ser Ile Val Leu Lys Val Lys Asn Thr
1 5 10 15

Asn Glu Cys Pro Ile Thr Lys Asp Val Ile Asn Glu Tyr Lys Lys Tyr
20 25 30

Tyr Asn Ile Cys Ser Glu Trp Ile Lys Asp Asn Leu Thr Ser Ile Thr
35 40 45

Ile Gly Asp Ile Ala Ser Phe Leu Lys Glu Ala Thr Asn Lys Asp Thr
50 55 60

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

Pro Ile Tyr His Leu Phe Thr Asp Asp Tyr His Glu Lys Ser Ala Asn
85 90 95

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

Gly Asn Ile Leu Asn Leu Ser Glu Thr Tyr Tyr Arg Arg Asn Gly Tyr
115 120 125

Phe Lys Ser Val Val Gly Asn Tyr Arg Thr Lys Ile Arg Thr Leu Asn
130 135 140

Tyr Lys Ile Lys Arg Lys Asn Val Asp Glu Asn Ser Thr Asn Glu Asp
145 150 155 160

Ile Glu Leu Gln Val Met Tyr Glu Ile Ala Lys Arg Lys Leu Asn Ile
165 170 175

Lys Lys Asp Trp Glu Asn Tyr Ile Ser Tyr Ile Glu Asn Val Glu Asn
180 185 190

Ile Asn Ile Lys Asn Ile Asp Arg Tyr Asn Leu Leu Tyr Lys His Phe
195 200 205

```
Cys Glu Asn Glu Ser Thr Ile Asn Cys Lys Met Glu Leu Leu Ser Val
    210                 215                 220

Glu Gln Leu Lys Glu Phe Gly Gly Cys Val Met Lys Gln His Ile Asn
225                 230                 235                 240

Ser Met Thr Ile Asn Ile Gln Asp Phe Lys Ile Glu Asn Lys Glu Asn
                245                 250                 255

Ser Leu Gly Phe Ile Leu Asn Leu Pro Leu Asn Lys Lys Lys Tyr Gln
            260                 265                 270

Ile Glu Leu Trp Gly Asn Arg Gln Ile Lys Lys Gly Asn Lys Asp Asn
        275                 280                 285

Tyr Lys Thr Leu Val Asp Phe Ile Asn Thr Tyr Gly Gln Asn Ile Ile
    290                 295                 300

Phe Thr Ile Lys Asn Asn Lys Ile Tyr Val Val Phe Ser Tyr Glu Cys
305                 310                 315                 320

Glu Leu Lys Glu Lys Glu Ile Asn Phe Asp Lys Ile Val Gly Ile Asp
                325                 330                 335

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

Pro Leu Gln Asp Asn Asn Gln Leu Lys Gly Tyr Ile Asn Leu Tyr Lys
        355                 360                 365

Tyr Leu Leu Glu His Asn Glu Phe Thr Ser Leu Leu Thr Lys Glu Glu
    370                 375                 380

Leu Asp Ile Tyr Lys Glu Ile Ala Lys Gly Val Thr Phe Cys Pro Leu
385                 390                 395                 400

Glu Tyr Asn Leu Leu Phe Thr Arg Ile Glu Asn Lys Gly Gly Lys Ser
                405                 410                 415

Asn Asp Lys Glu Gln Val Leu Ser Lys Leu Leu Tyr Ser Leu Gln Ile
            420                 425                 430
```

```
Lys Leu Lys Asn Glu Asn Lys Ile Gln Glu Tyr Ile Tyr Val Ser Cys
        435                 440                 445

Val Asn Lys Leu Arg Ala Lys Tyr Val Ser Tyr Phe Ile Leu Lys Glu
    450                 455                 460

Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Glu Met Gly Phe Thr
465                 470                 475                 480

Asp Asp Ser Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg Leu Glu
                485                 490                 495

Phe Pro Phe Arg Asn Thr Gln Ile Ala Asn Gly Phe Leu Glu Lys Leu
            500                 505                 510

Ser Asn Val Gln Gln Asp Ile Asn Gly Cys Leu Lys Asn Ile Ile Asn
        515                 520                 525

Tyr Ala Tyr Lys Val Phe Glu Gln Asn Gly Phe Gly Val Ile Ala Leu
    530                 535                 540

Glu Asn Leu Glu Asn Ser Asn Phe Glu Lys Thr Gln Val Leu Pro Thr
545                 550                 555                 560

Ile Lys Ser Leu Leu Glu Tyr His Lys Leu Glu Asn Gln Asn Ile Asn
                565                 570                 575

Asn Ile Asn Ala Ser Asp Lys Val Lys Glu Tyr Ile Glu Lys Glu Tyr
            580                 585                 590

Tyr Glu Leu Thr Thr Asn Glu Asn Asn Glu Ile Val Asp Ala Lys Tyr
        595                 600                 605

Thr Lys Lys Gly Ile Ile Lys Val Lys Lys Ala Asn Phe Phe Asn Leu
    610                 615                 620

Met Met Lys Ser Leu His Phe Ala Ser Asn Lys Asp Glu Phe Ile Leu
625                 630                 635                 640
```

```
Leu Ser Asn Asn Gly Lys Thr Gln Ile Ala Leu Val Pro Ser Glu Tyr
                645                 650                 655

Thr Ser Gln Met Asp Ser Ile Glu His Cys Leu Tyr Val Asp Lys Asn
            660                 665                 670

Gly Lys Lys Val Asp Lys Lys Lys Val Arg Gln Lys Gln Glu Thr His
        675                 680                 685

Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala Asn Asn Ile Lys Tyr
    690                 695                 700

Ile Ile Glu Asn Glu Asn Leu Arg Lys Leu Phe Cys Gly Lys Leu Lys
705                 710                 715                 720

Val Ser Gly Tyr Asn Thr Pro Ile Leu Asp Ala Thr Lys Lys Gly Gln
                725                 730                 735

Phe Asn Ile Leu Ala Glu Leu Lys Lys Gln Asn Lys Ile Lys Ile Phe
            740                 745                 750

Glu Ile Glu Lys
        755
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<210> 5
<211> 746
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 5

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Met Ala Ser His Lys Lys Thr Glu Ser Asn Gln Ile Ile Lys Thr Phe
1               5                   10                  15

Pro Phe Lys Leu Lys Asn Ala Asn Gly Leu Ser Leu Asp Val Leu Asn
            20                  25                  30

Asp Ala Ile Thr Glu Tyr Gln Asn Tyr Tyr Asn Ile Cys Ser Asp Trp
        35                  40                  45
```

```
Ile Lys Asp His Leu Thr Met Lys Ile Ser Glu Leu Tyr Lys Tyr Ile
    50                  55                  60

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

Glu Trp Lys Asp Lys Pro Met Tyr Met Met Phe Lys Lys Gly Tyr Pro
                85                  90                  95

Ala Asn Asn Arg Asp Asn Ala Ile Tyr Glu Thr Leu Asn Thr Cys Asn
            100                 105                 110

Thr Glu His Tyr Thr Gly Asn Ile Leu Asn Phe Pro Asp Thr Tyr Tyr
        115                 120                 125

Arg Arg Phe Gly Tyr Val Ala Ser Thr Ile Ser Asn Tyr Val Thr Lys
    130                 135                 140

Ile Ser Lys Met Ser Thr Gly Ser Arg Ser Lys Asn Ile Ser Asn Asp
145                 150                 155                 160

Ser Asp Val Asp Thr Ile Met Glu Gln Val Ile Tyr Glu Met Glu His
                165                 170                 175

Asn Gly Trp Thr Ser Val Lys Asp Trp Glu Asn Gln Met Glu Tyr Leu
            180                 185                 190

Glu Ser Lys Thr Asp Ser Asn Pro Asn Phe Val Tyr Arg Met Thr Thr
        195                 200                 205

Leu Tyr Glu Phe Tyr Lys Ser His Ile Asp Glu Val Asn Ser Lys Met
    210                 215                 220

Glu Thr Met Ser Ile Asp Leu Leu Ile Lys Phe Gly Gly Cys Arg Arg
225                 230                 235                 240

Lys Asp Ser Lys Lys Ser Met Tyr Ile Met Gly Gly Ser Asn Thr Pro
                245                 250                 255

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

```
Lys Asn Leu Asn Val Asp Val Phe Gly Arg Tyr Asp Val Ile Lys Asp
        275                 280                 285

Asn Thr Leu Leu Val Asp Ile Ile Asn Gly His Gly Ala Ser Phe Val
    290                 295                 300

Leu Lys Ile Ile Asn Asp Glu Ile Tyr Ile Asp Ile Asn Val Ser Val
305                 310                 315                 320

Pro Phe Asp Lys Lys Ile Ala Thr Thr Asn Lys Val Val Gly Ile Asp
                325                 330                 335

Val Asn Ile Lys His Met Leu Leu Ala Thr Asn Ile Leu Asp Asp Gly
            340                 345                 350

Asn Val Lys Gly Tyr Val Asn Ile Tyr Lys Glu Val Ile Asn Asp Ser
        355                 360                 365

Asp Phe Lys Lys Val Cys Asn Ser Thr Val Met Lys Tyr Phe Thr Asp
    370                 375                 380

Phe Ser Lys Phe Val Thr Phe Cys Pro Leu Glu Phe Asp Phe Leu Phe
385                 390                 395                 400

Ser Arg Val Cys Asn Gln Lys Gly Ile Tyr Asn Asp Asn Ser Val Met
                405                 410                 415

Glu Lys Ser Phe Ser Asp Val Leu Asn Lys Leu Lys Trp Asn Phe Ile
            420                 425                 430

Glu Thr Gly Asp Asn Thr Lys Arg Ile Tyr Ile Glu Asn Val Met Lys
        435                 440                 445

Leu Arg Thr Gln Met Lys Ala Tyr Ala Ile Val Lys Asn Ala Tyr Tyr
    450                 455                 460

Lys Gln Gln Ser Glu Tyr Asp Phe Gly Lys Ser Glu Glu Phe Ile Gln
465                 470                 475                 480
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```
Glu His Pro Phe Ser Asn Thr Asp Lys Gly Ile Glu Ile Leu His Lys
                485                 490                 495

Leu Asp Asn Ile Ser Lys Lys Ile Leu Gly Cys Arg Asn Asn Ile Ile
            500                 505                 510

Gln Tyr Ser Tyr Asn Leu Phe Glu Ile Asn Gly Tyr Asp Met Ile Ser
        515                 520                 525

Leu Glu Lys Leu Thr Ser Ser Gln Phe Lys Lys Lys Ser Phe Pro Thr
    530                 535                 540

Val Asn Ser Leu Leu Lys Tyr His Lys Ile Leu Gly Cys Thr Gln Glu
545                 550                 555                 560

Glu Met Glu Lys Lys Asp Ile Tyr Ser Val Ile Lys Lys Gly Tyr Tyr
                565                 570                 575

Asp Ile Ile Phe Asp Asn Asp Val Val Thr Asp Ala Lys Leu Ser Thr
            580                 585                 590

Lys Gly Glu Leu Ser Lys Phe Lys Asp Asp Phe Phe Asn Leu Met Ile
        595                 600                 605

Lys Ser Ile His Phe Ala Asp Ile Lys Asp Tyr Phe Ile Thr Leu Ser
    610                 615                 620

Asn Asn Gly Thr Ala Gly Val Ser Leu Val Pro Ser Phe Phe Thr Ser
625                 630                 635                 640

Gln Met Asp Ser Ile Asp His Lys Ile Tyr Phe Val Gln Asp Asn Lys
                645                 650                 655

Ser Gly Lys Leu Lys Leu Ala Asn Lys His Lys Val Arg Ser Ser Gln
            660                 665                 670

Glu Lys His Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Arg Asn
        675                 680                 685

Ile Ala Tyr Ile Met Glu Asn Thr Glu Cys Arg Asn Met Phe Met Lys
    690                 695                 700
```

```
Gln Ser Arg Thr Asp Lys Ser Leu Tyr Asn Lys Pro Ser Tyr Glu Thr
705                 710                 715                 720


Phe Ile Lys Thr Gln Gly Ser Ala Val Ala Lys Leu Lys Lys Glu Gly
                725                 730                 735


Phe Met Lys Ile Leu Asp Glu Ala Ser Val
            740                 745


<210> 6
<211> 733
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      bovine gut metagenome sequence

<400> 6
Met Ala His Lys Lys Asn Ile Gly Ala Glu Ile Val Lys Thr Tyr Ser
1               5                   10                  15


Phe Lys Val Lys Asn Thr Asn Gly Ile Thr Met Glu Lys Leu Met Asn
            20                  25                  30


Ala Ile Asp Glu Tyr Gln Ser Tyr Tyr Asn Leu Cys Ser Asp Trp Ile
        35                  40                  45


Cys Lys Asn Leu Thr Thr Met Thr Ile Gly Asp Leu Asp Arg Tyr Ile
    50                  55                  60


Pro Glu Lys Ala Lys Asp Asn Ile Tyr Ala Thr Val Leu Leu Asp Glu
65                  70                  75                  80


Val Trp Lys Asn Gln Pro Leu Tyr Lys Ile Phe Gly Lys Lys Tyr Ser
                85                  90                  95


Ser Asn Asn Arg Asn Asn Ala Leu Tyr Cys Ala Leu Ser Ser Val Ile
            100                 105                 110


Asp Met Thr Lys Glu Asn Val Leu Gly Phe Ser Lys Thr His Tyr Ile
        115                 120                 125
```

```
Arg Asn Gly Tyr Ile Leu Asn Val Ile Ser Asn Tyr Ala Ser Lys Leu
    130                 135                 140

Ser Lys Leu Asn Thr Gly Val Lys Ser Arg Ala Ile Lys Glu Thr Ser
145                 150                 155                 160

Asp Glu Ala Thr Ile Ile Glu Gln Val Ile Tyr Glu Met Glu His Asn
                165                 170                 175

Lys Trp Glu Ser Ile Glu Asp Trp Lys Asn Gln Ile Glu Tyr Leu Asn
            180                 185                 190

Ser Lys Thr Asp Tyr Asn Pro Thr Tyr Met Glu Arg Met Lys Thr Leu
        195                 200                 205

Ser Ala Tyr Tyr Ser Thr His Lys Ser Glu Val Asp Ala Lys Met Gln
    210                 215                 220

Glu Met Ala Val Glu Asn Leu Val Lys Phe Gly Gly Cys Arg Arg Asn
225                 230                 235                 240

Asn Ser Lys Lys Ser Met Phe Ile Met Gly Ser Asn Thr Thr Asn Tyr
                245                 250                 255

Thr Ile Ser Tyr Ile Gly Asp Asn Cys Phe Asn Ile Asn Phe Ala Asn
            260                 265                 270

Ile Leu Asn Phe Asp Val Tyr Gly Arg Arg Asp Val Val Lys Asn Gly
        275                 280                 285

Glu Val Leu Val Asp Ile Met Ala Asn His Gly Asp Ser Ile Val Leu
    290                 295                 300

Lys Ile Val Asn Gly Glu Leu Tyr Ala Asp Val Pro Cys Ser Val Thr
305                 310                 315                 320

Leu Asn Lys Val Glu Ser Asn Phe Asp Lys Val Val Gly Ile Asp Val
                325                 330                 335
```

```
Asn Met Lys His Met Leu Leu Ser Thr Ser Val Thr Asp Asn Gly Ser
            340                 345                 350

Ser Asp Phe Val Asn Ile Tyr Lys Glu Met Ser Asn Asn Ala Glu Phe
        355                 360                 365

Met Ala Leu Cys Pro Glu Lys Asp Arg Lys Tyr Tyr Lys Asp Ile Ser
    370                 375                 380

Gln Tyr Val Thr Phe Ala Pro Leu Glu Leu Asp Leu Leu Phe Ser Arg
385                 390                 395                 400

Ile Ser Lys Gln Gly Glu Val Lys Met Glu Lys Ala Tyr Ser Glu Ile
                405                 410                 415

Leu Glu Ser Leu Lys Trp Lys Phe Phe Ala Asn Gly Asp Asn Lys Asn
            420                 425                 430

Arg Ile Tyr Val Glu Ser Ile Gln Lys Ile Arg Gln Gln Ile Lys Ala
        435                 440                 445

Leu Cys Val Ile Lys Asn Ala Tyr Tyr Glu Gln Gln Ser Ala Tyr Asp
    450                 455                 460

Ile Asp Lys Thr Gln Glu Tyr Ile Glu Thr His Pro Phe Ser Leu Thr
465                 470                 475                 480

Glu Lys Gly Met Ser Ile Lys Ser Lys Met Asp Lys Ile Cys Gln Thr
                485                 490                 495

Ile Ile Gly Cys Arg Asn Asn Ile Ile Asp Leu Ala Tyr Ser Phe Phe
            500                 505                 510

Glu Arg Asn Gly Tyr Ser Ile Ile Gly Leu Glu Lys Leu Thr Ser Ser
        515                 520                 525

Gln Phe Lys Asn Thr Lys Ser Met Pro Thr Cys Lys Ser Leu Leu Asn
    530                 535                 540

Leu His Lys Val Leu Gly His Thr Leu Ser Glu Leu Glu Thr Leu Pro
545                 550                 555                 560
```

```
Ile Asn Asp Ile Val Lys Tyr Tyr Thr Phe Thr Thr Asp Asn Glu Gly
                565                 570                 575

Arg Ile Thr Asp Ala Ser Leu Ser Glu Lys Gly Lys Ile Arg Lys Met
            580                 585                 590

Lys Asp Arg Phe Leu Asn Gln Ala Ile Lys Ala Ile His Phe Ala Asp
        595                 600                 605

Val Lys Asp Tyr Phe Ala Thr Leu Ser Asn Asn Gly Gln Thr Gly Ile
    610                 615                 620

Phe Phe Val Pro Ser Gln Phe Thr Ser Gln Met Asp Ser Asn Thr His
625                 630                 635                 640

Asn Leu Tyr Phe Glu Val Asp Lys Asn Gly Gly Leu Lys Met Ala Ser
                645                 650                 655

Lys Asp Lys Thr Arg Pro Lys Gln Glu Tyr His Arg Asn Gly Leu Pro
            660                 665                 670

Ala Asp Tyr Asn Ala Ala Arg Asn Ile Ala Tyr Ile Gly Leu Asp Glu
        675                 680                 685

Thr Met Arg Asn Thr Phe Leu Lys Lys Val Asn Ser Asn Lys Ser Leu
    690                 695                 700

Tyr Asn Gln Pro Ile Tyr Asp Thr Gly Ile Lys Lys Thr Ala Gly Val
705                 710                 715                 720

Phe Ser Arg Met Lys Lys Leu Lys Arg Tyr Glu Ile Ile
                725                 730
```

<210> 7
<211> 744
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 7
Met Ile Lys Ser Ile Lys Leu Lys Val Lys Gly Asp Cys Pro Ile Thr
1   5   10   15

Lys Asp Val Ile Asn Glu Tyr Lys Glu Tyr Tyr Asn Arg Cys Ser Asp
            20   25   30

Trp Ile Lys Asn Asn Leu Thr Ser Ile Thr Ile Gly Glu Ile Gly Lys
        35   40   45

Phe Leu Gln Asp Val Thr Gly Lys Thr Thr Gly Tyr Ile Glu Val Ala
    50   55   60

Leu Ser Asp Lys Trp Lys Asp Lys Pro Met Tyr Tyr Leu Phe Thr Asp
65   70   75   80

Gln Tyr Asp Thr Asn His Ala Asn Asn Leu Leu Tyr Ser Phe Ile Gln
                85   90   95

Glu Asn Asn Leu Asp Gly Tyr Asp Gly Asn Ser Leu Asn Ile Ser Gly
            100   105   110

Thr Tyr Tyr Arg Lys Gln Gly Tyr Phe Lys Leu Val Ser Ser Asn Tyr
        115   120   125

Arg Thr Lys Ile Arg Thr Leu Asn Cys Lys Ile Lys Arg Lys Lys Val
    130   135   140

Asp Val Asp Ser Thr Ser Glu Asp Ile Glu Ser Gln Val Met Tyr Glu
145   150   155   160

Ile Ile Asn Arg Ser Leu Asn Lys Lys Ser Asp Trp Asp Ser Phe Ile
                165   170   175

Ser Tyr Ile Glu Asn Val Glu Asn Pro Asn Ile Asp Ser Ile Asn Arg
            180   185   190

Tyr Thr Leu Leu Arg Asp Tyr Phe Cys Asp Asn Glu Asp Val Ile Lys
        195   200   205

```
Asn Lys Ile Glu Leu Leu Ser Ile Glu Gln Leu Lys Asp Phe Gly Gly
    210                 215                 220

Cys Ile Met Lys Gln His Ile Asn Thr Met Ser Leu Asn Ile Gln His
225                 230                 235                 240

Phe Lys Ile Glu Glu Lys Glu Asn Ser Leu Gly Phe Ile Leu Tyr Leu
                245                 250                 255

Pro Leu Asn Lys Lys Gln Tyr Gln Ile Glu Leu Trp Gly His Arg Gln
            260                 265                 270

Ile Lys Lys Gly Ser Lys Glu Ser Cys Glu Thr Leu Val Asp Phe Ile
        275                 280                 285

Asn Thr Tyr Gly Glu Asn Ile Val Phe Thr Ile Asn Asn Asp Glu Leu
    290                 295                 300

Tyr Val Val Phe Ser Tyr Glu Ser Glu Phe Gly Lys Glu Glu Thr Asn
305                 310                 315                 320

Phe Glu Lys Ser Val Gly Leu Asp Ile Asn Phe Lys His Ala Leu Phe
                325                 330                 335

Val Thr Ser Glu Leu Asp Asn Asp Gln Phe Asp Gly Tyr Ile Asn Leu
            340                 345                 350

Tyr Lys Tyr Ile Leu Ser His Ser Glu Phe Thr Asn Leu Leu Thr Glu
        355                 360                 365

Asp Glu Arg Lys Asp Tyr Glu Glu Leu Ser Lys Val Val Thr Phe Cys
    370                 375                 380

Pro Phe Glu Asn Gln Leu Leu Phe Ala Arg Tyr Asp Lys Met Ser Lys
385                 390                 395                 400

Phe Cys Lys Lys Glu Gln Val Leu Ser Lys Leu Leu Tyr Ser Leu Gln
                405                 410                 415

Lys Lys Leu Lys Asn Glu Asn Arg Thr Lys Glu Tyr Ile Tyr Val Ser
            420                 425                 430
```

```
Cys Val Asn Lys Leu Arg Ala Lys Tyr Ile Ser Tyr Phe Ile Leu Arg
        435                 440                 445

Glu Lys Tyr Asp Glu Lys Asn Lys Glu Tyr Asp Ile Glu Met Gly Phe
    450                 455                 460

Val Asp Asp Ser Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg Phe
465                 470                 475                 480

Glu Asn Pro Phe Arg Asn Thr Leu Val Ala Asn Glu Leu Leu Ala Lys
                485                 490                 495

Met Ser Lys Val Gln Gln Asp Ile Asn Gly Cys Met Ser Asn Ile Ile
            500                 505                 510

Asn Tyr Val Tyr Lys Val Phe Glu Gln Asn Gly Tyr Asn Ile Ile Ala
        515                 520                 525

Leu Glu Asn Leu Glu Asn Ser Asn Phe Glu Lys Arg Gln Val Leu Pro
    530                 535                 540

Thr Ile Lys Ser Leu Leu Lys Tyr His Lys Leu Glu Asn Gln Asn Ile
545                 550                 555                 560

Asn Asp Ile Lys Ala Ser Asp Lys Ile Lys Glu Tyr Ile Glu Asn Gly
                565                 570                 575

Tyr Tyr Ser Phe Thr Thr Asn Glu Asn Asn Glu Ile Val Asp Ala Lys
            580                 585                 590

Tyr Thr Ala Lys Gly Asp Ile Lys Val Lys Asn Ala Lys Phe Phe Asn
        595                 600                 605

Leu Met Met Lys Ile Leu His Phe Ala Ser Ile Lys Asp Glu Phe Val
    610                 615                 620

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

Tyr Thr Ser Gln Met Asp Ser Ile Asp His Cys Ile Tyr Met Thr Glu
645 650 655

Asn Asp Lys Gly Lys Ile Val Lys Val Asp Lys Arg Lys Val Arg Thr
660 665 670

Lys Gln Glu Arg His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
675 680 685

Asn Asn Ile Lys Tyr Ile Val Ser Asn Glu Lys Trp Arg Asn Val Phe
690 695 700

Cys Thr Pro Lys Lys Ala Lys Tyr Asn Thr Pro Ala Leu Asp Ala Thr
705 710 715 720

Lys Lys Gly Gln Phe Arg Ile Leu Asp Asp Met Lys Lys Leu Asn Ala
725 730 735

Thr Lys Leu Leu Glu Ile Glu Lys
740

<210> 8
<211> 754
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 8
Met Tyr Gln Leu Asn Gln Tyr Ile Met Ala Ser His Lys Lys Thr Glu
1 5 10 15

Ser Asn Gln Ile Ile Lys Thr Phe Ser Phe Lys Ile Lys Asn Ala Asn
20 25 30

Gly Leu Ser Leu Asp Val Leu Asn Asp Ala Ile Thr Glu Tyr Gln Asn
35 40 45

Tyr Tyr Asn Ile Cys Ser Asp Trp Ile Lys Asp His Leu Thr Met Lys
50 55 60

```
Ile Ser Glu Leu Tyr Lys Tyr Ile Pro Asp Glu Lys Lys Asn Ser Gly
65                  70                  75                  80

Tyr Ala Leu Thr Leu Ile Ser Asp Glu Trp Lys Asp Lys Pro Met Tyr
                85                  90                  95

Met Met Phe Lys Lys Gly Tyr Pro Ala Asn Asn Arg Asp Asn Ala Ile
            100                 105                 110

Tyr Glu Thr Leu Asn Thr Cys Asn Thr Glu His Tyr Thr Gly Asn Ile
        115                 120                 125

Leu Asn Phe Ser Asp Thr Tyr Tyr Arg Arg Phe Gly Tyr Val Ala Ser
    130                 135                 140

Ala Ile Ser Asn Tyr Val Thr Lys Ile Ser Lys Met Ser Thr Gly Ser
145                 150                 155                 160

Arg Tyr Lys Asn Ile Ser Asn Asp Ser Asp Val Asp Thr Ile Met Glu
                165                 170                 175

Gln Val Ile Tyr Glu Met Glu His Asn Gly Trp Thr Ser Val Lys Asp
            180                 185                 190

Trp Glu Asn Gln Met Glu Tyr Leu Glu Ser Lys Thr Asp Ser Asn Pro
        195                 200                 205

Asn Phe Val Tyr Arg Met Thr Thr Leu Tyr Glu Phe Tyr Lys Ser His
    210                 215                 220

Ile Asp Glu Val Asn Ser Lys Met Glu Thr Met Ser Ile Asp Ser Leu
225                 230                 235                 240

Ile Lys Phe Gly Gly Cys Arg Arg Lys Asp Ser Lys Lys Ser Met Tyr
                245                 250                 255

Ile Met Gly Gly Ser Asn Thr Pro Phe Asp Ile Thr Gln Ile Gly Gly
            260                 265                 270

Asn Ser Leu Asn Ile Lys Phe Ser Lys Asn Leu Asn Val Asp Val Phe
        275                 280                 285
```

```
Gly Arg Tyr Asp Val Ile Lys Asp Asn Thr Leu Leu Val Asp Ile Ile
    290                 295                 300

Asn Gly His Gly Ala Ser Phe Val Leu Lys Ile Ile Asn Asp Glu Ile
305                 310                 315                 320

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

Thr Asn Lys Val Val Gly Ile Asp Val Asn Ile Lys His Met Leu Leu
            340                 345                 350

Ala Thr Asn Ile Leu Asp Asp Gly Asn Val Lys Gly Tyr Val Asn Ile
        355                 360                 365

Tyr Lys Glu Val Ile Asn Asp Ser Asp Phe Lys Lys Val Cys Asn Ser
    370                 375                 380

Thr Val Met Lys Tyr Phe Thr Asp Phe Ser Lys Phe Val Thr Phe Cys
385                 390                 395                 400

Pro Leu Glu Phe Asp Phe Leu Phe Ser Arg Val Cys Asn Gln Lys Gly
                405                 410                 415

Ile Tyr Asn Asp Asn Ser Ala Met Glu Lys Ser Phe Ser Asp Val Leu
            420                 425                 430

Asn Lys Leu Lys Trp Asn Phe Ile Glu Thr Gly Asp Asn Thr Lys Arg
        435                 440                 445

Ile Tyr Ile Glu Asn Val Met Lys Leu Arg Ser Gln Met Lys Ala Tyr
    450                 455                 460

Ala Ile Val Lys Asn Ala Tyr Tyr Lys Gln Gln Ser Glu Tyr Asp Phe
465                 470                 475                 480

Gly Lys Ser Glu Glu Phe Ile Gln Glu His Pro Phe Ser Asn Thr Asp
                485                 490                 495
```

```
Lys Gly Ile Glu Ile Leu His Lys Leu Asp Asn Ile Ser Lys Lys Ile
            500                 505                 510

Leu Gly Cys Arg Asn Asn Ile Ile Gln Tyr Ser Tyr Asn Leu Phe Glu
        515                 520                 525

Ile Asn Gly Tyr Asp Met Ile Ser Leu Glu Lys Leu Thr Ser Ser Gln
    530                 535                 540

Phe Lys Lys Lys Pro Phe Pro Thr Val Asn Ser Leu Leu Lys Tyr His
545                 550                 555                 560

Lys Ile Leu Gly Cys Thr Gln Glu Glu Met Glu Lys Lys Asp Ile Tyr
                565                 570                 575

Ser Val Ile Lys Lys Gly Tyr Tyr Asp Ile Ile Phe Asp Asn Gly Val
            580                 585                 590

Val Ile Asp Ala Lys Leu Ser Ala Lys Gly Glu Leu Ser Lys Phe Lys
        595                 600                 605

Asp Asp Phe Phe Asn Leu Met Ile Lys Ser Ile His Phe Ala Asp Ile
    610                 615                 620

Lys Asp Tyr Phe Ile Thr Leu Ser Asn Asn Gly Thr Ala Gly Val Ser
625                 630                 635                 640

Leu Val Pro Ser Tyr Phe Thr Ser Gln Met Asp Ser Ile Asp His Lys
                645                 650                 655

Ile Tyr Phe Val Gln Asp Asn Lys Ser Gly Lys Leu Lys Leu Ala Asn
            660                 665                 670

Lys His Lys Val Arg Ser Ser Gln Glu Lys His Ile Asn Gly Leu Asn
        675                 680                 685

Ala Asp Tyr Asn Ala Ala Arg Asn Ile Ala Tyr Ile Met Glu Asn Thr
    690                 695                 700

Glu Cys Arg Asn Met Phe Met Lys Gln Ser Arg Thr Asp Lys Ser Leu
705                 710                 715                 720
```

Tyr Asn Lys Pro Ser Tyr Glu Thr Phe Ile Lys Thr Gln Gly Ser Ala
725 730 735

Val Ser Lys Leu Lys Lys Asp Gly Phe Val Lys Ile Leu Asp Glu Ala
740 745 750

Ser Val

<210> 9
<211> 746
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 9
Met Ala Ser His Lys Lys Thr Glu Ser Asn Gln Ile Ile Lys Thr Phe
1 5 10 15

Ser Phe Lys Ile Lys Asn Ala Asn Gly Leu Ser Leu Asp Val Leu Asn
20 25 30

Asp Ala Ile Thr Glu Tyr Gln Asn Tyr Tyr Asn Ile Cys Ser Asp Trp
35 40 45

Ile Lys Asp His Leu Thr Met Lys Ile Ser Glu Leu Tyr Lys Tyr Ile
50 55 60

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

Glu Trp Lys Asp Lys Pro Met Tyr Met Met Phe Lys Lys Gly Tyr Pro
85 90 95

Ala Asn Asn Arg Asp Asn Ala Ile Tyr Glu Thr Leu Asn Thr Cys Asn
100 105 110

Thr Glu His Tyr Thr Gly Asn Ile Leu Asn Phe Ser Asp Thr Tyr Tyr
115 120 125

```
Arg Arg Phe Gly Tyr Val Ala Ser Ala Ile Ser Asn Tyr Val Thr Lys
    130                 135                 140

Ile Ser Lys Met Ser Thr Gly Ser Arg Tyr Lys Asn Ile Ser Asn Asp
145                 150                 155                 160

Ser Asp Val Asp Thr Ile Met Glu Gln Val Ile Tyr Glu Met Glu His
                165                 170                 175

Asn Gly Trp Thr Ser Val Lys Asp Trp Glu Asn Gln Met Glu Tyr Leu
            180                 185                 190

Glu Ser Lys Thr Asp Ser Asn Pro Asn Phe Val Tyr Arg Met Thr Thr
        195                 200                 205

Leu Tyr Glu Phe Tyr Lys Ser His Ile Asp Glu Val Asn Ser Lys Met
    210                 215                 220

Glu Thr Met Ser Ile Asp Ser Leu Ile Lys Phe Gly Gly Cys Arg Arg
225                 230                 235                 240

Lys Asp Ser Lys Lys Ser Met Tyr Ile Met Gly Gly Ser Asn Thr Pro
                245                 250                 255

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

Lys Asn Leu Asn Val Asp Val Phe Gly Arg Tyr Asp Val Ile Lys Asp
        275                 280                 285

Asn Thr Leu Leu Val Asp Ile Ile Asn Gly His Gly Ala Ser Phe Val
    290                 295                 300

Leu Lys Ile Ile Asn Asp Glu Ile Tyr Ile Asp Ile Asn Val Ser Val
305                 310                 315                 320

Pro Phe Asp Lys Lys Ile Ala Thr Thr Asn Lys Val Val Gly Ile Asp
                325                 330                 335
```

```
Val Asn Ile Lys His Met Leu Leu Ala Thr Asn Ile Leu Asp Asp Gly
            340                 345                 350

Asn Val Lys Gly Tyr Val Asn Ile Tyr Lys Glu Val Ile Asn Asp Ser
        355                 360                 365

Asp Phe Lys Lys Val Cys Asn Ser Thr Val Met Lys Tyr Phe Thr Asp
    370                 375                 380

Phe Ser Lys Phe Val Thr Phe Cys Pro Leu Glu Phe Asp Phe Leu Phe
385                 390                 395                 400

Ser Arg Val Cys Asn Gln Lys Gly Ile Tyr Asn Asp Asn Ser Ala Met
                405                 410                 415

Glu Lys Ser Phe Ser Asp Val Leu Asn Lys Leu Lys Trp Asn Phe Ile
            420                 425                 430

Glu Thr Gly Asp Asn Thr Lys Arg Ile Tyr Ile Glu Asn Val Met Lys
        435                 440                 445

Leu Arg Ser Gln Met Lys Ala Tyr Ala Ile Val Lys Asn Ala Tyr Tyr
    450                 455                 460

Lys Gln Gln Ser Glu Tyr Asp Phe Gly Lys Ser Glu Glu Phe Ile Gln
465                 470                 475                 480

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

Leu Asp Asn Ile Ser Lys Lys Ile Leu Gly Cys Arg Asn Asn Ile Ile
            500                 505                 510

Gln Tyr Ser Tyr Asn Leu Phe Glu Ile Asn Gly Tyr Asp Met Ile Ser
        515                 520                 525

Leu Glu Lys Leu Thr Ser Ser Gln Phe Lys Lys Lys Pro Phe Pro Thr
    530                 535                 540

Val Asn Ser Leu Leu Lys Tyr His Lys Ile Leu Gly Cys Thr Gln Glu
545                 550                 555                 560
```

```
Glu Met Glu Lys Lys Asp Ile Tyr Ser Val Ile Lys Lys Gly Tyr Tyr
                565                 570                 575

Asp Ile Ile Phe Asp Asn Gly Val Val Ile Asp Ala Lys Leu Ser Ala
            580                 585                 590

Lys Gly Glu Leu Ser Lys Phe Lys Asp Asp Phe Phe Asn Leu Met Ile
        595                 600                 605

Lys Ser Ile His Phe Ala Asp Ile Lys Asp Tyr Phe Ile Thr Leu Ser
    610                 615                 620

Asn Asn Gly Thr Ala Gly Val Ser Leu Val Pro Ser Tyr Phe Thr Ser
625                 630                 635                 640

Gln Met Asp Ser Ile Asp His Lys Ile Tyr Phe Val Gln Asp Asn Lys
                645                 650                 655

Ser Gly Lys Leu Lys Leu Ala Asn Lys His Lys Val Arg Ser Ser Gln
            660                 665                 670

Glu Lys His Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Arg Asn
        675                 680                 685

Ile Ala Tyr Ile Met Glu Asn Thr Glu Cys Arg Asn Met Phe Met Lys
    690                 695                 700

Gln Ser Arg Thr Asp Lys Ser Leu Tyr Asn Lys Pro Ser Tyr Glu Thr
705                 710                 715                 720

Phe Ile Lys Thr Gln Gly Ser Ala Val Ser Lys Leu Lys Lys Asp Gly
                725                 730                 735

Phe Val Lys Ile Leu Asp Glu Ala Ser Val
            740                 745
```

<210> 10
<211> 745
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 10
Met Ile Lys Ser Ile Gln Leu Lys Val Lys Gly Glu Cys Pro Ile Thr
1 5 10 15

Lys Asp Val Ile Asn Glu Tyr Lys Glu Tyr Tyr Asn Asn Cys Ser Asp
20 25 30

Trp Ile Lys Asn Asn Leu Thr Ser Ile Thr Ile Gly Glu Met Ala Lys
35 40 45

Phe Leu Gln Ser Leu Ser Asp Lys Glu Val Ala Tyr Ile Ser Met Gly
50 55 60

Leu Ser Asp Glu Trp Lys Asp Lys Pro Leu Tyr His Leu Phe Thr Lys
65 70 75 80

Lys Tyr His Thr Lys Asn Ala Asp Asn Leu Leu Tyr Tyr Tyr Ile Lys
85 90 95

Glu Lys Asn Leu Asp Gly Tyr Lys Gly Asn Thr Leu Asn Ile Ser Asn
100 105 110

Thr Ser Phe Arg Gln Phe Gly Tyr Phe Lys Leu Val Val Ser Asn Tyr
115 120 125

Arg Thr Lys Ile Arg Thr Leu Asn Cys Lys Ile Lys Arg Lys Lys Ile
130 135 140

Asp Ala Asp Ser Thr Ser Glu Asp Ile Glu Met Gln Val Met Tyr Glu
145 150 155 160

Ile Ile Lys Tyr Ser Leu Asn Lys Lys Ser Asp Trp Asp Asn Phe Ile
165 170 175

Ser Tyr Ile Glu Asn Val Glu Asn Pro Asn Ile Asp Asn Ile Asn Arg
180 185 190

```
Tyr Lys Leu Leu Arg Glu Cys Phe Cys Glu Asn Glu Asn Met Ile Lys
        195                 200                 205

Asn Lys Leu Glu Leu Leu Ser Val Glu Gln Leu Lys Lys Phe Gly Gly
    210                 215                 220

Cys Ile Met Lys Pro His Ile Asn Ser Met Thr Ile Asn Ile Gln Asp
225                 230                 235                 240

Phe Lys Ile Glu Glu Lys Glu Asn Ser Leu Gly Phe Ile Leu His Leu
                245                 250                 255

Pro Leu Asn Lys Lys Gln Tyr Gln Ile Glu Leu Leu Gly Asn Arg Gln
            260                 265                 270

Ile Lys Lys Gly Thr Lys Glu Ile His Glu Thr Leu Val Asp Ile Thr
        275                 280                 285

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

Tyr Ile Val Phe Ser Tyr Glu Ser Glu Phe Glu Lys Glu Glu Val Asn
305                 310                 315                 320

Phe Ala Lys Thr Val Gly Leu Asp Val Asn Phe Lys His Ala Phe Phe
                325                 330                 335

Val Thr Ser Glu Lys Asp Asn Cys His Leu Asp Gly Tyr Ile Asn Leu
            340                 345                 350

Tyr Lys Tyr Leu Leu Glu His Asp Glu Phe Thr Asn Leu Leu Thr Glu
        355                 360                 365

Asp Glu Arg Lys Asp Tyr Glu Glu Leu Ser Lys Val Val Thr Phe Cys
    370                 375                 380

Pro Phe Glu Asn Gln Leu Leu Phe Ala Arg Tyr Asn Lys Met Ser Lys
385                 390                 395                 400

Phe Cys Lys Lys Glu Gln Val Leu Ser Lys Leu Leu Tyr Ala Leu Gln
                405                 410                 415
```

```
Lys Lys Leu Lys Asp Glu Asn Arg Thr Lys Glu Tyr Ile Tyr Val Ser
            420                 425                 430

Cys Val Asn Lys Leu Arg Ala Lys Tyr Val Ser Tyr Phe Ile Leu Lys
        435                 440                 445

Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Glu Met Gly Phe
    450                 455                 460

Val Asp Asp Ser Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg Thr
465                 470                 475                 480

Glu Tyr Pro Phe Arg Asn Thr Pro Val Ala Asn Glu Leu Leu Ser Lys
                485                 490                 495

Leu Asn Asn Val Gln Gln Asp Ile Asn Gly Cys Leu Lys Asn Ile Ile
            500                 505                 510

Asn Tyr Ile Tyr Lys Ile Phe Glu Gln Asn Gly Tyr Lys Val Val Ala
        515                 520                 525

Leu Glu Asn Leu Glu Asn Ser Asn Phe Glu Lys Lys Gln Val Leu Pro
    530                 535                 540

Thr Ile Lys Ser Leu Leu Lys Tyr His Lys Leu Glu Asn Gln Asn Val
545                 550                 555                 560

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

Tyr Tyr Glu Leu Met Thr Asn Glu Asn Asn Glu Ile Val Asp Ala Lys
            580                 585                 590

Tyr Thr Glu Lys Gly Ala Met Lys Val Lys Asn Ala Asn Phe Phe Asn
        595                 600                 605

Leu Met Met Lys Ser Leu His Phe Ala Ser Val Lys Asp Glu Phe Val
    610                 615                 620
```

```
Leu Leu Ser Asn Asn Gly Lys Thr Gln Ile Ala Leu Val Pro Ser Glu
625                 630                 635                 640

Phe Thr Ser Gln Met Asp Ser Thr Asp His Cys Leu Tyr Met Lys Lys
                645                 650                 655

Asn Asp Lys Gly Lys Leu Val Lys Ala Asp Lys Lys Glu Val Arg Thr
            660                 665                 670

Lys Gln Glu Arg His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
        675                 680                 685

Asn Asn Ile Lys Tyr Ile Val Glu Asn Glu Val Trp Arg Gly Ile Phe
    690                 695                 700

Cys Thr Arg Pro Lys Lys Thr Glu Tyr Asn Val Pro Ser Leu Asp Thr
705                 710                 715                 720

Thr Lys Lys Gly Pro Ser Ala Ile Leu Asn Met Leu Lys Lys Ile Glu
                725                 730                 735

Ala Ile Lys Val Leu Glu Thr Glu Lys
            740                 745
```

<210> 11
<211> 744
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 11

```
Met Ile Lys Ser Ile Val Phe Lys Val Lys Gly Asp Cys Pro Ile Thr
1               5                   10                  15

Lys Asp Val Ile Lys Glu Tyr Lys Glu Tyr Tyr Asn Arg Cys Ser Glu
            20                  25                  30

Trp Ile Lys Asn Asn Leu Thr Ser Ile Thr Ile Gly Glu Ile Gly Lys
        35                  40                  45
```

```
Phe Leu Gln Asp Thr Met Gly Lys Thr His Gly Tyr Ile Lys Val Ala
    50                  55                  60

Leu Ser Asp Glu Trp Lys Asp Lys Pro Met Tyr Tyr Leu Phe Thr Glu
65                  70                  75                  80

Lys Tyr Asp Thr Lys His Ala Asn Asn Leu Leu Tyr Tyr Phe Ile Gln
                85                  90                  95

Glu Asn Asn Leu Asp Arg Tyr Glu Gly Asn Ser Leu Asn Ile Pro Ser
            100                 105                 110

Tyr Tyr Tyr Lys Arg Glu Gly Tyr Phe Lys Leu Val Thr Ser Asn Tyr
        115                 120                 125

Arg Thr Lys Ile Arg Thr Leu Asn Cys Lys Ile Lys Arg Lys Lys Ile
    130                 135                 140

Asp Val Asp Ser Thr Cys Val Asp Ile Glu Asn Gln Val Ile Tyr Glu
145                 150                 155                 160

Ile Ile Lys Lys Gly Leu Asn Lys Lys Ser Asp Trp Asp Asn Tyr Ile
                165                 170                 175

Ser Tyr Ile Glu Asn Ile Glu Met Pro Asn Ile Asp Ser Ile Asn Arg
            180                 185                 190

Tyr Lys Leu Leu Arg Asp Tyr Phe Cys Glu Asn Glu Asn Val Ile Lys
        195                 200                 205

Asn Lys Ile Glu Leu Leu Ser Ile Glu Gln Leu Lys Asn Phe Gly Gly
    210                 215                 220

Cys Ile Met Lys Gln His Ile Asn Thr Met Ile Leu Asn Ile Lys Arg
225                 230                 235                 240

Leu Lys Ile Glu Glu Lys Glu Asn Ser Leu Gly Phe Ile Leu His Leu
                245                 250                 255

Pro Leu Asn Lys Lys Gln Tyr Gln Ile Glu Leu Trp Gly Asn Arg Gln
            260                 265                 270
```

```
Ile Lys Lys Gly Thr Lys Glu Ser Asn Glu Thr Leu Val Asp Phe Ile
        275                 280                 285

Asn Thr Tyr Gly Glu Asp Val Val Phe Thr Ile Lys Lys Asn Glu Leu
    290                 295                 300

Tyr Ala Lys Phe Ser Tyr Glu Cys Glu Phe Glu Lys Glu Glu Thr Asn
305                 310                 315                 320

Phe Glu Lys Ser Val Gly Leu Asp Ile Asn Phe Lys His Ala Leu Phe
                325                 330                 335

Val Thr Ser Glu Leu Asp Asp Asp Gln Phe Tyr Gly Tyr Ile Asn Leu
            340                 345                 350

Tyr Lys Tyr Ile Leu Ser His Ser Glu Phe Thr Asn Leu Leu Thr Glu
        355                 360                 365

Asp Glu Lys Lys Asp Tyr Glu Asp Leu Ser Asn Ala Ile Thr Phe Cys
    370                 375                 380

Pro Phe Glu Asn Gln Leu Leu Phe Thr Arg Tyr Asp Lys Lys Ser Lys
385                 390                 395                 400

Leu Tyr Lys Lys Glu Gln Val Leu Ser Lys Ile Leu Tyr Ser Leu Gln
                405                 410                 415

Lys Lys Leu Lys Asp Glu Asn Arg Lys Gln Glu Tyr Ile Tyr Val Ser
            420                 425                 430

Cys Val Asn Lys Leu Arg Ala Lys Tyr Val Ser Tyr Phe Ile Leu Lys
        435                 440                 445

Glu Lys Tyr Asn Glu Lys Gln Lys Glu Tyr Asp Ile Glu Met Gly Phe
    450                 455                 460

Val Asp Asp Ser Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg Tyr
465                 470                 475                 480
```

```
Glu Tyr Pro Phe Arg Asn Thr Pro Val Ala Asn Glu Leu Leu Glu Lys
                485                 490                 495

Met Asn Asn Val Gln Gln Asp Ile Ser Gly Cys Leu Lys Asn Ile Ile
            500                 505                 510

Asn Tyr Ala Tyr Lys Val Phe Glu Gln Asn Gly Tyr Asn Ile Val Ala
        515                 520                 525

Leu Glu Asn Leu Glu Asn Ser Asn Phe Glu Lys Arg Asn Val Leu Pro
    530                 535                 540

Thr Ile Lys Ser Leu Leu Lys Tyr His Lys Leu Glu Asn Gln Asn Ile
545                 550                 555                 560

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

Tyr Tyr Glu Leu Ile Thr Asn Glu Asn Asn Glu Ile Ile Asp Ala Lys
            580                 585                 590

Tyr Thr Glu Asn Gly Asp Ile Lys Val Lys Asn Ala Arg Phe Phe Asn
        595                 600                 605

Leu Met Met Lys Ser Leu His Phe Ala Ser Ile Lys Asp Glu Phe Val
    610                 615                 620

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

Tyr Thr Ser Gln Met Asp Ser Thr Asp His Cys Ile Tyr Met Thr Glu
                645                 650                 655

Asn Asp Lys Gly Lys Leu Val Lys Val Asp Lys Arg Lys Val Arg Thr
            660                 665                 670

Lys Gln Glu Arg His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
        675                 680                 685

Asn Asn Ile Lys Tyr Ile Val Glu Asn Glu Lys Trp Arg Lys Val Phe
    690                 695                 700
```

```
Cys Ala Pro Gln Lys Ala Lys Tyr Asn Thr Pro Thr Leu Asp Ala Thr
705                 710                 715                 720


Lys Lys Gly Gln Phe Arg Ile Leu Glu Asp Leu Lys Lys Leu Lys Ala
                725                 730                 735


Thr Lys Leu Leu Glu Ile Gly Lys
            740


<210> 12
<211> 745
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      bovine gut metagenome sequence

<400> 12
Met Ile Lys Ser Ile Gln Leu Lys Val Lys Gly Glu Cys Pro Ile Thr
1               5                   10                  15


Lys Asp Val Ile Asn Glu Tyr Lys Glu Tyr Tyr Asn Asn Cys Ser Asp
            20                  25                  30


Trp Ile Lys Asn Asn Leu Thr Ser Ile Thr Ile Gly Glu Met Ala Lys
        35                  40                  45


Phe Leu Gln Ser Leu Ser Asp Lys Glu Val Ala Tyr Ile Ser Met Gly
    50                  55                  60


Leu Ser Asp Glu Trp Lys Asp Lys Pro Leu Tyr His Leu Phe Thr Lys
65                  70                  75                  80


Lys Tyr His Thr Lys Asn Ala Asp Asn Leu Leu Tyr Tyr Tyr Ile Lys
                85                  90                  95


Glu Lys Asn Leu Asp Gly Tyr Lys Gly Asn Thr Leu Asn Ile Ser Asn
            100                 105                 110


Thr Ser Phe Arg Gln Phe Gly Tyr Phe Lys Leu Val Val Ser Asn Tyr
        115                 120                 125
```

```
Arg Thr Lys Ile Arg Thr Leu Asn Cys Lys Ile Lys Arg Lys Lys Ile
    130                 135                 140

Asp Ala Asp Ser Thr Ser Glu Asp Ile Glu Met Gln Val Met Tyr Glu
145                 150                 155                 160

Ile Ile Lys Tyr Ser Leu Asn Lys Lys Ser Asp Trp Asp Asn Phe Ile
                165                 170                 175

Ser Tyr Ile Glu Asn Val Glu Asn Pro Asn Ile Asp Asn Ile Asn Arg
            180                 185                 190

Tyr Lys Leu Leu Arg Glu Cys Phe Cys Glu Asn Glu Asn Met Ile Lys
        195                 200                 205

Asn Lys Leu Glu Leu Leu Ser Val Glu Gln Leu Lys Lys Phe Gly Gly
    210                 215                 220

Cys Ile Met Lys Pro His Ile Asn Ser Met Thr Ile Asn Ile Gln Asp
225                 230                 235                 240

Phe Lys Ile Glu Glu Lys Glu Asn Ser Leu Gly Phe Ile Leu His Leu
                245                 250                 255

Pro Leu Asn Lys Lys Gln Tyr Gln Ile Glu Leu Leu Gly Asn Arg Gln
            260                 265                 270

Ile Lys Lys Gly Thr Lys Glu Ser His Glu Thr Leu Val Asp Ile Thr
        275                 280                 285

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

Tyr Ile Val Phe Ser Tyr Glu Ser Glu Phe Glu Lys Glu Glu Val Asn
305                 310                 315                 320

Phe Ala Lys Thr Val Gly Leu Asp Val Asn Phe Lys His Ala Phe Phe
                325                 330                 335
```

```
Val Thr Ser Glu Lys Asp Asn Cys His Leu Asp Gly Tyr Ile Asn Leu
            340                 345                 350

Tyr Lys Tyr Leu Leu Glu His Asp Glu Phe Thr Asn Leu Leu Thr Glu
        355                 360                 365

Asp Glu Arg Lys Asp Tyr Glu Glu Leu Ser Lys Val Val Thr Phe Cys
    370                 375                 380

Pro Phe Glu Asn Gln Leu Leu Phe Ala Arg Tyr Asn Lys Met Ser Lys
385                 390                 395                 400

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

Lys Lys Leu Lys Asp Glu Asn Arg Thr Lys Glu Tyr Ile Tyr Val Ser
            420                 425                 430

Cys Val Asn Lys Leu Arg Ala Lys Tyr Val Ser Tyr Phe Ile Leu Lys
        435                 440                 445

Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Glu Met Gly Phe
    450                 455                 460

Val Asp Asp Ser Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg Thr
465                 470                 475                 480

Glu Tyr Pro Phe Arg Asn Thr Pro Val Ala Asn Glu Leu Leu Ser Lys
                485                 490                 495

Leu Asn Asn Val Gln Gln Asp Ile Asn Gly Cys Leu Lys Asn Ile Ile
            500                 505                 510

Asn Tyr Ile Tyr Lys Ile Phe Glu Gln Asn Gly Tyr Lys Val Val Ala
        515                 520                 525

Leu Glu Asn Leu Glu Asn Ser Asn Phe Glu Lys Lys Gln Val Leu Pro
    530                 535                 540

Thr Ile Lys Ser Leu Leu Lys Tyr His Lys Leu Glu Asn Gln Asn Val
545                 550                 555                 560
```

```
Asn Asp Ile Lys Ala Ser Asp Lys Val Lys Glu Tyr Ile Glu Asn Gly
                565                 570                 575

Tyr Tyr Glu Leu Met Thr Asn Glu Asn Asn Glu Ile Val Asp Ala Lys
            580                 585                 590

Tyr Thr Glu Lys Gly Ala Met Lys Val Lys Asn Ala Asn Phe Phe Asn
        595                 600                 605

Leu Met Met Lys Ser Leu His Phe Ala Ser Val Lys Asp Glu Phe Val
    610                 615                 620

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

Phe Thr Ser Gln Met Asp Ser Thr Asp His Cys Leu Tyr Met Lys Lys
                645                 650                 655

Asn Asp Lys Gly Lys Leu Val Lys Ala Asp Lys Lys Glu Val Arg Thr
            660                 665                 670

Lys Gln Glu Arg His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
        675                 680                 685

Asn Asn Ile Lys Tyr Ile Val Glu Asn Glu Val Trp Arg Gly Ile Phe
    690                 695                 700

Cys Thr Arg Pro Lys Lys Thr Glu Tyr Asn Val Pro Ser Leu Asp Thr
705                 710                 715                 720

Thr Lys Lys Gly Pro Ser Ala Ile Leu Asn Met Leu Lys Lys Ile Glu
                725                 730                 735

Ala Val Lys Ile Leu Glu Thr Glu Lys
            740                 745
```

<210> 13
<211> 712
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 13
Met Lys Asn Asn Leu Thr Thr Val Thr Ile Gly Glu Met Ala Lys Phe
1 5 10 15

Leu Gln Glu Thr Thr Gly Lys Asn Val Thr Tyr Ile Thr Met Gly Leu
20 25 30

Ser Glu Glu Trp Lys Asp Lys Pro Leu Tyr His Leu Phe Tyr Gly Lys
35 40 45

Tyr His Thr Lys Asn Ala Asp Asn Leu Leu Tyr Tyr Phe Ile Lys Ala
50 55 60

Lys Lys Leu Asp Glu Tyr Asp Gly Asn Met Leu Asn Leu Gly Asp Thr
65 70 75 80

Tyr Tyr Arg Gln Phe Gly Tyr Phe Lys Leu Val Val Ser Asn Tyr Arg
85 90 95

Thr Lys Ile Arg Thr Leu Asn Leu Asn Val Lys Arg Lys Arg Val Asp
100 105 110

Val Asp Ser Thr Ser Glu Asp Ile Glu Ser Gln Val Met Tyr Glu Ile
115 120 125

Val Lys Arg Asn Leu Asn Thr Ile Ser Asp Trp Glu Asn Tyr Ile Ser
130 135 140

Tyr Ile Glu Asp Val Glu Thr Pro Asn Ile Asp Asn Ile Asn Arg Tyr
145 150 155 160

Lys Phe Leu Gln Asn Tyr Phe Cys Glu Asn Glu Glu Asp Ile Lys Asn
165 170 175

Lys Ile Glu Phe Leu Ser Ile Glu Gln Leu Lys Asp Phe Gly Gly Cys
180 185 190

```
Ile Met Lys Pro His Ile Asn Ser Met Thr Ile Asn Ile Gln Asp Phe
        195                 200                 205

Lys Ile Glu Glu Ile Glu Asn Ser Leu Gly Phe Val Leu Gln Leu Pro
    210                 215                 220

Leu Asn Lys Lys Tyr His Gln Ile Glu Leu Tyr Gly Asn Arg Gln Val
225                 230                 235                 240

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

Thr His Gly Glu Asn Ile Val Phe Thr Ile Glu Asn Asn Glu Leu Tyr
            260                 265                 270

Val Val Phe Ser Tyr Glu Tyr Glu Leu Lys Lys Lys Asp Ile Asn Phe
        275                 280                 285

Glu Lys Met Ala Gly Ile Asp Val Asn Phe Lys His Ala Leu Phe Val
    290                 295                 300

Thr Ser Glu Thr Asp Asn Asn Gln Leu Asn His Tyr Ile Asn Leu Tyr
305                 310                 315                 320

Lys His Ile Leu Glu His Asn Glu Phe Thr Thr Leu Leu Thr Asp Ser
                325                 330                 335

Glu Arg Lys Asp Tyr Glu Glu Ile Ala Lys Thr Val Thr Phe Cys Pro
            340                 345                 350

Phe Glu Tyr Gln Leu Leu Phe Thr Arg Phe Asp Lys Asn Ser Asn Ala
        355                 360                 365

Asn Val Lys Glu Gln Ala Leu Ser Lys Ile Leu Tyr Asp Leu Gln Lys
    370                 375                 380

Lys Leu Lys Ser Gln Asn Lys Ile Lys Glu Tyr Ile Tyr Val Ser Cys
385                 390                 395                 400

Val Asn Lys Leu Arg Ala Lys Tyr Val Ser Tyr Phe Ile Leu Lys Glu
                405                 410                 415
```

```
Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Gln Met Gly Phe Val
            420                 425                 430

Asp Asp Ser Thr Glu Ser Lys Ser Ser Met Val Lys Arg Arg Val Glu
        435                 440                 445

Tyr Pro Phe Arg Asn Thr Pro Val Ala Asn Ala Leu Leu Ala Ile Val
    450                 455                 460

Asn Asn Val Gln Gln Asp Ile Asn Gly Cys Leu Lys Asn Ile Ile Asn
465                 470                 475                 480

Tyr Ala Tyr Lys Val Phe Glu Leu Asn Asp Tyr Asn Val Val Ala Leu
                485                 490                 495

Glu Asn Leu Glu Asn Ala Asn Phe Glu Lys Lys Gln Val Ile Pro Thr
            500                 505                 510

Ile Lys Ser Leu Leu Lys Tyr His Lys Leu Glu Met Gln Asn Ile Asn
        515                 520                 525

Asp Ile Lys Ala Asn Asp Thr Ile Lys Lys Tyr Ile Glu Asn Glu Tyr
    530                 535                 540

Tyr Gln Leu Ile Thr Asn Glu Asn Asn Glu Ile Val Asn Ala Ile Tyr
545                 550                 555                 560

Thr Pro Lys Gly Ile Thr Lys Leu Lys Tyr Ala Asn Phe Phe Asn Leu
                565                 570                 575

Leu Met Lys Ser Leu His Phe Ala Ser Ile Lys Asp Glu Phe Ile Leu
            580                 585                 590

Leu Ser Asn Asn Gly Asn Thr Asn Ile Ala Leu Val Pro His Glu Tyr
        595                 600                 605

Thr Ser Gln Met Asp Ser Ile Asp His Cys Ile Tyr Met Val Gln Asn
    610                 615                 620
```

```
Asp Lys Gly Asn Leu Val Lys Ala His Lys Thr Lys Val Arg Thr Lys
625                 630                 635                 640


Gln Glu Lys His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala Asn
                645                 650                 655


Asn Ile Lys Tyr Ile Val Glu Asn Glu Lys Trp Arg Asn Ile Phe Cys
            660                 665                 670


Lys Ile Pro Lys Lys Ile Glu Tyr Asn Thr Pro Val Leu Asp Val Thr
        675                 680                 685


Lys Lys Gly Gln Ser Asn Ile Ile Lys Thr Leu Lys Asn Leu Asn Ala
    690                 695                 700


Thr Lys Ile Leu Glu Ile Lys Lys
705                 710
```

<210> 14
<211> 741
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
terrestrial metagenome sequence

<400> 14

```
Met Lys Lys Ser Ile Lys Phe Lys Val Lys Gly Asn Cys Pro Ile Thr
1               5                   10                  15


Lys Asp Val Ile Asn Glu Tyr Lys Glu Tyr Tyr Asn Lys Cys Ser Asp
            20                  25                  30


Trp Ile Lys Asn Asn Leu Thr Ser Ile Thr Ile Gly Glu Met Ala Lys
        35                  40                  45


Phe Leu Gln Glu Thr Leu Gly Lys Asp Val Ala Tyr Ile Ser Met Gly
    50                  55                  60


Leu Ser Asp Glu Trp Lys Asp Lys Pro Leu Tyr His Leu Phe Thr Lys
65                  70                  75                  80
```

```
Lys Tyr His Thr Asn Asn Ala Asp Asn Leu Leu Tyr Tyr Tyr Ile Lys
                85                  90                  95

Glu Lys Asn Leu Asp Gly Tyr Lys Gly Asn Thr Leu Asn Ile Gly Asn
            100                 105                 110

Thr Phe Phe Arg Gln Phe Gly Tyr Phe Lys Leu Val Val Ser Asn Tyr
        115                 120                 125

Arg Thr Lys Ile Arg Thr Leu Asn Cys Glu Ile Lys Arg Lys Lys Ile
    130                 135                 140

Asp Ala Asp Ser Thr Ser Glu Asp Ile Glu Met Gln Thr Met Tyr Glu
145                 150                 155                 160

Ile Ile Lys His Asn Leu Asn Lys Lys Thr Asp Trp Asp Glu Phe Ile
                165                 170                 175

Ser Tyr Ile Glu Asn Val Glu Asn Pro Asn Ile Asp Asn Ile Asn Arg
            180                 185                 190

Tyr Lys Leu Leu Arg Lys Cys Phe Cys Glu Asn Glu Asn Met Ile Lys
        195                 200                 205

Asn Lys Leu Glu Leu Leu Ser Ile Glu Gln Leu Lys Asn Phe Gly Gly
    210                 215                 220

Cys Ile Met Lys Gln His Ile Asn Ser Met Thr Leu Ile Ile Gln His
225                 230                 235                 240

Phe Lys Ile Glu Glu Lys Glu Asn Ser Leu Gly Phe Ile Leu Asn Leu
                245                 250                 255

Pro Leu Asn Lys Lys Gln Tyr Gln Ile Glu Leu Trp Gly Asn Arg Gln
            260                 265                 270

Val Asn Lys Gly Thr Lys Glu Arg Asp Ala Phe Leu Asn Thr Tyr Gly
        275                 280                 285

Glu Asn Ile Val Phe Ile Ile Asn Asn Asp Glu Leu Tyr Val Val Phe
    290                 295                 300
```

```
Ser Tyr Glu Tyr Glu Leu Glu Lys Glu Glu Ala Asn Phe Val Lys Thr
305                 310                 315                 320

Val Gly Leu Asp Val Asn Phe Lys His Ala Phe Phe Val Thr Ser Glu
                325                 330                 335

Lys Asp Asn Cys His Leu Asp Gly Tyr Ile Asn Leu Tyr Lys Tyr Leu
            340                 345                 350

Leu Glu His Asp Glu Phe Thr Asn Leu Leu Thr Asn Asp Glu Lys Lys
        355                 360                 365

Asp Tyr Glu Glu Leu Ser Lys Val Val Thr Phe Cys Pro Phe Glu Asn
    370                 375                 380

Gln Leu Leu Phe Ala Arg Tyr Asn Lys Met Ser Lys Phe Cys Lys Lys
385                 390                 395                 400

Glu Gln Val Leu Ser Lys Leu Leu Tyr Ala Leu Gln Lys Gln Leu Lys
                405                 410                 415

Asp Glu Asn Arg Thr Lys Glu Tyr Ile Tyr Val Ser Cys Val Asn Lys
            420                 425                 430

Leu Arg Ala Lys Tyr Val Ser Tyr Phe Ile Leu Lys Glu Lys Tyr Tyr
        435                 440                 445

Glu Lys Gln Lys Glu Tyr Asp Ile Glu Met Gly Phe Val Asp Asp Ser
    450                 455                 460

Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg Thr Glu Phe Pro Phe
465                 470                 475                 480

Arg Asn Thr Pro Val Ala Asn Glu Leu Leu Ser Lys Leu Asn Asn Val
                485                 490                 495

Gln Gln Asp Ile Asn Gly Cys Leu Lys Asn Ile Ile Asn Tyr Ile Tyr
            500                 505                 510
```

```
Lys Ile Phe Glu Gln Asn Gly Tyr Lys Ile Val Ala Leu Glu Asn Leu
        515                 520                 525

Glu Asn Ser Asn Phe Glu Lys Lys Gln Val Leu Pro Thr Ile Lys Ser
    530                 535                 540

Leu Leu Lys Tyr His Lys Leu Glu Asn Gln Asn Val Asn Asp Ile Lys
545                 550                 555                 560

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

Ile Thr Asn Glu Asn Asn Glu Ile Val Asp Ala Lys Tyr Thr Glu Lys
            580                 585                 590

Gly Ala Met Lys Val Lys Asn Ala Asn Phe Phe Asn Leu Met Met Lys
        595                 600                 605

Ser Leu His Phe Ala Ser Val Lys Asp Glu Phe Val Leu Leu Ser Asn
    610                 615                 620

Asn Gly Lys Thr Gln Ile Ala Leu Val Pro Ser Glu Phe Thr Ser Gln
625                 630                 635                 640

Met Asp Ser Thr Asp His Cys Leu Tyr Met Lys Lys Asn Asp Lys Gly
                645                 650                 655

Lys Leu Val Lys Ala Asp Lys Lys Glu Val Arg Thr Lys Gln Glu Lys
            660                 665                 670

His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala Asn Asn Ile Lys
        675                 680                 685

Tyr Ile Val Glu Asn Glu Val Trp Arg Glu Ile Phe Cys Thr Arg Pro
    690                 695                 700

Lys Lys Ala Glu Tyr Asn Val Pro Ser Leu Asp Thr Thr Lys Lys Gly
705                 710                 715                 720

Pro Ser Ala Ile Leu His Met Leu Lys Lys Ile Glu Ala Ile Lys Ile
                725                 730                 735
```

Leu Glu Thr Glu Lys
740

<210> 15
<211> 752
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
feces metagenome sequence

<400> 15
Met Ala Lys Ser Ile Met Lys Lys Ser Ile Lys Phe Lys Val Lys Gly
1 5 10 15

Asn Ser Pro Ile Asn Glu Asp Ile Ile Asn Glu Tyr Lys Gly Tyr Tyr
20 25 30

Asn Thr Cys Ser Asn Trp Ile Asn Asn Asn Leu Thr Ser Ile Thr Ile
35 40 45

Gly Glu Met Gly Lys Phe Leu Lys Asp Val Met Arg Lys Thr Thr Gly
50 55 60

Tyr Ile Asp Val Ala Leu Ser Asp Glu Trp Lys Asp Lys Pro Met Tyr
65 70 75 80

Tyr Leu Phe Thr Lys Lys Tyr Asn Pro Lys His Ala Asn Asn Leu Leu
85 90 95

Tyr Tyr Phe Ile Lys Glu Lys Lys Leu Asp Lys Phe Asn Gly Asn Ile
100 105 110

Leu Asn Val Pro Glu Tyr Tyr Tyr Arg Lys Glu Gly Tyr Phe Lys Leu
115 120 125

Val Ala Gly Asn Tyr Arg Thr Lys Ile Asn Thr Leu Asn Phe Lys Ile
130 135 140

Lys Ser Lys Lys Val Asp Ala Asn Ser Leu Ser Glu Asp Ile Glu Met
145 150 155 160

```
Gln Thr Ile Tyr Glu Ile Val Lys Arg Gly Leu Asn Lys Lys Ser Asp
                165                 170                 175

Trp Asp Ser Tyr Ile Ser Tyr Ile Glu Cys Val Gln Asn Pro Asn Ile
            180                 185                 190

Asp Asn Ile Asn Arg Tyr Lys Leu Leu Arg Asp Tyr Phe Cys Glu Asn
        195                 200                 205

Glu Asp Val Ile Lys Asn Lys Ile Glu Ile Leu Ser Ile Glu Gln Ile
    210                 215                 220

Lys Glu Phe Gly Gly Cys Ile Met Lys Pro His Ile Asn Ser Met Thr
225                 230                 235                 240

Phe Gly Ile Gln Lys Phe Lys Ile Glu Glu Ile Glu Asn Ser Leu Gly
                245                 250                 255

Phe Thr Phe Asn Leu Pro Leu Asn Lys Asn Asn Tyr Lys Ile Glu Leu
            260                 265                 270

Trp Gly His Arg Gln Leu Lys Lys Gly Asn Lys Glu Ser Asn Val Asn
        275                 280                 285

Val Ser Leu Asp Asp Phe Ile Asn Thr Tyr Gly Gln Asn Val Val Phe
    290                 295                 300

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

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

Asn Phe Lys His Ser Leu Phe Val Thr Ser Glu Ile Asp Asn Asn Gln
            340                 345                 350

Phe Asp Gly Tyr Ile Asn Leu Tyr Lys Tyr Ile Leu Ser Asn Asn Glu
        355                 360                 365
```

```
Phe Thr Ser Leu Leu Thr Asp Ser Glu Arg Lys Asp Tyr Glu Asp Leu
    370                 375                 380

Ala Asn Ile Val Thr Phe Cys Pro Phe Glu Tyr Gln Leu Leu Phe Ser
385                 390                 395                 400

Arg Tyr Asp Lys Leu Ser Lys Ile Ser Glu Lys Glu Lys Val Leu Ser
                405                 410                 415

Lys Ile Leu Tyr Ser Leu Gln Lys Lys Leu Lys Asn Glu Lys Arg Thr
            420                 425                 430

Lys Glu Tyr Ile Tyr Val Ser Cys Val Asn Lys Leu Arg Ala Lys Tyr
        435                 440                 445

Val Ser Tyr Phe Lys Leu Lys Gln Lys Tyr Asn Glu Lys Gln Lys Glu
    450                 455                 460

Tyr Asp Ile Glu Met Gly Phe Val Asp Asp Ser Thr Glu Ser Lys Glu
465                 470                 475                 480

Ser Met Asp Lys Arg Arg Phe Glu Asn Pro Phe Ile Asn Thr Pro Val
                485                 490                 495

Ala Lys Glu Leu Leu Glu Lys Met Asn Asn Val Lys Gln Asp Ile Asn
            500                 505                 510

Gly Cys Lys Lys Asn Ile Val Val Tyr Ala Tyr Lys Val Leu Glu Gln
        515                 520                 525

Asn Gly Tyr Asn Ile Ile Ala Leu Glu Asn Leu Glu Asn Ser Asn Phe
    530                 535                 540

Glu Lys Ile Arg Val Leu Pro Lys Ile Lys Ser Leu Leu Glu Tyr His
545                 550                 555                 560

Lys Phe Glu Asn Lys Asn Ile Asn Asp Ile Lys Asn Ser Asp Lys Tyr
                565                 570                 575

Lys Glu Phe Ile Glu Pro Gly Tyr Phe Glu Leu Ile Thr Asn Glu Asn
            580                 585                 590
```

```
Asn Glu Ile Ile Asp Ala Lys Tyr Thr Gln Lys Gly Asp Ile Lys Ile
        595                 600                 605

Lys Asn Ala Asp Phe Ile Asn Ile Met Ile Lys Ala Leu Asn Phe Ala
    610                 615                 620

Ser Ile Lys Asp Glu Phe Ile Leu Leu Ser His Asn Gly Lys Ser Gln
625                 630                 635                 640

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

His Cys Ile Tyr Met Thr Lys Asn Asp Lys Gly Lys Leu Val Lys Val
            660                 665                 670

Asp Lys Arg Lys Val Arg Thr Lys Gln Glu Arg His Ile Asn Gly Leu
        675                 680                 685

Asn Ala Asp Phe Asn Ala Ala Cys Asn Ile Lys Tyr Ile Val Thr Asn
    690                 695                 700

Glu Asp Trp Arg Lys Val Phe Cys Ile Lys Pro Lys Lys Glu Asp Tyr
705                 710                 715                 720

Asn Thr Pro Leu Leu Asp Ala Thr Lys Asn Gly Gln Phe Arg Ile Leu
                725                 730                 735

Asp Lys Leu Lys Lys Leu Asn Ala Thr Lys Leu Leu Glu Met Glu Lys
            740                 745                 750
```

<210> 16
<211> 766
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
feces metagenome sequence

<400> 16

```
Met Ala Asn Lys Lys Phe Lys Leu Thr Lys Asn Glu Val Val Lys Ser
1               5                   10                  15
```

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

Thr Leu Gln Glu Tyr Lys Asn Tyr Tyr Asn Lys Val Ser Gln Trp Ile
        35                  40                  45

Asn Asn Asn Leu Thr Lys Met Thr Ile Gly Asp Leu Ile Gln Tyr Ala
    50                  55                  60

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

Tyr Asp Thr Pro Leu Tyr Val Thr Tyr Ala Met Ser Asp Glu Trp Lys
                85                  90                  95

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

Ala Asn Asn Leu Leu Tyr Glu Ala Ile Arg Asn Leu Asn Val Asp Glu
        115                 120                 125

Tyr Asp Gly Asn Gln Leu Asn Phe Asn Ser Thr Tyr Tyr Arg Thr Gln
    130                 135                 140

Gly Tyr Val Asn Arg Val Phe Ser Asn Tyr Arg Thr Lys Ile Asn Thr
145                 150                 155                 160

Leu Asp Ile Lys Ile Lys Lys Ser Lys Val Asp Glu Asn Ser Asp Val
                165                 170                 175

Glu Thr Leu Glu Leu Gln Thr Met Tyr Glu Ile Asn Lys Leu Asn Leu
            180                 185                 190

Lys Thr Asn Lys Asp Trp Glu Glu Arg Leu Gln Tyr Leu Thr Met Gln
        195                 200                 205

Glu Asn Pro Asn Gln Asn Thr Ile Asp Arg Thr Lys Ile Leu Phe Asn
    210                 215                 220
```

```
Tyr Phe Ile Asn Asn Asn Asp Thr Ile Phe Gln Lys Met Glu Glu Leu
225                 230                 235                 240


Ser Ile Lys Gln Leu Thr Glu Phe Gly Gly Cys Lys Met Lys Asp Asn
                245                 250                 255


Thr Thr Ser Met Thr Ile Asn Ile Gln Asp Phe Lys Ile Lys Arg Lys
            260                 265                 270


Glu Asn Ser Ile Gly Tyr Ile Met Thr Ile Pro Phe Asn Lys Lys Asn
        275                 280                 285


Val Asp Val Glu Leu Tyr Gly His Lys Gln Thr Ile Lys Gly His Lys
    290                 295                 300


Asn Ser Tyr Thr Glu Ile Val Asp Ile Val Asn Lys His Gly Asn Thr
305                 310                 315                 320


Ile Thr Phe Lys Ile Lys Asn Asn Gln Leu Phe Ala Ile Ile Thr Ser
                325                 330                 335


Asp Thr Glu Val Thr Lys Pro Glu Pro Gln Tyr Glu Lys Ile Val Gly
            340                 345                 350


Val Asp Val Asn Ile Lys His Thr Leu Met Val Thr Ser Glu Lys Asp
        355                 360                 365


Asn Gly Lys Leu Lys Gly Tyr Ile Asn Leu Tyr Lys Glu Val Leu Lys
    370                 375                 380


Asn Asp Glu Phe Lys Lys Leu Leu Asn Lys Thr Glu Leu Asp Asn Phe
385                 390                 395                 400


Lys Ser Leu Ser Gln Ile Val Thr Phe Cys Pro Ile Glu Tyr Asp Phe
                405                 410                 415


Leu Phe Ser Arg Ile Phe Asp Asp Glu Asn Thr Lys Lys Glu Leu Ala
            420                 425                 430


Phe Ser Asn Val Leu Tyr Asp Ile Gln Lys Gln Leu Lys Asn Thr Asn
        435                 440                 445
```

```
Asn Ile Leu Gln Tyr Asn Tyr Ile Ala Cys Val Asn Lys Leu Arg Ala
    450                 455                 460

Lys Tyr Lys Ala Tyr Phe Val Leu Lys Met Ser Tyr Met Lys Gln Gln
465                 470                 475                 480

Lys Ile Tyr Asp Thr Asn Met Gly Phe Phe Asp Ile Ser Thr Glu Ser
                485                 490                 495

Lys Glu Thr Met Asp Gln Arg Arg Ser Leu Tyr Pro Phe Ile Asn Thr
            500                 505                 510

Glu Ile Ala Gln Asn Ile Ile Thr Lys Met Asn Asn Val Gln Gln Asp
        515                 520                 525

Ile Asn Gly Cys Leu Lys Asn Ile Phe Lys Tyr Thr Tyr Thr Val Phe
    530                 535                 540

Glu Asn Asn Asn Tyr Asp Thr Ile Val Leu Glu Asn Leu Glu Asn Ala
545                 550                 555                 560

Asn Phe Glu Lys His Asn Pro Leu Pro Asn Ile Thr Ser Leu Leu Lys
                565                 570                 575

Tyr His Lys Val Gln Gly Leu Thr Ile Gln Glu Ala Glu Gln His Glu
            580                 585                 590

Lys Val Gly Asn Leu Ile Gln Asn Asp Asn Tyr Ile Phe Gln Leu Asn
        595                 600                 605

Glu Asp Asn Lys Ile Ile Asn Ala Asp Tyr Ser Gln Lys Ala Tyr Tyr
    610                 615                 620

Lys Val Cys Lys Ala Leu Phe Phe Asn Gln Ala Ile Lys Thr Leu His
625                 630                 635                 640

Phe Ala Ser Val Lys Asp Glu Met Ile Lys Leu Ser Asn Asn Asn Lys
                645                 650                 655
```

Val Cys Val Ala Ile Ile Pro Pro Glu Tyr Thr Ser Gln Ile Asp Ser
            660   665   670

Asn Thr His Lys Leu Tyr Phe Ile Asn Lys Asp Gly Lys Leu Leu Lys
        675   680   685

Ala Asp Lys Lys Thr Val Arg Lys Thr Gln Glu Lys His Ile Asn Gly
    690   695   700

Leu Asn Ala Asp Phe Asn Ala Ala Ser Asn Ile Lys Tyr Ile Val Gln
705   710   715   720

Asn Glu Thr Trp Arg Asn Leu Phe Thr Asn Lys Thr Asn Asn Thr Tyr
                725   730   735

Gly Leu Pro Ile Leu Thr Pro Ser Lys Lys Gly Gln Ser Asn Ile Ile
            740   745   750

Thr Gln Leu Met Lys Ile Asn Ala Thr Gln Glu Leu Val Val
        755   760   765

<210> 17
<211> 784
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      sheep gut metagenome sequence

<400> 17
Met Tyr Asn Ser Lys Lys Lys Gly Glu Gly Asp Ile Gln Lys Ser Phe
1   5   10   15

Lys Phe Lys Val Lys Thr Asp Lys Glu Thr Val Glu Leu Phe Arg Lys
            20   25   30

Ala Ala Val Glu Tyr Ser Glu Tyr Tyr Lys Arg Leu Thr Thr Phe Leu
        35   40   45

Cys Glu Arg Leu Thr Asp Met Thr Trp Gly Glu Val Ala Ser Phe Ile
    50   55   60

```
Pro Glu Lys Tyr Arg Lys Asn Glu Tyr Tyr Lys Tyr Leu Ile Lys Glu
65                  70                  75                  80

Glu Asn Lys Asp Leu Pro Leu Tyr Lys Met Phe Thr Lys Ala Ala Ser
                85                  90                  95

Ser Met Phe Ile Asp His Ser Ile Glu Arg Tyr Val Glu Ala Leu Asn
            100                 105                 110

Pro Glu Gly Asn Thr Gly Asn Ile Leu Gly Phe Cys Lys Ser Ser Tyr
        115                 120                 125

Val Arg Gly Gly Tyr Leu Lys Asn Val Val Ser Asn Ile Arg Thr Lys
    130                 135                 140

Phe Ala Thr Leu Lys Thr Gly Ile Lys Tyr Lys Lys Phe Asn Pro Ala
145                 150                 155                 160

Glu Asp Asp Glu Glu Thr Ile Leu Gly Gln Thr Val Phe Glu Met Glu
                165                 170                 175

Lys Arg Gly Leu Glu Phe Lys Cys Asp Phe Glu Lys Thr Ile Lys Tyr
            180                 185                 190

Leu Asn Glu Lys Gly Lys Thr Gln Glu Ala Glu Arg Leu Gln Cys Leu
        195                 200                 205

Met Glu Tyr Phe Ser Thr Asn Thr Asp Lys Ile Asn Glu Tyr Arg Glu
    210                 215                 220

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

Lys Ser Asn Ser Phe Ser Val Thr Leu Glu Lys Ala Asp Ile Lys Glu
                245                 250                 255

Asp Gly Leu Thr Gly Tyr Thr Met Lys Val Ser Lys Lys Leu Lys Glu
            260                 265                 270

Ile His Leu Leu Gly His Arg Arg Val Val Glu Val Val Asn Gly Arg
        275                 280                 285
```

```
Arg Val Asn Leu Val Asp Ile Cys Gly Asp Lys Ser Gly Asp Ser Lys
    290                 295                 300

Val Phe Val Val Asp Gly Asp Asn Leu Tyr Val Cys Ile Ser Ala Pro
305                 310                 315                 320

Val Lys Phe Ser Lys Asn Gly Met Glu Ala Lys Lys Tyr Ile Gly Val
                325                 330                 335

Asp Met Asn Met Lys His Ser Ile Ile Ser Val Ser Asp Asn Ala Ser
            340                 345                 350

Asp Met Lys Gly Phe Leu Asn Ile Tyr Lys Glu Leu Leu Lys Asp Glu
        355                 360                 365

Gly Phe Arg Lys Thr Leu Asn Ala Thr Glu Leu Glu Lys Tyr Glu Lys
    370                 375                 380

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

Glu Arg Ile Val Lys Gln Lys Lys Glu Asn Ser Val Asp Gly Leu Lys
                405                 410                 415

Val Gln Ala Glu Lys Lys Leu Ile Glu Arg Glu Ala Ala Ile Glu Arg
            420                 425                 430

Val Leu Asp Lys Leu Arg Lys Gly Thr Ser Asp Thr Asp Thr Glu Asn
        435                 440                 445

Tyr Ile Asn Tyr Asn Lys Ile Leu Arg Ala Lys Ile Lys Ser Ala Tyr
    450                 455                 460

Ile Leu Lys Asp Lys Tyr Tyr Glu Met Leu Gly Lys Tyr Asp Ser Glu
465                 470                 475                 480

Arg Ala Gly Ser Gly Asp Leu Ser Glu Glu Asn Lys Ile Lys Tyr Lys
                485                 490                 495
```

```
Asp Glu Phe Asn Glu Thr Glu Lys Gly Lys Glu Ile Leu Gly Lys Leu
            500                 505                 510

Asn Asn Val Tyr Lys Asp Ile Ile Gly Cys Arg Asp Asn Ile Val Thr
        515                 520                 525

Tyr Ala Val Asn Leu Phe Ile Arg Asn Gly Tyr Asp Thr Val Ala Leu
    530                 535                 540

Glu Tyr Leu Glu Ser Ser Gln Met Lys Ala Arg Arg Ile Pro Ser Thr
545                 550                 555                 560

Gly Gly Leu Leu Lys Gly His Lys Leu Glu Gly Lys Pro Glu Gly Glu
                565                 570                 575

Val Thr Ala Tyr Leu Lys Ala Asn Lys Ile Pro Lys Ser Tyr Tyr Ser
            580                 585                 590

Phe Glu Tyr Asp Gly Asn Gly Met Leu Thr Asp Val Lys Tyr Ser Asp
        595                 600                 605

Met Gly Glu Lys Ala Arg Gly Arg Asn Arg Phe Lys Asn Leu Val Pro
    610                 615                 620

Lys Phe Leu Arg Trp Ala Ser Ile Lys Asp Lys Phe Val Gln Leu Ser
625                 630                 635                 640

Asn Tyr Lys Asp Ile Gln Met Val Tyr Val Pro Ser Pro Tyr Thr Ser
                645                 650                 655

Gln Thr Asp Ser Arg Thr His Ser Leu Tyr Tyr Ile Glu Thr Val Lys
            660                 665                 670

Val Asp Glu Lys Thr Gly Lys Glu Lys Lys Glu His Ile Val Ala Pro
        675                 680                 685

Lys Glu Ser Val Arg Thr Glu Gln Glu Ser Phe Val Asn Gly Met Asn
    690                 695                 700

Ala Asp Thr Asn Ser Ala Asn Asn Ile Lys Tyr Ile Phe Glu Asn Glu
705                 710                 715                 720
```

Thr Leu Arg Asp Lys Phe Leu Lys Arg Thr Lys Asp Gly Thr Glu Met
725 730 735

Tyr Asn Arg Pro Ala Phe Asp Leu Lys Glu Cys Tyr Lys Lys Asn Ser
740 745 750

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

Gly Lys Leu Asp Glu Asn Gly Asn Phe Ile Glu Asn Glu Cys Asn Lys
770 775 780

<210> 18
<211> 782
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
gut metagenome sequence

<400> 18
Met Ala Gly His Ser Lys Ile Lys Glu Asn His Ile Met Lys Ala Phe
1 5 10 15

Leu Met Lys Val Lys Glu Thr Arg Lys Lys Gln Trp Gln Ser Asn Phe
20 25 30

Ile Arg Ser Glu Ile Ala Lys Phe Thr Asn Tyr Tyr Asn Gly Leu Ser
35 40 45

Lys Phe Ile Ala Asp Arg Leu Leu Asp Asp Met Val Thr Thr Leu Ala
50 55 60

Pro Leu Ile Glu Glu Lys Lys Arg Asn Ser Glu Tyr Tyr Lys Tyr Leu
65 70 75 80

Thr Asn Gly Asp Trp Asp Gly Lys Pro Leu Tyr Phe Ile Phe Lys Glu
85 90 95

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

```
Arg Val Tyr Cys Glu Gln Asn Tyr Thr Gly Asn Gly Phe Gly Leu Ser
        115                 120                 125

Tyr Ser Tyr Tyr Val Val Ile Gly Phe Ala Lys Glu Val Ile Ala Asn
    130                 135                 140

Tyr Arg Ser Ser Phe Gln Lys Pro Lys Val Lys Ile Lys Lys Lys Lys
145                 150                 155                 160

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

Thr Ile Tyr Tyr Glu Phe Asn Glu Lys Lys Asp Ile Gln Lys Trp Lys
            180                 185                 190

Asp Glu Ile Lys Phe Leu Lys Glu Arg Gly Glu Ser Lys Glu Thr Arg
        195                 200                 205

Leu Lys Arg Ile Gln Thr Leu Phe Glu Phe Tyr Lys Asp Lys Ser His
    210                 215                 220

Lys Glu Leu Val Asp Glu Arg Val Ala Asn Leu Val Val Asp Asn Ile
225                 230                 235                 240

Lys Glu Phe Gly Gly Cys Lys Arg Asp Ile Asp Cys Pro Ser Met Gly
                245                 250                 255

Ile Gln Ile Gln His Asn Phe Asp Ile Ser Ile Asn Glu Lys Arg Asn
            260                 265                 270

Gly Tyr Thr Ile Cys Phe Gly Pro Asn Lys Lys Asn Leu Thr Lys Leu
        275                 280                 285

Glu Val Phe Gly Asn Arg Met Val Leu Leu Asn Gly Glu Glu Ile Val
    290                 295                 300

Asp Leu Pro Asn Thr His Gly Glu Lys Leu Thr Leu Ile Asp Arg Gly
305                 310                 315                 320
```

```
Asn Ala Ile Tyr Ala Ala Ile Thr Ala Gln Val Pro Phe Glu Lys His
                325                 330                 335

Met Pro Asp Gly Asn Lys Thr Val Gly Ile Asp Leu Asn Leu Lys His
            340                 345                 350

Ser Val Phe Ala Thr Ser Ile Val Asp Asn Gly Lys Leu Ala Gly Tyr
        355                 360                 365

Ile Ser Ile Tyr Lys Glu Leu Leu Lys Asp Asp Glu Phe Val Lys Tyr
    370                 375                 380

Cys Pro Lys Asp Leu Leu Arg Phe Met Lys Asp Ala Ser Lys Tyr Val
385                 390                 395                 400

Phe Phe Ala Pro Ile Glu Ile Glu Leu Leu Arg Ser Arg Val Ile Tyr
                405                 410                 415

Asn Lys Gly Tyr Ala Cys Val Glu Asn Tyr Glu Asn Val Tyr Lys Ala
            420                 425                 430

Glu Val Ala Phe Val Asn Val Ile Lys Arg Leu Gln Ser Gln Cys Glu
        435                 440                 445

Ala Asn Gly Asp Ala Gln Gly Ala Leu Tyr Met Ser Tyr Leu Ser Lys
    450                 455                 460

Met Arg Ala Gln Leu Lys Asn Tyr Ile Asn Leu Lys Leu Ala Tyr Tyr
465                 470                 475                 480

Asp His Gln Ser Ala Tyr Asp Leu Lys Met Gly Phe Thr Asp Ile Ser
                485                 490                 495

Thr Glu Ser Lys Glu Thr Met Asp Glu Arg Arg Lys Leu Phe Pro Phe
            500                 505                 510

Asn Lys Glu Lys Glu Ala Gln Glu Ile Leu Ala Lys Met Lys Asn Ile
        515                 520                 525

Ser Asn Val Ile Ile Ala Cys Arg Asn Asn Ile Ala Val Tyr Met Tyr
    530                 535                 540
```

```
Lys Met Phe Glu Arg Asn Gly Tyr Asp Phe Ile Gly Leu Glu Lys Leu
545                 550                 555                 560

Glu Ser Ser Gln Met Lys Lys Arg Gln Ser Arg Ser Phe Pro Thr Val
                565                 570                 575

Lys Ser Leu Leu Asn Tyr His Lys Leu Ala Gly Met Thr Met Asp Glu
            580                 585                 590

Ile Lys Lys Gln Glu Val Ser Ser Asn Ile Lys Lys Gly Phe Tyr Asp
        595                 600                 605

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

Lys Gly Asn Val His Phe Ile Glu Asp Glu Phe Tyr Ile Ser Gly Leu
625                 630                 635                 640

Lys Ala Ile His Phe Ala Asp Met Lys Asp Tyr Phe Val Arg Leu Ser
                645                 650                 655

Asn Asn Gly Lys Val Ser Val Ala Leu Val Pro Pro Ser Phe Thr Ser
            660                 665                 670

Gln Met Asp Ser Val Glu His Lys Phe Phe Met Lys Lys Asn Ala Asn
        675                 680                 685

Gly Lys Leu Ile Val Ala Asp Lys Lys Asp Val Arg Ser Cys Gln Glu
    690                 695                 700

Lys His Lys Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Cys Asn
705                 710                 715                 720

Ile Gly Phe Ile Val Glu Asp Asp Tyr Met Arg Glu Ser Leu Leu Gly
                725                 730                 735

Ser Pro Thr Gly Gly Thr Tyr Asp Thr Ala Tyr Phe Asp Thr Lys Ile
            740                 745                 750
```

```
Gln Gly Ser Lys Gly Val Tyr Asp Lys Ile Lys Glu Asn Gly Glu Thr
        755                 760                 765


Tyr Ile Ala Val Leu Ser Asp Asp Val Ile Thr Ala Glu Val
    770                 775                 780


<210> 19
<211> 735
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      human gut metagenome sequence

<400> 19
Met Ala His Lys Lys Asn Val Gly Ala Glu Ile Val Lys Thr Tyr Ser
1               5                   10                  15


Phe Lys Val Lys Asn Thr Asn Gly Ile Thr Met Glu Lys Leu Met Asn
            20                  25                  30


Ala Ile Asp Glu Phe Gln Ser Tyr Tyr Asn Leu Cys Ser Asp Trp Ile
        35                  40                  45


Cys Lys Asn Leu Thr Thr Met Thr Ile Gly Asp Leu Asp Gln Tyr Ile
    50                  55                  60


Pro Glu Lys Ala Lys Gly Asn Thr Tyr Ala Thr Val Leu Leu Asp Glu
65                  70                  75                  80


Ala Trp Lys Asn Gln Pro Leu Tyr Lys Ile Phe Gly Lys Lys Tyr Ser
                85                  90                  95


Ser Asn Asn Arg Asn Asn Ala Leu Tyr Cys Ala Leu Ser Ser Val Ile
            100                 105                 110


Asp Met Thr Lys Glu Asn Val Leu Gly Phe Ser Lys Thr His Tyr Ile
        115                 120                 125


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

```
Ser Lys Leu Asn Thr Gly Val Lys Ser Arg Ala Ile Lys Glu Thr Ser
145                 150                 155                 160

Asp Glu Ala Thr Ile Ile Glu Gln Val Ile Tyr Glu Met Glu His Asn
                165                 170                 175

Lys Trp Glu Ser Ile Glu Asp Trp Lys Asn Gln Ile Glu Tyr Leu Asn
            180                 185                 190

Ser Lys Thr Asp Tyr Asn Pro Thr Tyr Met Glu Arg Met Lys Thr Leu
        195                 200                 205

Ser Ala Tyr Tyr Ser Thr His Lys Ser Glu Val Asp Ala Lys Met Gln
    210                 215                 220

Glu Met Ala Val Glu Asn Leu Val Lys Phe Gly Gly Cys Arg Arg Asn
225                 230                 235                 240

Asn Ser Lys Lys Ser Met Phe Ile Met Gly Ser Asn Thr Thr Asn Tyr
                245                 250                 255

Thr Ile Ser Tyr Ile Gly Gly Asn Ser Phe Asn Ile Asn Phe Ala Asn
            260                 265                 270

Ile Leu Asn Phe Asp Val Tyr Gly Arg Arg Asp Val Val Lys Asn Gly
        275                 280                 285

Glu Val Leu Val Asp Ile Met Ala Asn His Gly Asp Ser Ile Val Leu
    290                 295                 300

Lys Ile Val Asn Gly Glu Leu Tyr Ala Asp Val Pro Cys Ser Val Thr
305                 310                 315                 320

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

Asn Met Lys His Met Leu Leu Ser Thr Ser Ile Thr Asp Asn Gly Ser
            340                 345                 350

Ser Asp Phe Leu Asn Ile Tyr Lys Glu Met Ser Asn Asn Ala Glu Phe
        355                 360                 365
```

```
Met Ala Leu Cys Pro Glu Glu Asp Arg Lys Tyr Tyr Lys Asp Ile Ser
    370                 375                 380

Lys Tyr Val Thr Phe Ala Pro Leu Glu Leu Asp Leu Leu Phe Ser Arg
385                 390                 395                 400

Ile Ser Lys Gln Gly Lys Val Lys Met Glu Lys Val Tyr Ser Glu Ile
                405                 410                 415

Leu Glu Ala Leu Lys Trp Lys Phe Phe Ala Asn Gly Asp Asn Lys Asn
            420                 425                 430

Arg Ile Tyr Val Glu Ser Ile Gln Lys Ile Arg Gln Gln Ile Lys Ala
        435                 440                 445

Leu Cys Val Ile Lys Asn Ala Tyr Tyr Glu Gln Gln Ser Ala Tyr Asp
    450                 455                 460

Ile Asp Lys Thr Gln Glu Tyr Ile Glu Thr His Pro Phe Ser Leu Thr
465                 470                 475                 480

Glu Lys Gly Met Ser Ile Lys Ser Lys Met Asp Lys Ile Cys Gln Thr
                485                 490                 495

Ile Ile Gly Cys Arg Asn Asn Ile Ile Asp Tyr Ala Tyr Ser Phe Phe
            500                 505                 510

Glu Arg Asn Gly Tyr Ser Ile Ile Gly Leu Glu Lys Leu Thr Ser Ser
        515                 520                 525

Gln Phe Glu Lys Thr Lys Ser Met Pro Thr Cys Lys Ser Leu Leu Asn
    530                 535                 540

Phe His Lys Val Leu Gly His Thr Leu Ser Glu Leu Glu Thr Leu Pro
545                 550                 555                 560

Ile Asn Asp Val Val Lys Lys Gly Tyr Tyr Thr Phe Thr Thr Asp Asn
                565                 570                 575
```

```
Glu Gly Lys Ile Thr Asp Ala Ser Leu Ser Glu Lys Gly Lys Val Arg
            580                 585                 590

Lys Met Lys Asp Asp Phe Phe Asn Gln Ala Ile Lys Ala Ile His Phe
        595                 600                 605

Ala Asp Val Lys Asp Tyr Phe Ala Thr Leu Ser Asn Asn Gly Gln Thr
    610                 615                 620

Gly Ile Phe Phe Val Pro Ser Gln Phe Thr Ser Gln Met Asp Ser Asn
625                 630                 635                 640

Thr His Asn Leu Tyr Phe Glu Asn Ala Lys Asn Gly Gly Leu Lys Leu
                645                 650                 655

Ala Pro Lys Tyr Lys Val Arg Gln Thr Gln Glu Tyr His Leu Asn Gly
            660                 665                 670

Leu Pro Ala Asp Tyr Asn Ala Ala Arg Asn Ile Ala Tyr Ile Gly Leu
        675                 680                 685

Asp Glu Thr Met Arg Asn Thr Phe Leu Lys Lys Ala Asn Ser Asn Lys
    690                 695                 700

Ser Leu Tyr Asn Gln Pro Ile Tyr Asp Thr Gly Ile Lys Lys Thr Ala
705                 710                 715                 720

Gly Val Phe Ser Arg Met Lys Lys Leu Lys Arg Tyr Glu Ile Ile
                725                 730                 735
```

<210> 20
<211> 774
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-asian elephant fecal-elephas maximus sequence

<400> 20

```
Met Leu Asn Ile Lys Asn Asn Gly Glu Ser Val Asp Met Asn Thr Ile
1               5                   10                  15
```

```
Glu Leu Ala Met Lys Glu Tyr Asn Arg Tyr Tyr Asn Ile Cys Ser Asp
            20                  25                  30

Trp Ile Cys Asn Asn Leu Met Thr Pro Ile Gly Ser Leu Tyr Gln Tyr
        35                  40                  45

Ile Asp Asp Lys Cys Lys Asn Asn Ala Tyr Ala Gln Asn Leu Ile Ala
    50                  55                  60

Glu Glu Trp Lys Asp Lys Pro Leu Tyr Tyr Met Phe Tyr Lys Gly Tyr
65                  70                  75                  80

Asn Ala Asn Asn Cys Ala Asn Ala Ile Cys Cys Ala Ile Arg Ser Gln
                85                  90                  95

Val Pro Glu Val Asn Lys Ala Glu Asn Ile Leu Asn Leu Ser Tyr Thr
            100                 105                 110

Tyr Tyr Phe Arg Asn Gly Val Ile Lys Ser Val Ile Ser Asn Tyr Ala
        115                 120                 125

Ser Lys Met Arg Ile Leu Ser Asp Lys Gln Ile Lys Tyr Cys Ile Val
    130                 135                 140

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

Leu Lys Arg Arg His Glu Asp Leu Lys Asp Trp Glu Glu Asn Leu Lys
                165                 170                 175

Tyr Leu Ile Leu Lys Gly Asn Glu Ser Ala Ile Thr Arg Phe Thr Ile
            180                 185                 190

Leu Lys Asp Phe Tyr Ser Lys Asn Ile Glu Arg Val Lys Glu Glu Arg
        195                 200                 205

Glu Ile Met Ala Ile Ala Glu Leu Lys Asp Phe Gly Gly Cys Arg Arg
    210                 215                 220

Lys Asp Asp Lys Leu Ser Met Cys Ile Gln Ser Ala Gly Asn Ser Lys
225                 230                 235                 240
```

```
Asp Ile Lys Val Ser Arg Val Lys Thr Thr His Asn Tyr Thr Glu Leu
                245                 250                 255

Val Asp Asp Tyr Thr Glu Asn Phe Asn Ile Lys Phe Ser Ala Leu Asp
            260                 265                 270

Phe Asn Val Met Gly Arg Arg Asp Val Val Lys Thr Lys Leu Asn Lys
        275                 280                 285

Thr Glu Asp Asp Ser Asn Thr Trp Gly Gly Thr Glu Leu Leu Val Asp
    290                 295                 300

Ile Ile Asn Asn His Gly Cys Ser Leu Thr Phe Lys Leu Val Asp Asp
305                 310                 315                 320

Lys Leu Tyr Val Asp Ile Pro Ile Asp Thr Glu His Ile Asn Lys Thr
                325                 330                 335

Thr Asp Phe Lys Lys Ser Val Gly Ile Asp Val Asn Leu Lys His Ser
            340                 345                 350

Leu Leu Asn Thr Asp Ile Leu Asp Asn Gly Gly Ile Asn Gly Tyr Ile
        355                 360                 365

Asn Ile Tyr Lys Lys Leu Leu Ala Asp Asp Ala Phe Met Ser Ala Cys
    370                 375                 380

Thr Lys Ala Asp Leu Val Asn Tyr Ile Asp Ile Ala Lys Thr Val Thr
385                 390                 395                 400

Phe Cys Pro Ile Glu Ala Asp Phe Ile Ile Ser Asn Val Val Glu Lys
                405                 410                 415

Tyr Leu His Met Lys Asp Asn Thr Asn Lys Met Glu Ile Ala Phe Ser
            420                 425                 430

Ser Val Leu Met Asn Ile Arg Lys Glu Leu Glu Ile Lys Leu Leu His
        435                 440                 445
```

```
Ser Ser Lys Glu Glu Ser Pro Leu Ile Arg Lys Gln Ile Ile Tyr Ile
    450                 455                 460

Asn Cys Ile Ile Cys Leu Arg Asn Glu Leu Lys Gln Tyr Ala Ile Ala
465                 470                 475                 480

Lys His Arg Tyr Tyr Lys Lys Gln Gln Glu Tyr Asp Thr Leu Cys Asp
                485                 490                 495

Thr Leu His Gly Val Asp Tyr Lys Gln Ile His Pro Tyr Ala Gln Ser
            500                 505                 510

Lys Glu Gly Ala Glu Gln Met Lys Lys Met Lys Thr Ile Glu Asn Asn
        515                 520                 525

Leu Ile Ala Asn Arg Asn Asn Ile Ile Glu Tyr Ala Tyr Thr Val Phe
    530                 535                 540

Glu Leu Asn Asn Phe Asp Leu Ile Ala Leu Glu Asn Ile Thr Lys Asp
545                 550                 555                 560

Ile Met Glu Asp Lys Lys Lys Arg Lys Ser Phe Pro Ser Ile Asn Ser
                565                 570                 575

Leu Leu Lys Tyr His Lys Val Ile Asn Cys Thr Glu Asp Asn Ile Asn
            580                 585                 590

Asp Asn Glu Thr Tyr Gln Lys Phe Ala Lys Tyr Tyr Asn Val Ser Tyr
        595                 600                 605

Glu Asn Gly Lys Val Thr Gly Ala Thr Leu Ser Gln Glu Gly Asn Lys
    610                 615                 620

Val Lys Leu Lys Asp Asp Phe Tyr Asp Lys Leu Leu Lys Val Leu His
625                 630                 635                 640

Phe Thr Ser Ile Lys Asp Tyr Phe Thr Thr Leu Ser Asn Lys Arg Lys
                645                 650                 655

Ile Ala Val Ala His Val Pro Ala Tyr Tyr Thr Ser Gln Ile Asp Ser
            660                 665                 670
```

Ile Asp Asn Lys Ile Cys Met Ile Lys Ser Thr Asp Lys Asn Gly Lys
675 680 685

Ser Thr Tyr Lys Ile Ala Asp Lys Thr Ile Val Arg Pro Thr Gln Glu
690 695 700

Lys His Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Arg Asn Ile
705 710 715 720

Asn Phe Ile Val Ala Asp Glu Lys Trp Arg Lys Lys Phe Val Arg Pro
725 730 735

Thr Asn Thr Asn Lys Pro Leu Tyr Asn Ser Pro Val Phe Ser Pro Ala
740 745 750

Val Lys Ser Glu Gly Gly Thr Ile Lys Asn Leu Gln Ile Leu Ser Ala
755 760 765

Thr Lys Thr Ile Ile Leu
770

<210> 21
<211> 755
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-cattle and sheep rumen sequence

<400> 21
Met Ala His Val Arg Thr Lys Asn Glu Gly Asn Met Ala Lys Thr Tyr
1 5 10 15

Ser Phe Lys Val Arg Glu Thr Asn Leu Lys Lys Asp Val Met Ile Glu
20 25 30

Tyr Asn Glu Tyr Tyr Asn Arg Leu Ser Asp Trp Ile Cys Gly Asn Leu
35 40 45

Thr Lys Met Thr Ile Gly Glu Leu Ala Glu Leu Val Pro Glu Lys Lys
50 55 60

```
Arg Asn Thr Ser Tyr Tyr Leu Ala Ala Thr Asp Glu Lys Trp Ile Asn
65                  70                  75                  80

Glu Pro Met Tyr Lys Leu Phe Thr Asp Glu Tyr Thr Lys Lys Ser Ser
                85                  90                  95

Phe Thr Asp Pro Leu Val Ala Asn Ser Asn Asn Cys Asp Asn Leu Ile
            100                 105                 110

Leu Thr Ala Thr Asp Val Leu Asn Pro Glu Gly Tyr Glu Gly Asn Leu
        115                 120                 125

Leu Ser Leu Cys Lys Ser Thr Tyr Arg Thr Phe Gly Tyr Ala Lys Gln
    130                 135                 140

Ile Ile Ser Asn Met Lys Thr Lys Ile Gly Ala Leu Lys Pro Asn Val
145                 150                 155                 160

Lys Arg Arg Val Leu Gly Glu Asn Pro Thr Tyr Asp Glu Lys Met Ile
                165                 170                 175

Gln Val Leu Tyr Glu Met Tyr Asn Asn Gly Ile Ala Asp Val Thr Gly
            180                 185                 190

Phe Asn Asp Arg Ile Lys Tyr Leu Lys Lys Gln Glu Thr Pro Asn Glu
        195                 200                 205

Lys Leu Ile Ser Arg Met Lys Met Leu Arg Asp Phe Phe Lys Glu Asn
    210                 215                 220

Arg Asn Asp Ile Met Asp Lys Cys Arg Ile Met Ala Val Glu Gln Leu
225                 230                 235                 240

Val Ser Phe Gly Gly Cys Lys Arg Asn Ile Asn Gly Ala Ser Met Thr
                245                 250                 255

Leu Arg Asn Gln Cys Ile Ser Val Lys Arg Lys Asp Gly Cys Gln Gly
            260                 265                 270
```

```
Tyr Val Val Ala Ile Pro Val Gly Thr Lys Asn Ser Ile Val Phe Asp
        275                 280                 285

Leu Tyr Gly Arg Arg Asp Val Ile Lys Asp Gly Val Glu Leu Val Asp
    290                 295                 300

Val Cys Gly Lys His Thr Asp Thr Ile Thr Ile Lys Ser Val Asn Gly
305                 310                 315                 320

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

Gly Lys Cys Thr Lys Thr Val Gly Ile Asp Val Asn Thr Lys His Met
            340                 345                 350

Leu Ile Gln Thr Ser Val Lys Asp Asn Gly Lys Phe Asp Tyr Tyr Val
        355                 360                 365

Asn Leu Tyr Lys Ile Phe Ala Glu Asp Glu Glu Leu Asn Lys Ile Leu
    370                 375                 380

Gly Asp Asp Glu Val Met Val Asn Ile Lys Lys Asn Ala Glu Asn Leu
385                 390                 395                 400

Ser Phe Leu Pro Leu Glu Met Asp Leu Leu Tyr Ser Arg Ile Leu Asp
                405                 410                 415

Gly Pro Gln Lys Tyr Lys Leu Ala Glu Asp Arg Ile Thr Glu Leu Leu
            420                 425                 430

Lys Gln Trp Gly Ile Asn Phe Asp Ala Gly Cys Met Ser Gln Glu Arg
        435                 440                 445

Ile Tyr Val Gln Cys Val Arg Lys Leu Arg Gly Asn Leu Lys Arg Leu
    450                 455                 460

Leu Tyr Leu Gln Asn Lys Tyr Tyr Glu Ala Gln Gln Glu Tyr Asp Lys
465                 470                 475                 480

Lys Met Gly Phe Asp Asp Lys Ser Thr Asp Ser Lys Glu Thr Met Asp
                485                 490                 495
```

```
Lys Arg Arg Trp Glu Ser Pro Phe Arg Asn Thr Glu Glu Gly Thr Lys
            500                 505                 510

Leu Tyr Asp Glu Ile Asn Thr Tyr Gln Asn Arg Ile Ile Gly Ile Arg
        515                 520                 525

Asn Ser Ile Ile Asp Tyr Ala Tyr Leu Val Leu Glu Tyr Asn Gly Tyr
    530                 535                 540

Asp Asn Leu Ser Leu Glu Tyr Leu Thr Ser Ser Gln Phe Lys Val Asn
545                 550                 555                 560

Lys Thr Phe Pro Thr Thr Asn Ser Leu Leu Lys Tyr His Lys Leu Gln
                565                 570                 575

Gly Lys Thr Lys Thr Glu Ala Glu Lys Cys Asp Ala Tyr Ile Ser His
            580                 585                 590

Lys Ser Lys Tyr Lys Leu Ser Leu Lys Asp Gly Val Ile Asp Ser Ile
        595                 600                 605

Asp Tyr Ser Ala Glu Gly Leu Lys Gln Ile Lys Lys Asp Arg Ser Arg
    610                 615                 620

Asn Ile Ile Ile Lys Ala Ile His Phe Ala Asp Val Lys Asp Arg Phe
625                 630                 635                 640

Val Leu Ser Ser Asn Asn Gly Asn Ala Ser Val Thr Phe Val Pro Ser
                645                 650                 655

Tyr His Thr Ser Gln Ile Asp Ser Thr Asp His Lys Met Phe Val Thr
            660                 665                 670

Asn Lys Gly Lys Ile Val Asp Lys Arg Lys Val Arg Gln Ile Gln Glu
        675                 680                 685

Thr His Val Asn Gly Leu Asn Ser Asp Phe Asn Ala Ala Arg Asn Ile
    690                 695                 700
```

```
Gln Tyr Ile Ser Glu Asn Glu Glu Trp Arg Asn Ala Leu Cys Lys Pro
705                 710                 715                 720


Thr Glu Asn Met Tyr Asn Glu Pro Ile Tyr Val Pro Leu Val Lys Ser
                725                 730                 735


Gln Asn Gly Met Phe Lys Ala Ile Lys Lys Leu Gly Ala Thr Lys Ile
            740                 745                 750


Trp Gln Glu
        755
```

<210> 22
<211> 789
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-cattle and sheep rumen sequence

<400> 22

```
Met Ala His Arg Asn Lys Asn Leu Ala Glu Asn Cys Ile Asn Lys Thr
1               5                   10                  15


Phe Ser Phe Lys Val Lys Ala Glu Lys Glu Glu Ile Asn Ser Lys Trp
            20                  25                  30


Ile Pro Ala Ile Lys Glu Tyr Thr Ala Tyr Tyr Asn Arg Ile Ser Asp
        35                  40                  45


Trp Ile Cys Asp Arg Leu Thr Asn Thr Thr Val Gly Glu Leu Ile Gly
    50                  55                  60


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


Lys Asp Gly Ser Ser Glu Lys Tyr Arg Asn Leu Pro Leu Tyr Cys Met
                85                  90                  95


Phe Lys Lys Asn Phe Pro Ala Thr Thr Ala Asp Asn Ile Met Tyr Gln
            100                 105                 110
```

```
Val Ile Glu Lys Leu Gly Val Asp Lys Tyr Asn Gly Asn Ser Leu Gly
        115                 120                 125

Leu Ser Gly Thr Tyr Tyr Arg Arg Ile Gly Tyr Ile Ala Asn Val Ile
    130                 135                 140

Gly Asn Tyr Arg Thr Lys Val Arg Gly Met Lys Ala Ser Val Lys Tyr
145                 150                 155                 160

Arg Asn Phe Asp Pro Asn Asp Val Thr Glu Asp Val Leu Glu Asn Gln
                165                 170                 175

Thr Ile Phe Glu Ile Asn Lys Asn Gly Phe Glu Cys Lys Gly Asp Phe
            180                 185                 190

Glu Lys His Ile Glu Tyr Leu Lys Asn Arg Glu Leu Thr Asp Arg Leu
        195                 200                 205

Asn Lys Leu Ile Leu Arg Met Glu Cys Leu Tyr Asn Tyr Tyr Val Glu
    210                 215                 220

His Glu Asp Ala Val Lys Ala Lys Met Glu Asn Tyr Ala Ile Glu Ser
225                 230                 235                 240

Phe Lys Thr Phe Gly Gly Cys His Arg Asn Ser Asn Arg Ser Met Ser
                245                 250                 255

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

Thr Ser Phe Asp Leu Tyr Met Pro Ile Asn Gly Glu Val Ala Cys Leu
        275                 280                 285

Gln Leu Met Gly Asn Lys Gln Ala Val Cys Val Gly Glu Asn Gly Glu
    290                 295                 300

Arg Cys Asp Leu Val Asp Ile Val Asn Ser His Ser Lys Thr Ile Thr
305                 310                 315                 320

Ile Lys Ile Ile Asn Gly Glu Met Tyr Val Asp Ile Pro Cys Val Val
                325                 330                 335
```

```
Asn Phe Glu Lys Lys Asp Glu Asp Thr Ile Lys Ser Val Gly Val Asp
            340                 345                 350

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

Gln Leu Asn Gly Tyr Phe Asn Ile Tyr Lys Glu Leu Ile Asn Asn Lys
    370                 375                 380

Glu Phe Val Asp Thr Phe Asn Gly Asp Ile Lys Ala Phe Glu Ala Phe
385                 390                 395                 400

Lys Asp Asn Ala Ala Tyr Val Thr Phe Gly Leu Leu Glu Pro Asp Leu
                405                 410                 415

Leu Phe Thr Arg Phe Tyr Glu Arg Ser Gly Phe Glu Lys Asp Asp Arg
            420                 425                 430

His Ile Lys Leu Arg Glu Arg Glu Arg Ile Leu Thr Gly Ile Leu Lys
        435                 440                 445

Arg Ile Gly Gln Glu His Ser Asp Val Asp Val Arg Asn Tyr Val Arg
    450                 455                 460

Phe Val Asn Met Leu Arg Ser Lys Tyr Glu Ser Tyr Phe Val Leu Lys
465                 470                 475                 480

Asn Lys Tyr Tyr Glu Lys Met Gln Glu Phe Asp Ser Thr Gln Asn Tyr
                485                 490                 495

Val Asp Val Ser Thr Ala Ser Lys Glu Thr Met Asp Lys Arg Arg Phe
            500                 505                 510

Asp Asn Pro Phe Arg Asn Thr Glu Val Ala Asn Glu Leu Leu Gly Lys
        515                 520                 525

Ile Asp Asn Val Leu Gly Asp Ile Lys Gly Cys Met Ala Asn Ile Ile
    530                 535                 540
```

```
Thr Tyr Ala Phe Lys Val Leu Gln Lys Asn Gly Tyr Asn Thr Ile Gly
545                 550                 555                 560

Leu Glu Tyr Leu Asp Ser Ser Gln Phe Glu Asn Met Arg Thr Leu Thr
                565                 570                 575

Pro Thr Ser Ile Leu Lys Tyr His Lys Met Glu Gly Lys Ser Val Asp
            580                 585                 590

Ala Val Glu Ser Trp Ile Lys Glu Asn Lys Ile Pro Ser Asn Arg Tyr
        595                 600                 605

Asp Phe Ile Tyr Glu Asp Asn His Leu Thr Asp Val Leu Leu Asn Ser
    610                 615                 620

Asn Gly Ile Ala Tyr Gln Lys Lys Asn Leu Phe Met Asn Leu Val Ile
625                 630                 635                 640

Lys Ala Ile Ser Phe Ala Asp Ile Lys Asn Lys Phe Val Gln Leu Ser
                645                 650                 655

Asn Asn Thr Asn Val Ser Ile Leu Phe Ala Pro Ala Ala Phe Thr Ser
            660                 665                 670

Gln Met Asp Ser Asn Arg His Val Ile Tyr Thr Val Lys Asn Asn Lys
        675                 680                 685

Gly Lys Leu Ala Leu Val Asp Lys Lys Arg Val Arg Pro Asn Gln Glu
    690                 695                 700

Lys His Ile Asn Gly Leu His Ser Gly Tyr Asn Ala Ala Cys Asn Val
705                 710                 715                 720

Lys Phe Ile Cys Asp Asn Glu Phe Phe Arg Asn Thr Met Thr Ile Ser
                725                 730                 735

Asn Lys Gly Lys Asn Leu Tyr Ser Gln Pro Thr Tyr Asp Ile Lys Glu
            740                 745                 750

Ala Tyr Lys Lys Asn Ala Gly Cys Lys Val Ile Asn Asp Phe Ile Lys
        755                 760                 765
```

Asn Gly Asn Ala Val Ile Cys Cys Ile Glu Asn Asn Lys Leu Ile Glu
770 775 780

Thr Asn Gly Arg Gln
785

<210> 23
<211> 766
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-fecal sequence

<400> 23
Met Ala Asn Lys Lys Phe Lys Leu Thr Lys Asn Glu Val Val Lys Ser
1 5 10 15

Phe Val Leu Lys Val Ala Asn Gln Lys Lys Cys Ala Ile Thr Asn Glu
20 25 30

Thr Leu Gln Glu Tyr Lys Asn Tyr Tyr Asn Lys Val Ser Gln Trp Ile
35 40 45

Asn Asn Asn Leu Thr Lys Met Thr Ile Gly Asp Leu Ile Gln Tyr Ala
50 55 60

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

Tyr Asp Thr Pro Leu Tyr Val Thr Tyr Ala Met Ser Asp Glu Trp Lys
85 90 95

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

Ala Asn Asn Leu Leu Tyr Glu Ala Ile Arg Asn Leu Asn Val Asp Glu
115 120 125

Tyr Asp Gly Asn Gln Leu Asn Phe Asn Ser Thr Tyr Tyr Arg Thr Gln
130 135 140

```
Gly Tyr Val Asn Arg Val Phe Ser Asn Tyr Arg Thr Lys Ile Asn Thr
145                 150                 155                 160

Leu Asp Ile Lys Ile Lys Lys Ser Lys Val Asp Glu Asn Ser Asp Val
                165                 170                 175

Glu Thr Leu Glu Pro Gln Thr Met Tyr Glu Ile Asn Lys Leu Asn Leu
            180                 185                 190

Lys Thr Asn Lys Asp Trp Glu Glu Arg Leu Gln Tyr Leu Thr Met Gln
        195                 200                 205

Glu Asn Pro Asn Gln Asn Thr Ile Asp Arg Thr Lys Ile Leu Phe Asn
    210                 215                 220

Tyr Phe Ile Asn Asn Asn Asp Thr Ile Phe Gln Lys Met Glu Glu Leu
225                 230                 235                 240

Ser Ile Lys Gln Leu Thr Glu Phe Gly Gly Cys Lys Met Lys Asp Asn
                245                 250                 255

Thr Thr Ser Met Thr Ile Asn Ile Gln Asp Phe Lys Ile Lys Arg Lys
            260                 265                 270

Glu Asn Ser Ile Gly Tyr Ile Met Thr Ile Pro Phe Asn Lys Lys Asn
        275                 280                 285

Val Asp Val Glu Leu Tyr Gly His Lys Gln Thr Ile Lys Gly His Lys
    290                 295                 300

Asn Ser Tyr Thr Glu Ile Val Asp Ile Val Asn Lys His Gly Asn Thr
305                 310                 315                 320

Ile Thr Phe Lys Ile Lys Asn Asn Gln Leu Phe Ala Ile Ile Thr Ser
                325                 330                 335

Asp Thr Glu Val Thr Lys Pro Glu Pro Gln Tyr Glu Lys Ile Val Gly
            340                 345                 350
```

```
Val Asp Val Asn Ile Lys His Thr Leu Met Val Thr Ser Glu Lys Asp
        355                 360                 365

Asn Gly Lys Leu Lys Gly Tyr Ile Asn Leu Tyr Lys Glu Val Leu Lys
    370                 375                 380

Asn Asp Glu Phe Lys Lys Leu Leu Asn Lys Thr Glu Leu Asp Asn Phe
385                 390                 395                 400

Lys Ser Leu Ser Gln Ile Val Thr Phe Cys Pro Ile Glu Tyr Asp Phe
                405                 410                 415

Leu Phe Ser Arg Ile Phe Asp Asp Glu Asn Thr Lys Lys Glu Leu Ala
            420                 425                 430

Phe Ser Asn Val Leu Tyr Asp Ile Gln Lys Gln Leu Lys Asn Thr Asn
        435                 440                 445

Asn Ile Leu Gln Tyr Asn Tyr Ile Ala Cys Val Asn Lys Leu Arg Ala
    450                 455                 460

Lys Tyr Lys Ala Tyr Phe Val Leu Lys Met Ser Tyr Met Lys Gln Gln
465                 470                 475                 480

Lys Ile Tyr Asp Thr Asn Met Gly Phe Phe Asp Ile Ser Thr Glu Ser
                485                 490                 495

Lys Glu Thr Met Asp Gln Arg Arg Ser Leu Tyr Pro Phe Ile Asn Thr
            500                 505                 510

Glu Ile Ala Gln Asn Ile Ile Thr Lys Met Asn Asn Val Gln Gln Asp
        515                 520                 525

Ile Asn Gly Cys Leu Lys Asn Ile Phe Lys Tyr Thr Tyr Thr Val Phe
    530                 535                 540

Glu Asn Asn Asn Tyr Asp Thr Ile Val Leu Glu Asn Leu Glu Asn Ala
545                 550                 555                 560

Asn Phe Glu Lys His Asn Pro Leu Pro Asn Ile Thr Ser Leu Leu Lys
                565                 570                 575
```

```
Tyr His Lys Val Gln Gly Leu Thr Ile Gln Glu Ala Glu Gln His Glu
            580                 585                 590

Lys Val Gly Asn Leu Ile Gln Asn Asp Asn Tyr Ile Phe Gln Leu Asn
        595                 600                 605

Glu Asp Asn Lys Ile Ile Asn Ala Asp Tyr Ser Gln Lys Ala Tyr Tyr
    610                 615                 620

Lys Val Cys Lys Ala Leu Phe Phe Asn Gln Ala Ile Lys Thr Leu His
625                 630                 635                 640

Phe Ala Ser Val Lys Asp Glu Met Ile Lys Leu Ser Asn Asn Asn Lys
                645                 650                 655

Val Cys Val Ala Ile Ile Pro Pro Glu Tyr Thr Ser Gln Ile Asp Ser
            660                 665                 670

Asn Thr His Lys Leu Tyr Phe Ile Asn Lys Asp Gly Lys Leu Leu Lys
        675                 680                 685

Ala Asp Lys Lys Thr Val Arg Lys Thr Gln Glu Lys His Ile Asn Gly
    690                 695                 700

Leu Asn Ala Asp Phe Asn Ala Ala Ser Asn Ile Lys Tyr Ile Val Gln
705                 710                 715                 720

Asn Glu Thr Trp Arg Asn Leu Phe Thr Asn Lys Thr Asn Asn Thr Tyr
                725                 730                 735

Gly Leu Pro Ile Leu Thr Pro Ser Lys Lys Gly Gln Ser Asn Ile Ile
            740                 745                 750

Thr Gln Leu Met Lys Ile Asn Ala Thr Gln Glu Leu Val Val
        755                 760                 765
```

<210> 24
<211> 752
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-fecal sequence

<400> 24
Met Ala Lys Ser Ile Met Lys Lys Ser Ile Lys Phe Lys Val Lys Gly
1 5 10 15

Asn Ser Pro Ile Asn Glu Asp Ile Ile Asn Glu Tyr Lys Gly Tyr Tyr
20 25 30

Asn Thr Cys Ser Asn Trp Ile Asn Asn Asn Leu Thr Ser Ile Thr Ile
35 40 45

Gly Glu Met Gly Lys Phe Leu Lys Asp Val Met Arg Lys Thr Thr Gly
50 55 60

Tyr Ile Asp Val Ala Leu Ser Asp Glu Trp Lys Asp Lys Pro Met Tyr
65 70 75 80

Tyr Leu Phe Thr Lys Lys Tyr Asn Pro Lys His Ala Asn Asn Leu Leu
85 90 95

Tyr Tyr Phe Ile Lys Glu Lys Lys Leu Asp Lys Phe Asn Gly Asn Ile
100 105 110

Leu Asn Val Pro Glu Tyr Tyr Tyr Arg Lys Glu Gly Tyr Phe Lys Leu
115 120 125

Val Ala Gly Asn Tyr Arg Thr Lys Ile Asn Thr Leu Asn Phe Lys Ile
130 135 140

Lys Ser Lys Lys Val Asp Ala Asn Ser Leu Ser Glu Asp Ile Glu Met
145 150 155 160

Gln Thr Ile Tyr Glu Ile Val Lys Arg Gly Leu Asn Lys Lys Ser Asp
165 170 175

Trp Asp Ser Tyr Ile Ser Tyr Ile Glu Cys Val Gln Asn Pro Asn Ile
180 185 190

```
Asp Asn Ile Asn Arg Tyr Lys Leu Leu Arg Asp Tyr Phe Cys Glu Asn
        195                 200                 205

Glu Asp Val Ile Lys Asn Lys Ile Glu Ile Leu Ser Ile Glu Gln Ile
    210                 215                 220

Lys Glu Phe Gly Gly Cys Ile Met Lys Pro His Ile Asn Ser Met Thr
225                 230                 235                 240

Phe Gly Ile Gln Lys Phe Lys Ile Glu Glu Ile Glu Asn Ser Leu Gly
                245                 250                 255

Phe Thr Phe Asn Leu Pro Leu Asn Lys Asn Asn Tyr Lys Ile Glu Leu
            260                 265                 270

Trp Gly His Arg Gln Leu Lys Lys Gly Asn Lys Glu Ser Asn Val Asn
        275                 280                 285

Val Ser Leu Asp Asp Phe Ile Asn Thr Tyr Gly Gln Asn Val Val Phe
    290                 295                 300

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

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

Asn Phe Lys His Ser Leu Phe Val Thr Ser Glu Ile Asp Asn Asn Gln
            340                 345                 350

Phe Asp Gly Tyr Ile Asn Leu Tyr Lys Tyr Ile Leu Ser Asn Asn Glu
        355                 360                 365

Phe Thr Ser Leu Leu Thr Asp Ser Glu Arg Lys Asp Tyr Glu Asp Leu
    370                 375                 380

Ala Asn Ile Val Thr Phe Cys Pro Phe Glu Tyr Gln Leu Leu Phe Ser
385                 390                 395                 400

Arg Tyr Asp Lys Leu Ser Lys Ile Ser Glu Lys Glu Lys Val Leu Ser
                405                 410                 415
```

```
Lys Ile Leu Tyr Ser Leu Gln Lys Lys Leu Lys Asn Glu Lys Arg Thr
            420                 425                 430

Lys Glu Tyr Ile Tyr Val Ser Cys Val Asn Lys Leu Arg Ala Lys Tyr
        435                 440                 445

Val Ser Tyr Phe Lys Leu Lys Gln Lys Tyr Asn Glu Lys Gln Lys Glu
    450                 455                 460

Tyr Asp Ile Glu Met Gly Phe Val Asp Asp Ser Thr Glu Ser Lys Glu
465                 470                 475                 480

Ser Met Asp Lys Arg Arg Phe Glu Asn Pro Phe Ile Asn Thr Pro Val
                485                 490                 495

Ala Lys Glu Leu Leu Glu Lys Met Asn Asn Val Lys Gln Asp Ile Asn
            500                 505                 510

Gly Cys Lys Lys Asn Ile Val Val Tyr Ala Tyr Lys Val Leu Glu Gln
        515                 520                 525

Asn Gly Tyr Asn Ile Ile Ala Leu Glu Asn Leu Glu Asn Ser Asn Phe
    530                 535                 540

Glu Lys Ile Arg Val Leu Pro Lys Ile Lys Ser Leu Leu Glu Tyr His
545                 550                 555                 560

Lys Phe Glu Asn Lys Asn Ile Asn Asp Ile Lys Asn Ser Asp Lys Tyr
                565                 570                 575

Lys Glu Phe Ile Glu Pro Gly Tyr Phe Glu Leu Ile Thr Asn Glu Asn
            580                 585                 590

Asn Glu Ile Ile Asp Ala Lys Tyr Thr Gln Lys Gly Asp Ile Lys Ile
        595                 600                 605

Lys Asn Ala Asp Phe Ile Asn Ile Met Ile Lys Ala Leu Asn Phe Ala
    610                 615                 620
```

```
Ser Ile Lys Asp Glu Phe Ile Leu Leu Ser His Asn Gly Lys Ser Gln
625                 630                 635                 640


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


His Cys Ile Tyr Met Thr Lys Asn Asp Lys Gly Lys Leu Val Lys Val
            660                 665                 670


Asp Lys Arg Lys Val Arg Thr Lys Gln Glu Arg His Ile Asn Gly Leu
        675                 680                 685


Asn Ala Asp Phe Asn Ala Ala Cys Asn Ile Lys Tyr Ile Val Thr Asn
    690                 695                 700


Glu Asp Trp Arg Lys Val Phe Cys Ile Lys Pro Lys Lys Glu Asp Tyr
705                 710                 715                 720


Asn Thr Pro Leu Leu Asp Ala Thr Lys Asn Gly Gln Phe Arg Ile Leu
                725                 730                 735


Asp Lys Leu Lys Lys Leu Asn Ala Thr Lys Leu Leu Glu Met Glu Lys
            740                 745                 750


<210> 25
<211> 814
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-bos taurus sequence

<400> 25
Met Val Lys Val Phe Ile Asn Val Phe Leu Ser Glu Lys Asn Gln Ile
1               5                   10                  15


Thr Thr Asn Ile Phe Asp Thr Glu Lys Ile Ser Asn Ser Tyr Ile Asn
            20                  25                  30


His Ile Asn His Gln Phe Met Ala Thr His Lys Lys Thr Asp Asn Gln
        35                  40                  45
```

```
Thr Ile Val Lys Ala Tyr Val Met Lys Ala Lys Met Ser Lys His Asp
    50                  55                  60

Ile Glu Arg Val Trp Lys Pro Thr Ile Asp Glu Tyr Ile Asn Tyr Tyr
65                  70                  75                  80

Asn Lys Leu Ser Asp Trp Ile Cys Lys Asn Leu Thr Ser Val Thr Ile
                85                  90                  95

Gly Asp Leu Leu Lys Tyr Val Gly Glu Lys Gln Ile Asn Lys Gly Val
            100                 105                 110

Gly Tyr Tyr Thr Tyr Phe Ile Asp Glu Gln Lys Thr Asp Leu Pro Leu
        115                 120                 125

Tyr Thr Leu Phe Thr Asp Cys Pro Lys Thr His Ala Asp Asn Leu Leu
    130                 135                 140

Phe Glu Ala Val Arg Lys Ile Asn Pro Glu Asn Tyr Asn Gly Asn Leu
145                 150                 155                 160

Leu Ser Leu Phe Glu Thr Gly Tyr Arg Arg Asn Gly Tyr Phe Asp Asn
                165                 170                 175

Val Ile Ser Asn Tyr Arg Thr Lys Met Thr Thr Leu Lys Ile Asn Pro
            180                 185                 190

Lys Tyr Lys Arg Phe Ser Ser Glu Asn Met Pro Thr Asp Glu Val Leu
        195                 200                 205

Leu Glu Gln Thr Val Tyr Glu Val Thr Lys Asn Asp Phe Lys Asn Asp
    210                 215                 220

Asp Asp Trp Lys Lys Ser Ile Asp Tyr Met Lys Gln Lys Ser Glu Pro
225                 230                 235                 240

Asn Thr Ala Leu Ile Phe Arg Met Glu Thr Leu Phe Asp Tyr Trp Lys
                245                 250                 255

Asp His Lys Gln Asp Val Glu Gln Tyr Ile Asn Gln Lys Arg Val Glu
            260                 265                 270
```

```
Cys Leu Lys Asp Phe Gly Gly Cys Lys Arg Arg Ala Asp Gly Leu Ser
        275                 280                 285

Met Val Ile Leu Leu Asn Lys Lys Leu Thr Lys Ile Glu Ala Asp Gly
    290                 295                 300

Leu Thr Ser Tyr Lys Leu Thr Thr Asn Leu Phe Gly Gly Lys Tyr Met
305                 310                 315                 320

Ile Asn Ile Phe Gly His Arg Ala Leu Val Ser Val Cys Asn Gly Glu
                325                 330                 335

Arg Ala Glu Asn Glu Asn Ile Asp Ile Cys Asn Lys His Gly Glu Arg
            340                 345                 350

Phe Thr Phe Lys Ile Glu Asn Gly Asn Leu Phe Val Ala Leu Thr Ala
        355                 360                 365

Asp Tyr Asn Tyr Glu Lys Gln Pro Asn Leu Pro Lys Asn Ile Val Gly
    370                 375                 380

Val Asp Ile Asn Ile Lys His Ser Met Leu Asn Ser Ser Ile Glu Asp
385                 390                 395                 400

Lys Gly Lys Val Lys Gly Tyr Val Asn Leu Tyr Lys Glu Phe Leu Ser
                405                 410                 415

Asp Lys Asn Phe Arg Lys Thr Ile Thr Ser Asp Glu Glu Leu Asn Gln
            420                 425                 430

Tyr Ile Glu Leu Ser Lys Tyr Ala Thr Phe Gly Ile Thr Glu Leu Asp
        435                 440                 445

Ser Leu Phe Ala Arg Ala Thr Asp Thr Glu Lys Ser Ile Leu Cys Lys
    450                 455                 460

Arg Glu Leu Ala Met Gln Asp Val Phe Glu Lys Leu Glu Lys Arg Tyr
465                 470                 475                 480
```

```
Lys Asp Asp His Lys Ile Lys Phe Tyr Leu Gly Ser Thr Gln Lys Leu
                485                 490                 495

Arg Ala Gln Tyr Ile Ser Tyr Phe Lys Ile Lys Glu Ala Tyr Asn Arg
            500                 505                 510

Lys Gln Gln Glu Tyr Asp Leu Ala His Gly Lys Thr Asp Asn Pro Asp
        515                 520                 525

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

Leu Val Lys Leu Asn Arg Ile Glu Arg Lys Ile Ile Gly Cys Arg Asn
545                 550                 555                 560

Asn Ile Val Thr Tyr Ala Phe Asn Val Ile Lys Asn Asn Gly Tyr Asp
                565                 570                 575

Thr Ile Gly Val Glu Tyr Leu Thr Ser Ser Gln Phe Glu Lys Lys Arg
            580                 585                 590

Arg Leu Pro Ser Ile Lys Ser Leu Leu Asn Tyr Arg Lys Leu Leu Gly
        595                 600                 605

Lys Pro Lys Asp Glu Trp Asn Leu Lys Glu Trp Asn Asp Val Tyr Met
    610                 615                 620

Cys Tyr Arg Pro Glu Leu Asp Asp Ala Gly Asn Ile Met Asn Phe Thr
625                 630                 635                 640

Ile Thr Asn Glu Gly Ile Lys Arg Asn Lys Glu Ser Thr Phe Tyr Asn
                645                 650                 655

Ser Phe Ile Lys Ala Ile His Phe Ala Asp Val Lys Asp Lys Phe Ala
            660                 665                 670

Gln Leu Thr Asn Asn Asn Thr Met Asn Thr Val Phe Ile Pro Ser Ser
        675                 680                 685

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

```
Tyr Thr Glu Lys Cys Asp Asn Gly Lys Thr Lys Lys Val Val Lys Phe
705                 710                 715                 720


Ile Asn Lys Arg Val Leu Arg Lys Ile Gln Glu Gln His Leu Asn Gly
                725                 730                 735


Met Asn Ala Asp Asn Asn Ala Ala Arg Asn Ile Arg Asp Ile Thr Lys
            740                 745                 750


Asn Leu Arg Asp Val Phe Thr Lys Lys Gln Thr Asp Lys Asn Cys Tyr
        755                 760                 765


Asn Ser Ala Glu Phe Met Ile Gln Thr Lys Phe Lys Lys Arg Leu Pro
    770                 775                 780


Gln Ala Thr Val Phe Gly Glu Leu Asn Arg Asn Gly Tyr Val Lys Val
785                 790                 795                 800


Leu Thr Gln Glu Glu Tyr Asp Glu Leu Thr Lys Ser Ala Lys
                805                 810
```

<210> 26
<211> 776
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

```
<400> 26
Met Ala Thr His Lys Lys Thr Asp Asn Gln Thr Ile Val Lys Ala Tyr
1               5                   10                  15


Val Met Lys Ala Lys Met Ser Lys His Asp Ile Glu Arg Val Trp Lys
            20                  25                  30


Pro Thr Ile Asp Glu Tyr Ile Asn Tyr Tyr Asn Lys Leu Ser Asp Trp
        35                  40                  45


Ile Cys Lys Asn Leu Thr Ser Val Thr Ile Gly Asp Leu Leu Lys Tyr
    50                  55                  60
```

```
Val Gly Glu Lys Gln Ile Asn Lys Gly Val Gly Tyr Tyr Thr Tyr Phe
65                  70                  75                  80

Ile Asp Glu Gln Lys Thr Asp Leu Pro Leu Tyr Thr Leu Phe Thr Asp
                85                  90                  95

Cys Pro Lys Thr His Ala Asp Asn Leu Leu Phe Glu Ala Val Arg Lys
            100                 105                 110

Ile Asn Pro Glu Asn Tyr Asn Gly Asn Leu Leu Ser Leu Phe Glu Thr
        115                 120                 125

Gly Tyr Arg Arg Asn Gly Tyr Phe Asp Asn Val Ile Ser Asn Tyr Arg
    130                 135                 140

Thr Lys Met Thr Thr Leu Lys Ile Asn Pro Lys Tyr Lys Arg Phe Ser
145                 150                 155                 160

Ser Glu Asn Met Pro Thr Asp Glu Val Leu Leu Glu Gln Thr Val Tyr
                165                 170                 175

Glu Val Thr Lys Asn Asp Phe Lys Asn Asp Asp Asp Trp Lys Lys Ser
            180                 185                 190

Ile Asp Tyr Met Lys Gln Lys Ser Glu Pro Asn Thr Ala Leu Ile Phe
        195                 200                 205

Arg Met Glu Thr Leu Phe Asp Tyr Trp Lys Asp His Lys Gln Asp Val
    210                 215                 220

Glu Gln Tyr Ile Asn Gln Lys Arg Val Glu Cys Leu Lys Asp Phe Gly
225                 230                 235                 240

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

Lys Lys Leu Thr Lys Ile Glu Ala Asp Gly Leu Thr Ser Tyr Lys Leu
            260                 265                 270
```

```
Thr Thr Asn Leu Phe Gly Gly Lys Tyr Met Ile Asn Ile Phe Gly His
        275                 280                 285

Arg Ala Leu Val Ser Val Cys Asn Gly Glu Arg Ala Glu Asn Glu Asn
    290                 295                 300

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

Asn Gly Asn Leu Phe Val Ala Leu Thr Ala Asp Tyr Asn Tyr Glu Lys
                325                 330                 335

Gln Pro Asn Leu Pro Lys Asn Ile Val Gly Val Asp Ile Asn Ile Lys
            340                 345                 350

His Ser Met Leu Asn Ser Ser Ile Glu Asp Lys Gly Lys Val Lys Gly
        355                 360                 365

Tyr Val Asn Leu Tyr Lys Glu Phe Leu Ser Asp Lys Asn Phe Arg Lys
    370                 375                 380

Thr Ile Thr Ser Asp Glu Glu Leu Asn Gln Tyr Ile Glu Leu Ser Lys
385                 390                 395                 400

Tyr Ala Thr Phe Gly Ile Thr Glu Leu Asp Ser Leu Phe Ala Arg Ala
                405                 410                 415

Thr Asp Thr Glu Lys Ser Ile Leu Cys Lys Arg Glu Leu Ala Met Gln
            420                 425                 430

Asp Val Phe Glu Lys Leu Glu Lys Arg Tyr Lys Asp Asp His Lys Ile
        435                 440                 445

Lys Phe Tyr Leu Gly Ser Thr Gln Lys Leu Arg Ala Gln Tyr Ile Ser
    450                 455                 460

Tyr Phe Lys Ile Lys Glu Ala Tyr Asn Arg Lys Gln Gln Glu Tyr Asp
465                 470                 475                 480

Leu Ala His Gly Lys Thr Asp Asn Pro Asp Glu Val Tyr Lys Ser Asp
                485                 490                 495
```

```
Phe Ile Asn Glu Pro Ser Ala Lys Glu Met Leu Val Lys Leu Asn Arg
            500                 505                 510

Ile Glu Arg Lys Ile Ile Gly Cys Arg Asn Asn Ile Val Thr Tyr Ala
        515                 520                 525

Phe Asn Val Ile Lys Asn Asn Gly Tyr Asp Thr Ile Gly Val Glu Tyr
    530                 535                 540

Leu Thr Ser Ser Gln Phe Glu Lys Lys Arg Arg Leu Pro Ser Ile Lys
545                 550                 555                 560

Ser Leu Leu Asn Tyr Arg Lys Leu Leu Gly Lys Pro Lys Asp Glu Trp
                565                 570                 575

Asn Leu Lys Glu Trp Asn Asp Val Tyr Met Cys Tyr Arg Pro Glu Leu
            580                 585                 590

Asp Asp Ala Gly Asn Ile Met Asn Phe Thr Ile Thr Asn Glu Gly Ile
        595                 600                 605

Lys Arg Asn Lys Glu Ser Thr Phe Tyr Asn Ser Phe Ile Lys Ala Ile
    610                 615                 620

His Phe Ala Asp Val Lys Asp Lys Phe Ala Gln Leu Thr Asn Asn Asn
625                 630                 635                 640

Thr Met Asn Thr Val Phe Ile Pro Ser Ser Phe Thr Ser Gln Ile Asp
                645                 650                 655

Ser Lys Thr Arg Lys Leu Tyr Leu Leu Glu Tyr Thr Glu Lys Cys Asp
            660                 665                 670

Asn Gly Lys Thr Lys Lys Val Val Lys Phe Ile Asn Lys Arg Val Leu
        675                 680                 685

Arg Lys Ile Gln Glu Gln His Leu Asn Gly Met Asn Ala Asp Asn Asn
    690                 695                 700
```

```
Ala Ala Arg Asn Ile Arg Asp Ile Thr Lys Asn Leu Arg Asp Val Phe
705                 710                 715                 720


Thr Lys Lys Gln Thr Asp Lys Asn Cys Tyr Asn Ser Ala Glu Phe Met
                725                 730                 735


Ile Gln Thr Lys Phe Lys Lys Arg Leu Pro Gln Ala Thr Val Phe Gly
            740                 745                 750


Glu Leu Asn Arg Asn Gly Tyr Val Lys Val Leu Thr Gln Glu Glu Tyr
        755                 760                 765


Asp Glu Leu Thr Lys Ser Ala Lys
    770                 775


<210> 27
<211> 778
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-bos taurus sequence

<400> 27
Met Ala His Lys Gly Glu Lys Glu Gly Tyr Gln Ile Lys Thr Leu Lys
1               5                   10                  15


Phe Lys Val Arg Ser His Asp Ile Gly Lys Ser Leu Tyr Asp Ile Val
            20                  25                  30


Asn Glu Tyr Thr Asn Tyr Tyr Asn Lys Val Ser Lys Trp Ile Cys Asp
        35                  40                  45


Asn Leu Asp Thr Pro Ile Gly Glu Leu Ser Lys Asn Ile Ser Glu Lys
    50                  55                  60


Arg His Asn Ser Lys Tyr Tyr Arg Ala Thr Asn Asp Pro Asn Trp Lys
65                  70                  75                  80


Asn Glu Pro Met Trp Lys Ile Phe Thr Lys Lys Phe Ser Asn Gly Glu
                85                  90                  95
```

```
Thr Phe Ser Glu Gln Gly Lys Asn Asp Lys Leu Ala Asn Leu Ser Asn
            100                 105                 110

Cys Asp Asn Ile Leu Ser Tyr Ser Ile Ile Asp Tyr Asn Ile Asp Gly
        115                 120                 125

Tyr Thr Gly Asn Ile Leu Gly Leu Thr Asp Thr Ser Tyr Arg Leu Asn
    130                 135                 140

Gly Tyr Ile Ser Asn Cys Ile Ser Asn Tyr Lys Thr Lys Ile Arg Thr
145                 150                 155                 160

Ala Lys Pro Lys Val Arg Ser Thr Ala Ile Thr Glu His Ser Thr Val
                165                 170                 175

Glu Glu Lys Thr Asn Asn Thr Ile Tyr Glu Met Val Arg Lys Gly Phe
            180                 185                 190

Met Ser Pro Asn Asp Phe Lys Asn Gln Ile Lys Tyr Leu Thr Glu Lys
        195                 200                 205

Glu Asn Pro Asn Asp Lys Leu Ile Asp Arg Leu Ser Ile Leu His Ser
    210                 215                 220

Phe Tyr Thr Glu Asn Glu Glu Asp Val Asn Asn Ala Phe Ser Arg Met
225                 230                 235                 240

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

Lys Lys Thr Leu Asn Ile Ser Ser Ile Asp Tyr Lys Val Thr Arg Lys
            260                 265                 270

Glu Gly Cys Asp Gly Tyr Ile Leu Ser Phe Gly Ser Arg Asn Gln Lys
        275                 280                 285

Tyr Asn Ile Asp Leu Trp Gly Arg Arg Asp Thr Ile Ser Asn Gly Lys
    290                 295                 300

Glu Leu Ile Asp Leu Ser Glu His Gly Glu Pro Leu Thr Ile Thr Ser
305                 310                 315                 320
```

```
Glu Asn Gly Asp Tyr Tyr Val Cys Met Thr Val Asp Val Pro Phe Glu
                325                 330                 335

Lys Lys Ser Thr Gly Ser Thr Glu Lys Val Ala Ser Val Asp Val Asn
            340                 345                 350

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

Lys Gly Tyr Leu Asn Ile Tyr Lys Lys Leu Leu Leu Asp Thr Glu Leu
    370                 375                 380

Thr Ser Leu Leu His Lys Gln Asp Phe Asp Asp Met Lys Glu Leu Ser
385                 390                 395                 400

His Asn Val Cys Phe Gly Pro Ile Glu Tyr Asn Phe Leu Leu Ser Arg
                405                 410                 415

Ile Leu Asp Leu Asp Ala Tyr Glu Lys Lys Val Glu Asp Arg Ile Thr
            420                 425                 430

His Ser Met Lys Glu Met Leu Lys Thr Glu Thr Asp Glu Arg Asn Lys
        435                 440                 445

Met Tyr Leu Gly Ser Val Ile Lys Met Arg Ala Leu Leu Lys Val Tyr
    450                 455                 460

Ile Ser Thr Lys Asn Arg Tyr His Lys Glu Gln Gln Ser Tyr Asp Glu
465                 470                 475                 480

Ser Met Gly Phe Thr Asp Thr Ser Thr Ala Ser Lys Asp Thr Met Asp
                485                 490                 495

Lys Arg Arg Phe Glu Asn Pro Phe Ser Glu Thr Glu Thr Gly Lys Lys
            500                 505                 510

Leu Asn Asn Asp Leu Ser Ala Leu Ser Lys Lys Ile Ile Gly Cys Arg
        515                 520                 525
```

```
Asp Asn Ile Val Arg Tyr Ala Tyr Thr Thr Leu Gln Asp Asn Gly Tyr
    530                 535                 540

Thr Met Ile Gly Val Glu Asp Leu Asn Ser Ser Thr Phe Ala Asn Thr
545                 550                 555                 560

Arg Asn Pro Phe Pro Thr Ile Lys Ser Leu Leu Asn Tyr His His Leu
                565                 570                 575

Ser Gly Lys Thr Pro Glu Glu Ala Arg Asn Ile Asp Thr Tyr Ser Lys
            580                 585                 590

Phe Ser Asp His Tyr Thr Leu Thr Thr Asp Glu Glu Gly Lys Ile Thr
        595                 600                 605

Asp Ala Lys Tyr Thr Lys Lys Ala Glu Thr Lys Ile Lys Lys Lys Arg
    610                 615                 620

Ala Arg Asp Thr Ile Ile Lys Ala Ile His Phe Ala Glu Val Lys Asp
625                 630                 635                 640

Val Met Cys Val Met Ser Asn Asn Gly Thr Ala Ser Val Ala Phe Glu
                645                 650                 655

Pro Ser Tyr Phe Ser Ser Gln Met Asp Ser Ala Thr His Lys Val Tyr
            660                 665                 670

Thr Thr Arg Asn Lys Lys Gly Lys Asp Val Ile Ala Ser Lys Glu Thr
        675                 680                 685

Val Arg Pro Arg Gln Glu Lys His Ile Asn Gly Met Asn Cys Asp Ile
    690                 695                 700

Asn Ser Pro Lys Asn Leu Ser Tyr Leu Ile Thr Asn Glu Glu Phe Arg
705                 710                 715                 720

Glu Met Phe Leu Thr Pro Thr Lys Asn Gly Tyr Asn Glu Pro Phe Tyr
                725                 730                 735

Lys Ser Arg Val Lys Ser Ala Ala Ser Met Met Ser Gly Leu Lys Lys
            740                 745                 750
```

```
Leu Gly Ala Thr Met Pro Leu Thr Asp Glu Asn Ala Ile Phe Ser Thr
        755                 760                 765


Pro Lys Pro Lys Lys Asn Ile Gly Lys Gln
    770                 775


<210> 28
<211> 772
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-bos taurus sequence

<400> 28
Met Gly Asn Lys Val Gln Ser Asn Glu Thr Ile Val Lys Thr Tyr Thr
1               5                   10                  15


Phe Lys Val Arg Glu Phe Ile Ser Gly Ala Thr His Glu Ile Met Lys
            20                  25                  30


Ser Ala Ile Lys Gln Tyr Ile Glu Asp Ser Asn Asn Leu Ser Asp Trp
        35                  40                  45


Ile Asn Asn Gln Leu Thr Asn Lys Thr Ile Cys Glu Val Gly Ala Leu
    50                  55                  60


Ile Pro Ile Glu Lys Arg Glu Thr Ser Tyr Tyr Lys Ser Thr Val Asp
65                  70                  75                  80


Glu Leu Trp Ala Asn Lys Pro Cys Phe Lys Met Phe Thr Asn Asp Phe
                85                  90                  95


Thr Lys Glu Glu Asn Phe Ala Thr Arg Asn Ile Gly Asn Gly Lys Asn
            100                 105                 110


Cys Lys Asn Ile Ile Thr Ser Ala Tyr Lys Ser Thr Val Asn Pro Ser
        115                 120                 125


Phe Arg Asn Val Leu Asp Leu Thr Glu Lys Val Tyr Phe Ser Asp Gly
    130                 135                 140
```

```
Tyr Gly Ala Asn Val Cys Ser Asn Tyr Lys Thr Lys Leu Arg Thr Leu
145                 150                 155                 160

Lys Pro Ala Lys Ile Lys Leu Val Ser Ser Leu Ser Asp Cys Asp Asp
                165                 170                 175

Asn Thr Leu Thr Glu Gln Val Ile Arg Glu Lys Gln Lys Tyr Gly Tyr
            180                 185                 190

Ser Thr Pro Lys Asp Phe Glu Lys Arg Ile Glu Tyr Leu Asn Glu Lys
        195                 200                 205

Glu Lys Ser Glu Gln Asn Ser Lys Ile Ile Glu Arg Leu Gln Lys Leu
    210                 215                 220

Tyr Glu Phe Tyr Asp Asn Asn Thr Lys Leu Val Glu Glu Lys Glu Leu
225                 230                 235                 240

Glu Leu Ser Val Lys Ser Leu Val Glu Phe Gly Gly Cys Arg Arg Gly
                245                 250                 255

Glu Lys Thr Met Thr Leu Asn Leu Pro Asp Ile Gly Tyr Glu Ile Gln
            260                 265                 270

Arg Lys Asp Asp Lys Tyr Gly Tyr Ile Phe Thr Leu Lys Cys Ser Lys
        275                 280                 285

Lys Arg Lys Ile Ile Ile Asp Val Trp Gly Ser Lys Ala Thr Ile Asp
    290                 295                 300

Ser Asn Gly Asn Asp Lys Val Asp Ile Ile Asn Thr His Gly Lys Ser
305                 310                 315                 320

Ile Asn Phe Lys Ile Ile Asn Asn Glu Met Tyr Ile Asp Ile Thr Val
                325                 330                 335

Asp Val Pro Phe Ala Lys Arg Lys Leu Gly Ile Lys Lys Val Val Gly
            340                 345                 350
```

```
Ile Asp Val Asn Thr Lys His Met Leu Met Ala Thr Asn Ile Lys Val
        355                 360                 365

Thr Asp Ser Ile Lys Gly Tyr Val Asn Leu Tyr Lys Glu Phe Leu Asn
    370                 375                 380

Ser Lys Glu Ile Met Asp Val Ala Ser Pro Glu Thr Lys Lys Asn Phe
385                 390                 395                 400

Glu Asp Met Ser Met Phe Val Asn Phe Cys Pro Ile Glu Tyr Asn Thr
                405                 410                 415

Met Phe Ala Leu Ile Phe Lys Leu Asn Asn Gly Asp Ile Arg Thr Glu
            420                 425                 430

Gln Ala Ile Arg Arg Thr Leu His Gln Leu Ser Lys Lys Phe Ser Asp
        435                 440                 445

Gly Asn His Glu Thr Glu Arg Ile Tyr Val Gln Asn Val Phe Ser Ile
    450                 455                 460

Arg Glu Gln Leu Lys His Phe Ile Leu Leu Ser Asn Arg Tyr Tyr Ser
465                 470                 475                 480

Glu Gln Ser Asp Tyr Asp Thr Lys Met Gly Phe Ile Asp Glu Asn Thr
                485                 490                 495

Thr Ser Asn Ala Thr Met Asp Lys Arg Arg Phe Asp Lys Ser Leu Met
            500                 505                 510

Phe Arg Tyr Thr Gln Arg Gly Arg Gln Leu Tyr Glu Glu Arg Ile Glu
        515                 520                 525

Cys Gly Arg Lys Ile Thr Glu Ile Arg Asp Asn Ile Ile Thr Tyr Ala
    530                 535                 540

Arg Asn Val Phe Val Leu Asn Gly Tyr Asp Thr Ile Ala Leu Glu Tyr
545                 550                 555                 560

Leu Thr Asn Ala Thr Ile Gln Lys Pro Thr Arg Pro Thr Ser Pro Lys
                565                 570                 575
```

```
Ser Leu Leu Asp Tyr Phe Lys Leu Lys Gly Lys Pro Val Val Glu Ala
            580                 585                 590

Glu Lys Asn Glu Arg Ile Thr Lys Asn Arg Lys Tyr Tyr Asn Leu Ile
        595                 600                 605

Pro Asp Glu Asn Asp Asn Val Ile Asn Ile Glu Tyr Thr Glu Glu Gly
    610                 615                 620

Lys Val Ala Ile Lys Lys Ser Ile Ala Arg Asp His Ile Met Lys Ala
625                 630                 635                 640

Val His Phe Ala Glu Val Lys Asp Lys Phe Ile Gln Leu Ser Asn Asn
                645                 650                 655

Gly Lys Thr Gln Val Ala Leu Val Pro Ser Asn Tyr Thr Ser Gln Met
            660                 665                 670

Asn Ser Glu Thr His Thr Val Tyr Leu Met Lys Asn Pro Lys Thr Lys
        675                 680                 685

Lys Leu Val Ile Met Asp Lys Asp Lys Val Arg Pro Ile Gln Glu Lys
    690                 695                 700

Tyr Lys Leu Asn Gly Leu Asn Ala Asp Phe Asn Ser Ala Arg Asn Ile
705                 710                 715                 720

Ala Tyr Ile Val Glu Asn Glu Ile Leu Arg Asn Ser Phe Leu Lys Glu
                725                 730                 735

Glu Thr Lys Lys Tyr Thr Tyr Asn Thr Pro Leu Phe Thr Pro Arg Leu
            740                 745                 750

Lys Ser Ser Glu Lys Ile Ile Thr Glu Leu Lys Lys Leu Gly Met Thr
        755                 760                 765

Thr Val Ile Glu
    770
```

<210> 29
<211> 781
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 29
Met Ala Asn Lys Ser Thr Lys Gly Asn Leu Pro Lys Thr Ile Ile Met
1 5 10 15

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

Lys Glu Tyr Gln Ala Tyr Lys Asp Thr Leu Ser Lys Trp Val Ala Gln
35 40 45

Asn Leu Thr Ala Met Lys Ile Gly Asp Leu Leu Pro Tyr Leu Asp Lys
50 55 60

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

Tyr Tyr Gln Leu Cys Glu Gln His Lys Asp Glu Pro Leu Tyr Lys Leu
85 90 95

Phe Thr Tyr Asp Ser Asn Ser Arg Asn Asn Ala Met Tyr Glu Ile Ile
100 105 110

Arg Lys Thr Asn Cys Asp Gly Tyr Lys Gly Asn Ile Leu Gly Ile Ser
115 120 125

Glu Thr His Tyr Arg Arg Asn Gly Phe Val Lys Asn Ile Leu Ala Asn
130 135 140

Tyr Thr Thr Lys Ile Ser Thr Leu Glu Leu Ser Glu Arg Lys Arg Lys
145 150 155 160

Ile Asp Ser Asp Ser Pro Glu Asp Leu Ile Arg Ser Gln Val Val Tyr
165 170 175

```
Glu Met Gln Lys Asn Asn Ile Lys Asp Ala Lys Gly Phe Lys Ser Ile
            180                 185                 190

Ile Glu Tyr Leu Lys Ser Lys Lys Glu Val Asn Ile Gln Tyr Leu Glu
        195                 200                 205

Arg Leu Gln Ile Leu Tyr Glu Tyr Phe Lys Asn His Glu Asn Glu Ile
    210                 215                 220

Lys Glu Tyr Ile Thr Leu Ala Ala Val Glu Gln Leu Lys Ser Phe Gly
225                 230                 235                 240

Gly Val Arg Val Asn Asn Glu Lys Ser Ser Met Asn Leu Glu Ile Gln
                245                 250                 255

Gly Phe Ser Ile Thr Arg Val Asp Gly Ala Cys Thr Tyr Ile Leu His
            260                 265                 270

Leu Pro Ile Asn Gly Lys Ile His Gly Ile Lys Leu Trp Gly Asn Arg
        275                 280                 285

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

Thr Asn Gln His Gly Ser Thr Ile Asn Ile Thr Ile Lys Asn Gly Glu
305                 310                 315                 320

Ile Tyr Phe Ala Phe Thr Val Thr Ser Asp Phe Val Lys Pro Glu His
                325                 330                 335

Gln Ile Lys Asn Val Val Gly Val Asp Val Asn Thr Lys His Met Leu
            340                 345                 350

Met Gln Ser Asn Ile Thr Asp Asn Gly Asn Val Lys Gly Tyr Phe Asn
        355                 360                 365

Ile Tyr Lys Val Leu Val Glu Asp Arg Arg Phe Thr Ser Leu Leu Ser
    370                 375                 380

Glu Glu Gln Leu Lys Tyr Phe Cys Glu Leu Ala Asn Ile Val Ser Phe
385                 390                 395                 400
```

```
Cys Pro Ile Glu Thr Glu Phe Leu Phe Ala Arg Tyr Ala Glu Tyr Lys
                405                 410                 415

Lys Met Ser Asn Asn Ala Glu Met Arg Gln Ile Glu Lys Val Phe Ser
            420                 425                 430

Asp Ile Leu Asp Glu Gln Tyr Lys Lys Tyr Lys Asp Ile Asp Thr Ser
        435                 440                 445

Ile Ala Asn Tyr Ile Ser Tyr Val Arg Lys Leu Arg Ser Gln Cys Cys
    450                 455                 460

Ala Tyr Phe Lys Leu Lys Met Lys Tyr Lys Glu Leu Gln Arg Gln Phe
465                 470                 475                 480

Asp Lys Glu Gln Asp Tyr Lys Asp Leu Ser Thr Glu Ser Lys Glu Thr
                485                 490                 495

Met Asp Lys Arg Arg Trp Glu Asn Pro Phe Arg Asn Thr Pro Glu Ala
            500                 505                 510

Ser Lys Leu Ile Lys Lys Met Asp Asn Val Ser Arg Gln Leu Ile Gly
        515                 520                 525

Cys Arg Asp Asn Ile Ile Thr Tyr Ala Tyr Arg Val Phe Glu Lys Asn
    530                 535                 540

Gly Tyr Asp Thr Ile Ser Leu Glu Asn Leu Glu Ser Ser Gln Phe Glu
545                 550                 555                 560

Asn Asn Asp His Val Ile Ala Pro Lys Ser Leu Leu Glu Tyr His His
                565                 570                 575

Leu Lys Gly Lys Thr Met Asn Tyr Leu Leu Ser Asp Glu Cys Lys Val
            580                 585                 590

Arg Ile Thr Thr Lys Asp Gly Lys Val Lys Glu Trp Tyr His Val Glu
        595                 600                 605
```

```
Leu Asn Asp Lys Asp Glu Ile Asp Asn Ile Phe Leu Thr Pro Glu Gly
    610                 615                 620

Glu Thr Glu Lys Glu Lys Asn Leu Phe Asn Asn Met Val Ile Lys Ile
625                 630                 635                 640

Val His Phe Ala Asp Ile Lys Asp Lys Phe Ile Gln Leu Gly Asn Tyr
                645                 650                 655

Asn Lys Leu Gln Thr Val Leu Val Pro Ser Tyr Phe Thr Ser Gln Met
            660                 665                 670

Asp Ser Lys Thr His Ser Val Tyr Val Val Glu Thr Ala Asn Thr Lys
        675                 680                 685

Thr Ser Lys Lys Glu Leu Lys Leu Val Ser Lys Lys Arg Val Arg Arg
    690                 695                 700

Gln Gln Glu Trp His Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala
705                 710                 715                 720

Cys Asn Ile Ala His Ile Ala Lys Asn Ile Glu Leu Arg Gln Ile Met
                725                 730                 735

Cys Lys Thr Pro Gln Thr Lys Asn Gly Tyr Ser Ser Pro Val Leu Thr
            740                 745                 750

Ser Lys Val Lys Ser Gln Val Glu Met Val Arg Glu Leu Lys Lys Met
        755                 760                 765

Gly Lys Thr Ile Leu Tyr Ser Asn Asp Ser Leu Pro Phe
    770                 775                 780
```

<210> 30
<211> 798
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 30

```
Met Ala His Arg Lys Lys Lys Asp Asp Glu Ala Thr Leu Ser Tyr Lys
1               5                   10                  15

Phe Lys Val Lys Val Ile Glu Gly Asp Leu Thr Ala Asp Asp Ile Thr
            20                  25                  30

Lys Cys Ile Ala Glu Asn Ala Glu Gln Gly Asn His Phe Ser Glu Phe
        35                  40                  45

Ile His Lys Asn Leu Thr Ser Lys Thr Ile Gly Glu Phe Ala Ser Gln
    50                  55                  60

Leu Pro Val Glu Lys Arg Gln Phe Gly Tyr Tyr Gln Tyr Ala Ile Gly
65                  70                  75                  80

Gly Thr Met Pro Ala Lys Lys Asn Ala Ser Asp Glu Asp Lys Pro Lys
                85                  90                  95

Gly Glu Leu Ile Asp Trp Ser Lys Lys Pro Phe Tyr Val Leu Phe Ser
            100                 105                 110

Lys Gly Tyr Ser Ala Thr His Ala Val Asn Leu Ile Phe Asn Val Tyr
        115                 120                 125

Leu Asn Ser Glu Glu Gly Lys Ala Phe Ser Ala Lys Asn Ser Met Asn
    130                 135                 140

Leu Ser Lys Ser Gln Phe Ala Tyr Ser Gly Phe Val Gln Ile Val Cys
145                 150                 155                 160

Ala Asn Tyr Ala Ser Met Leu Ala Asn Ala Arg Pro Asp Lys Ile Lys
                165                 170                 175

Phe Glu Glu Ile Thr Glu Ala Thr Asp Asp Gly Thr Lys Lys Met Gln
            180                 185                 190

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

Ala Ser Arg Ile Glu Tyr Leu Glu Ala Asn Asn Thr Lys Gly Lys Phe
    210                 215                 220
```

```
Asp Lys Thr Ile Gln Arg Leu Arg Leu Leu Gln Pro Phe Phe Glu Lys
225                 230                 235                 240

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

Leu Glu His Ser Gly Gln Cys Thr Tyr Lys Gly Gly Arg Thr Ile Ser
            260                 265                 270

Ile Leu Glu Ile Gly Asp Ile Arg Ile Ser Arg Lys Glu Asn Ala Lys
        275                 280                 285

Gly Tyr Leu Leu Thr Ile Pro Ile Asn Arg Lys Ser Val Val Phe Asp
    290                 295                 300

Leu Tyr Gly Arg Lys Asp Thr Ile Gly Gly Asp Gly Arg Asp Leu Ile
305                 310                 315                 320

Asp Ile Met Asn Thr His Gly Ser Ser Leu Gln Phe Thr Ala Asp Gly
                325                 330                 335

Asn Asp Ile Tyr Leu Thr Ile Thr Ala Thr Lys Asn Phe Ile Lys Glu
            340                 345                 350

Lys Pro Thr Phe Asn Glu Asp Thr Val Leu Gly Gly Asp Val Asn Ile
        355                 360                 365

Lys His Ser Tyr Thr Val Phe Ser Thr Ser Pro Lys Asp Ile Pro Asp
    370                 375                 380

Phe Val Asn Phe Tyr Glu Tyr Phe Ala Lys Asp Gly Glu Ile Met Lys
385                 390                 395                 400

Leu Ala Pro Lys Pro Met Trp Asp Tyr Ile Val Ala Ala Ala Thr Lys
                405                 410                 415

Phe Leu Thr Ile Leu Pro Ile Glu Thr Pro Ala Ile Ser Ala Thr Val
            420                 425                 430
```

```
Tyr Gly Lys Arg Thr Glu Glu Gly Ile Ser Arg Ala Thr Phe Arg Glu
        435                 440                 445

Thr Gln Lys Leu Ile Ala Leu Glu Lys Ala Ile Glu Arg Val Met Lys
    450                 455                 460

Gln Val Phe Asp Lys Tyr Asn Asp Gly Lys His Pro Leu Glu Ala Ile
465                 470                 475                 480

Tyr Ile Gly Asn Ala Ile Lys Tyr Arg Arg Leu Ile Lys Gly Tyr Leu
                485                 490                 495

Ala Gln Lys Lys Lys Tyr Tyr Ser Ala His Ser Glu Tyr Asp Lys Ala
            500                 505                 510

Met Gly Tyr Thr Asp Asp Asp Thr Asp Arg Lys Glu Asn Met Asp Glu
        515                 520                 525

Arg Arg Phe Asp Asp Ser Lys Lys Phe Arg Tyr Thr Pro Glu Ala Gln
    530                 535                 540

Ala Leu Leu Asp Thr Met His Thr Ile Glu Lys Lys Ile Val Gly Cys
545                 550                 555                 560

Val Ser Asn Ala Ile Ser Tyr Ala Tyr His Lys Phe Asp Glu Asn Gly
                565                 570                 575

Phe Asn Val Ile Ala Leu Glu Asn Leu Thr Ser Ala Thr Phe Ala Lys
            580                 585                 590

Lys Tyr Lys Ser Asp Lys Pro Glu Ser Ile Lys Lys Leu Leu Asn Phe
        595                 600                 605

Asp Lys Leu Leu Gly Lys Thr Leu Asp Glu Ala Lys Ala Ser Lys Ser
    610                 615                 620

Ile Ser Lys His Pro Asn Trp Tyr Glu Leu Val Ala Asp Glu Asn Gly
625                 630                 635                 640

Cys Val Ser Asp Ile Arg Ile Thr Asp Glu Gly Gln Ser Ala Thr Tyr
                645                 650                 655
```

```
Arg Ser Leu Val Thr Glu Thr Ile Met Lys Val Ser His Phe Ala Glu
            660                 665                 670

Thr Lys Asp Arg Phe Ile Gly Leu Ala Asn Ser Gly Arg Leu Gln Val
        675                 680                 685

Gly Leu Val Pro Ser Gln Tyr Thr Ser Tyr Ile Asp Ser Thr Thr His
    690                 695                 700

Thr Leu Tyr Ala Val Ile Glu Asp Gly Lys Thr Val Leu Ala Pro Lys
705                 710                 715                 720

Glu Val Val Arg Ala Ser Gln Glu Arg His Ile Asn Gly Leu Asn Ala
                725                 730                 735

Asp Tyr Asn Ser Ala Leu Asn Leu Lys Tyr Met Ile Thr Asp Glu Asn
            740                 745                 750

Phe Arg Lys Thr Phe Thr Ser Glu Thr Ser Ala Asp Lys Phe Gly Trp
        755                 760                 765

Gly Lys Pro Met Phe Ser Pro Thr Thr Arg Ser Gln Asp Glu Val Phe
    770                 775                 780

Ser Ala Ile Lys Lys Ile Gly Ala Ile Thr Val Leu Glu Asp
785                 790                 795
```

<210> 31
<211> 786
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 31

```
Met Ala Gln His Lys Ser Asn Asn Glu Glu Ser Ala Ile Asn Lys Thr
1               5                   10                  15

Phe Ile Phe Lys Ala Lys Cys Glu Lys Asn Asp Val Ile Ser Leu Trp
            20                  25                  30
```

```
Glu Pro Ala Ala Lys Glu Tyr Gly Asp Tyr Tyr Asn Lys Val Ser Lys
        35                  40                  45

Trp Ile Ala Asp Asn Leu Ile Thr Met Lys Ile Gly Asp Leu Ala Gln
    50                  55                  60

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

Lys Lys Lys Asp Leu Pro Leu Tyr Arg Ile Phe Gln Lys Gly Phe Ser
                85                  90                  95

Ser Gln Cys Ala Asp Asn Ala Leu Tyr Cys Ala Ile Lys Ser Ile Asn
            100                 105                 110

Pro Glu Asn Tyr Lys Gly Asn Ser Leu Gly Ile Gly Glu Ser Asp Tyr
        115                 120                 125

Arg Arg Phe Gly Tyr Ile Gln Ser Val Val Ser Asn Phe Arg Thr Lys
    130                 135                 140

Met Ser Ser Leu Lys Val Ser Val Lys Tyr Lys Lys Phe Asp Val Ser
145                 150                 155                 160

Asn Val Asp Asp Glu Thr Leu Lys Ile Gln Thr Ile Tyr Asp Val Asp
                165                 170                 175

Lys Tyr Gly Ile Glu Thr Ala Lys Glu Phe Lys Glu Leu Ile Glu Thr
            180                 185                 190

Leu Lys Thr Arg Val Glu Thr Pro Gln Leu Asn Asp Thr Ile Ala Arg
        195                 200                 205

Leu Lys Cys Leu Cys Asp Tyr Tyr Ser Lys Asn Glu Lys Ala Ile Asn
    210                 215                 220

Asn Glu Ile Glu Thr Met Ala Ile Ala Asp Leu Gln Lys Phe Gly Gly
225                 230                 235                 240
```

```
Cys Gln Arg Lys Ser Leu Asn Ala Phe Thr Ile His Lys Gln Asp Ser
                245                 250                 255

Leu Met Glu Lys Val Gly Asn Thr Ser Phe Arg Leu Gln Leu Ser Phe
            260                 265                 270

Arg Lys Lys Thr Tyr Val Ile Asn Leu Leu Gly Asn Arg Gln Val Val
        275                 280                 285

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

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

His Ile Thr Ser Pro Ile Val Phe Asp Lys Asp Val Arg Asp Ile Arg
                325                 330                 335

Asn Val Val Gly Ile Asp Val Asn Ile Lys His Ser Met Leu Ala Thr
            340                 345                 350

Ser Ile Lys Asp Asp Gly Asn Val Lys Gly Tyr Ile Asn Leu Tyr Lys
        355                 360                 365

Glu Leu Leu Asn Asp Asp Val Phe Val Ser Thr Cys Asn Glu Ser Glu
    370                 375                 380

Leu Ala Leu Tyr Arg Gln Met Ser Glu Asn Val Asn Phe Gly Ile Leu
385                 390                 395                 400

Glu Thr Asp Ser Leu Phe Glu Arg Ile Val Asn Gln Ser Lys Gly Gly
                405                 410                 415

Cys Leu Lys Asn Lys Leu Ile Arg Arg Glu Leu Ala Met Gln Lys Val
            420                 425                 430

Phe Glu Arg Ile Thr Lys Thr Asn Lys Asp Gln Asn Ile Val Asp Tyr
        435                 440                 445

Val Asn Tyr Val Lys Met Met Arg Ala Lys Cys Lys Ala Ser Tyr Ile
    450                 455                 460
```

```
Leu Lys Glu Lys Tyr Asp Glu Lys Gln Lys Glu Tyr Tyr Val Lys Met
465                 470                 475                 480

Gly Phe Thr Asp Glu Ser Thr Glu Ser Lys Glu Thr Met Asp Lys Arg
                485                 490                 495

Arg Glu Glu Phe Pro Phe Val Asn Thr Asp Thr Ala Lys Glu Leu Leu
            500                 505                 510

Val Lys Gln Asn Asn Ile Arg Gln Asp Ile Ile Gly Cys Arg Asp Asn
        515                 520                 525

Ile Val Thr Tyr Ala Phe Asn Val Phe Lys Asn Asn Glu Tyr Asp Thr
    530                 535                 540

Leu Ser Val Glu Tyr Leu Asp Ser Ser Gln Phe Asp Lys Arg Arg Ile
545                 550                 555                 560

Pro Thr Pro Lys Ser Leu Leu Lys Tyr His Lys Phe Glu Gly Lys Thr
                565                 570                 575

Lys Asp Glu Val Glu Asn Met Met Lys Ser Glu Lys Leu Ser Asn Ala
            580                 585                 590

Tyr Tyr Thr Phe Lys Tyr Glu Asn Asp Val Val Ser Asp Ile Asp Tyr
        595                 600                 605

Ser Asp Glu Gly Asn Leu Arg Arg Ser Lys Leu Asn Phe Gly Asn Trp
    610                 615                 620

Ile Ile Lys Ala Ile His Phe Ala Asp Ile Lys Asp Lys Phe Val Gln
625                 630                 635                 640

Leu Ser Asn Asn Asn Lys Met Asn Ile Val Phe Cys Pro Ser Ala Phe
                645                 650                 655

Ser Ser Gln Met Asp Ser Ile Thr His Thr Leu Tyr Tyr Val Glu Lys
            660                 665                 670
```

```
Ile Thr Lys Asn Lys Lys Gly Lys Glu Lys Lys Lys Tyr Val Leu Ala
        675                 680                 685

Asn Lys Lys Met Val Arg Thr Gln Gln Glu Thr His Ile Asn Gly Leu
    690                 695                 700

Asn Ala Asp Tyr Asn Ser Ala Cys Asn Leu Lys Tyr Ile Ala Leu Asn
705                 710                 715                 720

Tyr Glu Leu Arg Asp Lys Met Thr Asp Arg Phe Lys Ala Ser Lys Lys
                725                 730                 735

Ile Lys Thr Met Tyr Asn Ile Pro Ala Tyr Asn Ile Lys Ser Asn Phe
            740                 745                 750

Lys Lys Asn Leu Ser Ala Lys Thr Ile Gln Thr Phe Arg Glu Leu Gly
        755                 760                 765

His Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Met Phe Val Glu Ile
    770                 775                 780

Leu Glu
785
```

<210> 32
<211> 781
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 32

```
Met Ala His Lys Asn Ser Asp Gly Glu Asn Thr Ile Asn Lys Thr Phe
1               5                   10                  15

Ile Phe Lys Val Lys Cys Glu Lys Asn Asp Ile Ile Ser Phe Trp Lys
            20                  25                  30

Pro Ala Ala Glu Glu Tyr Cys Asn Tyr Tyr Asn Lys Leu Ser Glu Trp
        35                  40                  45
```

```
Ile Gly Lys Asn Leu Ile Ser Met Lys Ile Gly Asp Leu Ala Lys Tyr
    50                  55                  60

Ile Asp Asn Pro Lys Ser Lys Tyr Tyr Leu Ser Val Thr Asp Glu Asn
65                  70                  75                  80

Lys Lys Asp Leu Pro Leu Tyr Lys Ile Phe Gln Lys Gly Phe Ser Ser
                85                  90                  95

Ile Asp Ala Asp Asn Ala Leu Tyr Cys Ala Ile Asp Lys Leu Asn Pro
            100                 105                 110

Glu Gly Tyr Asn Gly Asn Ile Leu Gly Val Gly Lys Ser Asp Tyr Arg
        115                 120                 125

Arg Asn Gly Tyr Val Ser Ser Val Ile Gly Asn Phe Arg Thr Lys Met
    130                 135                 140

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

Val Asp Glu Glu Thr Leu Arg Arg Gln Thr Ile Cys Asp Val Glu Lys
                165                 170                 175

Tyr Arg Ile Glu Ser Glu Lys Asp Phe Arg Asp Leu Ile Asp Ile Leu
            180                 185                 190

Lys Ala Arg Glu Glu Thr Pro Arg Leu Lys Glu Lys Ile Ser Arg Leu
        195                 200                 205

Glu Leu Leu Tyr Asp Tyr Tyr Ser Lys Asn Thr Lys Thr Ile Lys Ser
    210                 215                 220

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

Val Arg Lys Ser Leu Asn Thr Ile Thr Ile His Lys Gln Asp Ser Lys
                245                 250                 255

Ile Glu Lys Glu Gly Asn Thr Ser Phe Arg Leu His Met Val Phe Asn
            260                 265                 270
```

```
Lys Lys Pro Tyr Thr Ile Thr Leu Leu Gly Asn Arg Gln Val Val Lys
        275                 280                 285

Tyr Ile Asp Gly Lys Arg Val Asp Ile Val Asn Ile Val Glu Lys His
    290                 295                 300

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

Leu Thr Lys Cys Val Glu Phe Ser Lys Gly Gln Lys Glu Ile Lys Lys
                325                 330                 335

Ala Ala Gly Val Asp Val Asn Ile Lys His Ala Met Leu Ala Ala Ser
            340                 345                 350

Ile Val Asp Asp Gly Gln Leu Lys Gly Tyr Val Asn Leu Tyr Arg Glu
        355                 360                 365

Leu Ile Glu Asp Asp Asp Phe Val Ser Thr Phe Gly Asp Ser Asp Ser
    370                 375                 380

Gly Lys Thr Glu Leu Gly Met Tyr Gln Lys Met Ala Lys Thr Val Phe
385                 390                 395                 400

Phe Gly Val Leu Glu Val Glu Ser Leu Phe Glu Arg Val Val Asn Gln
                405                 410                 415

Gln Ser Gly Trp Lys Leu Asp Asn Gln Leu Ile Arg Arg Glu Arg Ala
            420                 425                 430

Met Glu Lys Val Phe Asp Arg Ile Val Lys Thr Thr Ser Asn Lys His
        435                 440                 445

Ile Ile Asp Tyr Val Asn Tyr Val Lys Met Leu Arg Ala Lys Tyr Lys
    450                 455                 460

Ala Tyr Phe Ile Leu Asp Glu Lys Tyr His Glu Lys Gln Arg Glu Tyr
465                 470                 475                 480
```

```
Asp Leu Ser Met Gly Phe Thr Asp Glu Ser Asp Glu Arg Arg Glu Leu
                485                 490                 495

Tyr Pro Phe Ile Asn Thr Glu Thr Ala Lys Glu Ile Leu Gly Lys Lys
            500                 505                 510

Arg Asn Val Glu Gln Asp Leu Ile Gly Cys Arg Asp Asn Ile Val Thr
        515                 520                 525

Tyr Ala Phe Asn Val Leu Arg Asn Asn Gly Tyr Asp Thr Ile Ser Val
    530                 535                 540

Glu Tyr Leu Asp Ser Ser Gln Phe Asp Lys Arg Arg Met Pro Thr Pro
545                 550                 555                 560

Lys Ser Leu Leu Glu Tyr His Lys Phe Lys Gly Lys Thr Gln Asp Glu
                565                 570                 575

Val Glu Arg Leu Met Ser Glu Lys Lys Phe Ala Lys Thr Asn Tyr Asp
            580                 585                 590

Ile His Tyr Asp Gly Glu Asn Lys Val Asp Gly Ile Val Tyr Ser Lys
        595                 600                 605

Glu Gly Glu Leu Arg Gln Lys Lys Leu Asn Phe Met Asn Leu Val Ile
    610                 615                 620

Lys Ala Ile His Phe Ala Asp Ile Lys Asp Lys Phe Ala Gln Leu Cys
625                 630                 635                 640

Asn Asn Asn Asp Val Asn Val Val Phe Gly Pro Ser Ala Phe Thr Ser
                645                 650                 655

Gln Met Asp Ser Glu Thr His Ser Leu Tyr Tyr Val Glu Lys Glu Thr
            660                 665                 670

Asn Gly Lys Asn Gly Lys Thr Gly Lys Lys Phe Val Leu Ala Asp Lys
        675                 680                 685

Lys Ser Val Arg Arg Arg Gln Glu Thr His Ile Asn Gly Leu Asn Ala
    690                 695                 700
```

```
Asp Phe Asn Ala Ala Arg Asn Leu Glu Tyr Ile Ala Ser Asn Pro Glu
705                 710                 715                 720


Leu Leu Glu Arg Met Thr Lys Arg Thr Lys Ser Gly Lys Asp Met Tyr
                725                 730                 735


Asn Thr Pro Ser Trp Asn Ile Arg Gln Glu Phe Lys Lys Asn Leu Ser
            740                 745                 750


Val Arg Thr Ile Asn Thr Phe Arg Glu Leu Gly Asn Val Lys Tyr Gly
        755                 760                 765


Lys Ile Asn Asn Glu Gly Leu Phe Val Glu Asp Asp Val
    770                 775                 780


<210> 33
<211> 798
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-bos taurus sequence

<400> 33
Met Ala His Arg Lys Lys Lys Asp Asp Glu Ala Thr Leu Ser Tyr Lys
1               5                   10                  15


Phe Lys Val Lys Val Ile Glu Gly Asp Leu Thr Ala Asp Asp Ile Thr
            20                  25                  30


Lys Cys Ile Ala Glu Asn Ala Glu Gln Gly Asn His Phe Ser Glu Phe
        35                  40                  45


Ile His Lys Asn Leu Thr Ser Lys Thr Ile Gly Glu Phe Ala Ser Gln
    50                  55                  60


Leu Pro Ala Glu Lys Arg Gln Phe Gly Tyr Tyr Gln Tyr Ala Ile Gly
65                  70                  75                  80


Gly Thr Met Pro Ala Lys Lys Asn Ala Ser Asp Glu Asp Lys Pro Lys
                85                  90                  95
```

```
Gly Glu Leu Ile Asp Trp Ser Lys Lys Pro Phe Tyr Val Leu Phe Ser
            100                 105                 110

Lys Gly Tyr Ser Ala Thr His Ala Val Asn Leu Ile Phe Asn Val Tyr
        115                 120                 125

Leu Asn Ser Glu Glu Gly Lys Ala Phe Ser Ala Lys Asn Ser Met Asn
    130                 135                 140

Leu Ser Lys Ser Gln Phe Ala Tyr Ser Gly Phe Val Gln Ile Val Cys
145                 150                 155                 160

Ala Asn Tyr Ala Ser Met Leu Ala Asn Ala Arg Pro Asp Lys Ile Lys
                165                 170                 175

Phe Glu Glu Ile Thr Glu Ala Thr Asp Asp Gly Thr Lys Lys Met Gln
            180                 185                 190

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

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

Asp Lys Thr Ile Gln Arg Leu Arg Leu Leu Gln Pro Phe Phe Glu Lys
225                 230                 235                 240

Asn Glu Glu Ser Ile Thr Glu Leu Tyr Tyr Asp Leu Ser Val Lys Ala
                245                 250                 255

Leu Glu His Ser Gly Gln Cys Thr Tyr Lys Gly Gly Arg Thr Ile Ser
            260                 265                 270

Ile Leu Glu Ile Gly Asp Ile Arg Ile Ser Arg Lys Glu Asn Ala Lys
        275                 280                 285

Gly Tyr Leu Leu Thr Ile Pro Ile Asn Arg Lys Ser Val Val Phe Asp
    290                 295                 300
```

```
Leu Tyr Gly Arg Lys Asp Thr Ile Gly Gly Asp Gly Arg Asp Leu Ile
305                 310                 315                 320

Asp Ile Met Asn Thr His Gly Ser Ser Leu Gln Phe Thr Ala Asp Glu
                325                 330                 335

Asn Asp Ile Tyr Leu Thr Ile Thr Ala Thr Lys Asn Phe Ile Lys Glu
            340                 345                 350

Lys Pro Thr Phe Asn Glu Asp Thr Val Leu Gly Gly Asp Val Asn Ile
        355                 360                 365

Lys His Ser Tyr Thr Val Phe Ser Ala Ser Pro Lys Asp Ile Pro Asp
    370                 375                 380

Phe Val Asn Phe Tyr Glu Tyr Phe Ala Lys Asp Gly Glu Ile Met Lys
385                 390                 395                 400

Leu Ala Pro Lys Pro Met Trp Asp Tyr Ile Val Ala Ala Ala Thr Lys
                405                 410                 415

Phe Leu Thr Ile Leu Pro Ile Glu Thr Pro Ala Ile Ser Ala Thr Val
            420                 425                 430

Tyr Gly Lys Arg Thr Glu Glu Gly Ile Ser Arg Ala Thr Phe Arg Glu
        435                 440                 445

Thr Gln Lys Leu Ile Ala Leu Glu Lys Ala Ile Glu Arg Val Met Lys
    450                 455                 460

Gln Val Phe Asp Lys Tyr Asn Asp Gly Lys His Pro Leu Glu Ala Ile
465                 470                 475                 480

Tyr Ile Gly Asn Ala Ile Lys Tyr Arg Arg Leu Ile Lys Gly Tyr Leu
                485                 490                 495

Ala Gln Lys Lys Lys Tyr Tyr Ser Ala His Ser Glu Tyr Asp Lys Ala
            500                 505                 510

Met Gly Tyr Thr Asp Asp Asp Thr Asp Arg Lys Glu Asn Met Asp Glu
        515                 520                 525
```

```
Arg Arg Phe Asp Asp Ser Lys Lys Phe Arg Tyr Thr Pro Glu Ala Gln
    530                 535                 540

Ala Leu Leu Asp Thr Met His Thr Ile Glu Lys Lys Ile Val Gly Cys
545                 550                 555                 560

Val Ser Asn Ala Ile Ser Tyr Ala Tyr His Lys Phe Asp Glu Asn Gly
                565                 570                 575

Phe Asn Val Ile Ala Leu Glu Asn Leu Thr Ser Ala Thr Phe Ala Lys
            580                 585                 590

Lys Tyr Lys Ser Asp Lys Pro Glu Ser Ile Lys Lys Leu Leu Asn Phe
        595                 600                 605

Asp Lys Leu Leu Gly Lys Thr Leu Asp Glu Ala Lys Ala Ser Lys Ser
    610                 615                 620

Ile Ser Lys His Pro Asn Trp Tyr Glu Leu Val Ala Asp Glu Asn Gly
625                 630                 635                 640

Cys Val Ser Asp Ile Arg Ile Thr Asp Glu Gly Gln Ser Ala Thr Tyr
                645                 650                 655

Arg Ser Leu Val Thr Glu Thr Ile Met Lys Val Ser His Phe Ala Glu
            660                 665                 670

Thr Lys Asp Arg Phe Ile Gly Leu Ala Asn Ser Gly Arg Leu Gln Val
        675                 680                 685

Gly Leu Val Pro Ser Gln Tyr Thr Ser Tyr Ile Asp Ser Thr Thr His
    690                 695                 700

Thr Leu Tyr Ala Val Ile Glu Asp Gly Lys Thr Val Leu Ala Pro Lys
705                 710                 715                 720

Glu Val Val Arg Ala Ser Gln Glu Arg His Ile Asn Gly Leu Asn Ala
                725                 730                 735
```

```
Asp Tyr Asn Ser Ala Leu Asn Leu Lys Tyr Met Ile Thr Asp Glu Asn
            740                 745                 750

Phe Arg Lys Thr Phe Thr Ser Glu Thr Ser Ala Asp Lys Phe Gly Trp
        755                 760                 765

Gly Lys Pro Met Phe Ser Pro Thr Thr Arg Ser Gln Asp Glu Val Phe
    770                 775                 780

Ser Ala Ile Lys Lys Ile Gly Ala Ile Thr Val Leu Glu Asp
785                 790                 795
```

<210> 34
<211> 724
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 34

```
Met Val Thr Thr Leu Ala Pro Leu Ile Glu Glu Lys Lys Arg Asp Ser
1               5                   10                  15

Glu Tyr Tyr Lys Tyr Leu Thr Asn Gly Asp Trp Asp Gly Lys Pro Leu
            20                  25                  30

Tyr Phe Ile Phe Lys Glu Gly Phe Asn Ser Thr Asn Ala Asp Asn Ile
        35                  40                  45

Leu Ala Asn Ser Leu Val Arg Val Tyr Cys Glu Gln Asn Tyr Thr Gly
    50                  55                  60

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

Lys Glu Val Ile Ala Asn Tyr Arg Ser Ser Phe Gln Lys Pro Lys Val
                85                  90                  95

Lys Ile Lys Lys Lys Lys Leu Ser Glu Asn Pro Thr Glu Asp Glu Leu
            100                 105                 110
```

```
Ile Glu Gln Cys Ile Tyr Thr Ile Tyr Tyr Glu Phe Asn Glu Lys Lys
        115                 120                 125

Asp Ile Lys Lys Trp Lys Asp Glu Ile Lys Phe Leu Lys Glu Arg Gly
    130                 135                 140

Glu Ser Lys Glu Thr Arg Leu Lys Arg Ile Gln Thr Leu Phe Glu Phe
145                 150                 155                 160

Tyr Lys Asp Lys Asn His Lys Glu Leu Val Asp Glu Arg Val Ala Asn
                165                 170                 175

Leu Val Val Asp Asn Ile Lys Glu Phe Gly Gly Cys Lys Arg Asp Ile
            180                 185                 190

Gly Cys Pro Ser Met Gly Ile Gln Ile Gln His Asn Phe Asp Ile Ser
        195                 200                 205

Ile Asn Glu Lys Arg Asn Gly Tyr Thr Ile Cys Phe Gly Pro Asn Lys
    210                 215                 220

Lys Asn Leu Thr Lys Leu Glu Val Phe Gly Asn Arg Met Val Leu Leu
225                 230                 235                 240

Asn Gly Glu Glu Ile Val Asp Leu Pro Asn Thr His Gly Glu Lys Leu
                245                 250                 255

Thr Leu Ile Asp Arg Gly Asn Ala Ile Tyr Ala Ala Leu Thr Ala Gln
            260                 265                 270

Val Pro Phe Glu Lys His Met Pro Asp Gly Asn Lys Thr Val Gly Ile
        275                 280                 285

Asp Leu Asn Leu Lys His Ser Val Phe Ala Thr Ser Ile Val Asp Asn
    290                 295                 300

Gly Lys Leu Ala Gly Tyr Ile Ser Ile Tyr Lys Glu Leu Leu Lys Asp
305                 310                 315                 320

Asp Glu Phe Val Lys Tyr Cys Pro Lys Asp Leu Leu Arg Phe Met Lys
                325                 330                 335
```

```
Asp Ala Ser Lys Tyr Val Phe Phe Ala Pro Ile Glu Ile Glu Leu Leu
            340                 345                 350

Arg Ser Arg Val Ile Tyr Asn Lys Gly Tyr Ala Cys Val Glu Asn Tyr
        355                 360                 365

Glu Asn Val Tyr Lys Ala Glu Val Ala Phe Val Asn Val Ile Lys Arg
    370                 375                 380

Leu Gln Ser Gln Cys Glu Ala Asn Gly Asp Ala Gln Gly Ala Leu Tyr
385                 390                 395                 400

Met Ser Tyr Leu Ser Lys Met Arg Ala Gln Leu Lys Asn Tyr Ile Asn
                405                 410                 415

Leu Lys Leu Ala Tyr Tyr Asp His Gln Ser Ala Tyr Asp Leu Lys Met
            420                 425                 430

Gly Phe Asn Asp Ile Ser Ala Glu Ser Lys Glu Thr Ile Asp Glu Arg
        435                 440                 445

Arg Lys Leu Phe Pro Phe Ser Lys Glu Lys Glu Ala Gln Glu Ile Leu
    450                 455                 460

Ala Lys Met Lys Asn Ile Ser Asn Val Ile Ile Ala Cys Arg Asn Asn
465                 470                 475                 480

Ile Ala Val Tyr Met Tyr Lys Met Phe Glu Arg Asn Gly Tyr Asp Phe
                485                 490                 495

Ile Gly Leu Glu Lys Leu Glu Ser Ser Gln Met Lys Lys Arg Gln Ser
            500                 505                 510

Arg Ser Phe Pro Thr Val Lys Ser Leu Leu Asn Tyr His Lys Leu Ala
        515                 520                 525

Gly Met Thr Met Asp Glu Ile Lys Lys Gln Glu Val Ser Ser Asn Ile
    530                 535                 540
```

```
Lys Lys Gly Phe Tyr Asp Leu Glu Phe Asp Ala Asp Gly Lys Leu Tyr
545                 550                 555                 560

Gly Ala Lys Tyr Ser Asn Lys Gly Asn Val His Phe Ile Glu Asp Glu
                565                 570                 575

Phe Tyr Ile Ser Gly Leu Lys Ala Ile His Phe Ala Asp Met Lys Asp
            580                 585                 590

Tyr Phe Val Arg Leu Ser Asn Asn Gly Lys Val Ser Val Ala Leu Val
        595                 600                 605

Pro Pro Ser Phe Thr Ser Gln Met Asp Ser Val Glu His Lys Phe Phe
    610                 615                 620

Met Lys Lys Asn Ala Asn Gly Lys Leu Ile Val Ala Asp Lys Lys Asp
625                 630                 635                 640

Val Arg Ser Cys Gln Glu Lys His Lys Ile Asn Gly Leu Asn Ala Asp
                645                 650                 655

Tyr Asn Ala Ala Cys Asn Ile Gly Phe Ile Val Glu Asp Asp Tyr Met
            660                 665                 670

Arg Glu Ser Leu Leu Gly Ser Pro Thr Gly Gly Thr Tyr Asp Thr Ala
        675                 680                 685

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

Lys Glu Asn Gly Glu Thr Tyr Ile Ala Val Leu Ser Asp Asp Val Ile
705                 710                 715                 720

Thr Ala Glu Glu
```

<210> 35
<211> 772
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 35

```
Met Gly Asn Lys Val Gln Ser Asn Glu Thr Ile Val Lys Thr Tyr Thr
1               5                  10                  15

Phe Lys Val Arg Glu Phe Ile Ser Gly Ala Thr His Glu Ile Met Lys
            20                  25                  30

Ser Ala Ile Lys Gln Tyr Ile Glu Asp Ser Asn Asn Leu Ser Asp Trp
        35                  40                  45

Ile Asn Asn Gln Leu Thr Asn Lys Thr Ile Cys Glu Val Gly Ala Leu
    50                  55                  60

Ile Pro Ile Glu Lys Arg Glu Thr Ser Tyr Tyr Lys Ser Thr Val Asp
65                  70                  75                  80

Glu Leu Trp Ala Asn Lys Pro Cys Phe Lys Met Phe Thr Asn Asp Phe
                85                  90                  95

Thr Lys Glu Glu Asn Phe Ala Thr Arg Asn Ile Gly Asn Gly Lys Asn
            100                 105                 110

Cys Lys Asn Ile Ile Thr Ser Ala Tyr Lys Ser Thr Val Asn Pro Ser
        115                 120                 125

Phe Arg Asn Val Leu Asp Leu Thr Glu Lys Val Tyr Phe Ser Asp Gly
    130                 135                 140

Tyr Gly Ala Asn Val Cys Ser Asn Tyr Lys Thr Lys Leu Arg Thr Leu
145                 150                 155                 160

Lys Pro Ala Lys Ile Lys Leu Val Ser Ser Leu Ser Asp Cys Asp Asp
                165                 170                 175

Asn Thr Leu Thr Glu Gln Val Ile Arg Glu Lys Gln Lys Tyr Gly Tyr
            180                 185                 190

Ser Thr Pro Lys Asp Phe Glu Lys Arg Ile Glu Tyr Leu Asn Glu Lys
        195                 200                 205
```

```
Glu Lys Ser Glu Gln Asn Ser Lys Ile Ile Glu Arg Leu Gln Lys Leu
    210                 215                 220

Tyr Glu Phe Tyr Asp Asn Asn Thr Lys Leu Val Glu Glu Lys Glu Leu
225                 230                 235                 240

Glu Leu Ser Val Lys Ser Leu Val Glu Phe Gly Gly Cys Arg Arg Gly
                245                 250                 255

Glu Lys Thr Met Thr Leu Asn Leu Pro Asp Ile Gly Tyr Glu Ile Gln
            260                 265                 270

Arg Lys Asp Asp Lys Tyr Gly Tyr Ile Phe Thr Leu Lys Cys Ser Lys
        275                 280                 285

Lys Arg Lys Ile Ile Ile Asp Val Trp Gly Ser Lys Ala Thr Ile Asp
    290                 295                 300

Ser Asn Gly Asn Asp Lys Val Asp Ile Ile Asn Thr His Gly Lys Ser
305                 310                 315                 320

Ile Asn Phe Lys Ile Ile Asn Asn Glu Met Tyr Ile Asp Ile Thr Val
                325                 330                 335

Asp Val Pro Phe Ala Lys Arg Lys Leu Gly Ile Lys Lys Val Val Gly
            340                 345                 350

Ile Asp Val Asn Thr Lys His Met Leu Met Ala Thr Asn Ile Lys Val
        355                 360                 365

Thr Asp Ser Ile Lys Gly Tyr Val Asn Leu Tyr Lys Glu Phe Leu Asn
    370                 375                 380

Ser Lys Glu Ile Met Asp Val Ala Ser Pro Glu Thr Lys Lys Asn Phe
385                 390                 395                 400

Glu Asp Met Ser Met Phe Val Asn Phe Cys Pro Ile Glu Tyr Asn Thr
                405                 410                 415
```

```
Met Phe Ala Leu Ile Phe Lys Leu Asn Asn Gly Asp Ile Arg Thr Glu
            420                 425                 430

Gln Ala Ile Arg Arg Thr Leu His Gln Leu Ser Lys Lys Phe Ser Asp
        435                 440                 445

Gly Asn His Glu Thr Glu Arg Ile Tyr Val Gln Asn Val Phe Ser Ile
    450                 455                 460

Arg Glu Gln Leu Lys His Phe Ile Leu Leu Ser Asn Arg Tyr Tyr Ser
465                 470                 475                 480

Glu Gln Ser Asp Tyr Asp Thr Lys Met Gly Phe Ile Asp Glu Asn Thr
                485                 490                 495

Thr Ser Asn Ala Thr Met Asp Lys Arg Arg Phe Asp Lys Ser Leu Met
            500                 505                 510

Phe Arg Tyr Thr Gln Arg Gly Arg Gln Leu Tyr Glu Glu Arg Ile Glu
        515                 520                 525

Cys Gly Arg Lys Ile Thr Glu Ile Arg Asp Asn Ile Ile Thr Tyr Ala
    530                 535                 540

Arg Asn Val Phe Val Leu Asn Gly Tyr Asp Thr Ile Ala Leu Glu Tyr
545                 550                 555                 560

Leu Thr Asn Ala Thr Ile Gln Lys Pro Thr Arg Pro Thr Ser Pro Lys
                565                 570                 575

Ser Leu Leu Asp Tyr Phe Lys Leu Lys Gly Lys Pro Val Val Glu Ala
            580                 585                 590

Glu Lys Asn Glu Arg Ile Thr Lys Asn Arg Lys Tyr Tyr Asn Leu Ile
        595                 600                 605

Pro Asp Glu Asn Asp Asn Val Ile Asn Ile Glu Tyr Thr Glu Glu Gly
    610                 615                 620

Lys Val Ala Ile Lys Lys Ser Ile Ala Arg Asp His Ile Met Lys Ala
625                 630                 635                 640
```

```
Val His Phe Ala Glu Val Lys Asp Lys Phe Ile Gln Leu Ser Asn Asn
                645                 650                 655


Gly Lys Thr Gln Val Ala Leu Val Pro Ser Asn Tyr Thr Ser Gln Met
            660                 665                 670


Asn Ser Glu Thr His Thr Val Tyr Leu Met Lys Asn Pro Lys Thr Lys
        675                 680                 685


Lys Leu Val Ile Met Asp Lys Asp Lys Val Arg Pro Ile Gln Glu Lys
    690                 695                 700


Tyr Lys Leu Asn Gly Leu Asn Ala Asp Phe Asn Ser Ala Arg Asn Ile
705                 710                 715                 720


Ala Tyr Ile Val Glu Asn Glu Ile Leu Arg Asn Ser Phe Leu Lys Glu
                725                 730                 735


Glu Thr Lys Lys Tyr Thr Tyr Asn Thr Pro Leu Phe Thr Pro Arg Leu
            740                 745                 750


Lys Ser Ser Glu Lys Ile Ile Thr Glu Leu Lys Lys Leu Gly Met Thr
        755                 760                 765


Thr Val Ile Glu
    770


<210> 36
<211> 781
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-bos taurus sequence

<400> 36
Met Ala Asn Lys Ser Thr Lys Gly Asn Leu Pro Lys Thr Ile Ile Met
1               5                   10                  15


Lys Ala Asn Leu Ser Pro Asp Gly Phe Thr Gln Trp Glu Arg Val Val
            20                  25                  30
```

```
Lys Glu Tyr Gln Ala Tyr Lys Asp Thr Leu Ser Lys Trp Val Ala Gln
        35                  40                  45

Asn Leu Thr Ala Met Lys Ile Gly Asp Leu Leu Pro Tyr Leu Asp Lys
    50                  55                  60

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

Tyr Tyr Gln Leu Cys Glu Gln His Lys Asp Glu Pro Leu Tyr Lys Leu
                85                  90                  95

Phe Thr Tyr Asp Ser Asn Ser Arg Asn Asn Ala Met Tyr Glu Ile Ile
            100                 105                 110

Arg Lys Thr Asn Cys Asp Gly Tyr Lys Gly Asn Ile Leu Gly Ile Ser
        115                 120                 125

Glu Thr His Tyr Arg Arg Asn Gly Phe Val Lys Asn Ile Leu Ala Asn
    130                 135                 140

Tyr Thr Thr Lys Ile Ser Thr Leu Glu Leu Ser Glu Arg Lys Arg Lys
145                 150                 155                 160

Ile Asp Ser Asp Ser Pro Glu Asp Leu Ile Arg Ser Gln Val Val Tyr
                165                 170                 175

Glu Met Gln Lys Asn Asn Ile Lys Asp Ala Lys Gly Phe Lys Ser Ile
            180                 185                 190

Ile Glu Tyr Leu Lys Ser Lys Lys Glu Val Asn Ile Gln Tyr Leu Glu
        195                 200                 205

Arg Leu Gln Ile Leu Tyr Glu Tyr Phe Lys Asn His Glu Asn Glu Ile
    210                 215                 220

Lys Glu Tyr Ile Thr Leu Ala Ala Val Glu Gln Leu Lys Ser Phe Gly
225                 230                 235                 240
```

```
Gly Val Arg Val Asn Asn Glu Lys Ser Ser Met Asn Leu Glu Ile Gln
                245                 250                 255

Gly Phe Ser Ile Thr Arg Val Asp Gly Ala Cys Thr Tyr Ile Leu His
            260                 265                 270

Leu Pro Ile Asn Gly Lys Ile His Gly Ile Lys Leu Trp Gly Asn Arg
        275                 280                 285

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

Thr Asn Gln His Gly Ser Thr Ile Asn Ile Thr Ile Lys Asn Gly Glu
305                 310                 315                 320

Ile Tyr Phe Ala Phe Thr Val Thr Ser Asp Phe Val Lys Pro Glu His
                325                 330                 335

Gln Ile Lys Asn Val Val Gly Val Asp Val Asn Thr Lys His Met Leu
            340                 345                 350

Met Gln Ser Asn Ile Thr Asp Asn Gly Asn Val Lys Gly Tyr Phe Asn
        355                 360                 365

Ile Tyr Lys Val Leu Val Glu Asp Arg Arg Phe Thr Ser Leu Leu Ser
    370                 375                 380

Glu Glu Gln Leu Lys Tyr Phe Cys Glu Leu Ala Asn Ile Val Ser Phe
385                 390                 395                 400

Cys Pro Ile Glu Thr Glu Phe Leu Phe Ala Arg Tyr Ala Glu Tyr Lys
                405                 410                 415

Lys Met Ser Asn Asn Ala Glu Met Arg Gln Ile Glu Lys Val Phe Ser
            420                 425                 430

Asp Ile Leu Asp Glu Gln Tyr Lys Lys Tyr Lys Asp Ile Asp Thr Ser
        435                 440                 445

Ile Ala Asn Tyr Ile Ser Tyr Val Arg Lys Leu Arg Ser Gln Cys Cys
    450                 455                 460
```

```
Ala Tyr Phe Lys Leu Lys Met Lys Tyr Lys Glu Leu Gln Arg Gln Phe
465                 470                 475                 480

Asp Lys Glu Gln Asp Tyr Lys Asp Leu Ser Thr Glu Ser Lys Glu Thr
                485                 490                 495

Met Asp Lys Arg Arg Trp Glu Asn Pro Phe Arg Asn Thr Pro Glu Ala
            500                 505                 510

Ser Lys Leu Ile Lys Lys Met Asp Asn Val Ser Arg Gln Leu Ile Gly
        515                 520                 525

Cys Arg Asp Asn Ile Ile Thr Tyr Ala Tyr Arg Val Phe Glu Lys Asn
    530                 535                 540

Gly Tyr Asp Thr Ile Ser Leu Glu Asn Leu Glu Ser Ser Gln Phe Glu
545                 550                 555                 560

Asn Asn Asp His Val Ile Ala Pro Lys Ser Leu Leu Glu Tyr His His
                565                 570                 575

Leu Lys Gly Lys Thr Met Asn Tyr Leu Leu Ser Asp Glu Cys Lys Val
            580                 585                 590

Arg Ile Thr Thr Lys Asp Gly Lys Val Lys Glu Trp Tyr His Val Glu
        595                 600                 605

Leu Asn Asp Lys Asp Glu Ile Asp Asn Ile Phe Leu Thr Pro Glu Gly
    610                 615                 620

Glu Thr Glu Lys Glu Lys Asn Leu Phe Asn Asn Met Val Ile Lys Ile
625                 630                 635                 640

Val His Phe Ala Asp Ile Lys Asp Lys Phe Ile Gln Leu Gly Asn Tyr
                645                 650                 655

Asn Lys Leu Gln Thr Val Leu Val Pro Ser Tyr Phe Thr Ser Gln Met
            660                 665                 670
```

```
Asp Ser Lys Thr His Ser Val Tyr Val Val Glu Thr Ala Asn Thr Lys
        675                 680                 685

Thr Ser Lys Lys Glu Leu Lys Leu Val Ser Lys Lys Arg Val Arg Arg
    690                 695                 700

Gln Gln Glu Trp His Ile Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala
705                 710                 715                 720

Cys Asn Ile Ala His Ile Ala Lys Asn Ile Glu Leu Arg Gln Ile Met
                725                 730                 735

Cys Lys Thr Pro Gln Thr Lys Asn Gly Tyr Ser Ser Pro Val Leu Thr
            740                 745                 750

Ser Lys Val Lys Ser Gln Val Glu Met Val Arg Glu Leu Lys Lys Met
        755                 760                 765

Gly Lys Thr Ile Leu Tyr Ser Asn Asp Ser Leu Pro Phe
    770                 775                 780
```

<210> 37
<211> 798
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 37

```
Met Ala His Arg Lys Lys Lys Asp Asp Glu Ala Thr Leu Ser Tyr Lys
1               5                   10                  15

Phe Lys Val Lys Val Ile Glu Gly Asp Leu Thr Ala Asp Asp Ile Thr
            20                  25                  30

Lys Cys Ile Ala Glu Asn Ala Glu Gln Gly Asn His Phe Ser Glu Phe
        35                  40                  45

Ile His Lys Asn Leu Thr Ser Lys Thr Ile Gly Glu Phe Ala Ser Gln
    50                  55                  60
```

```
Leu Pro Val Glu Lys Arg Gln Phe Gly Tyr Tyr Gln Tyr Ala Ile Gly
65                  70                  75                  80

Gly Thr Met Pro Ala Lys Lys Asn Ala Ser Asp Glu Asp Lys Pro Lys
                85                  90                  95

Gly Glu Leu Ile Asp Trp Ser Lys Lys Pro Phe Tyr Val Leu Phe Ser
            100                 105                 110

Lys Gly Tyr Ser Ala Thr His Ala Val Asn Leu Ile Phe Asn Val Tyr
        115                 120                 125

Leu Asn Ser Glu Glu Gly Lys Ala Phe Ser Ala Lys Asn Ser Met Asn
    130                 135                 140

Leu Ser Lys Ser Gln Phe Ala Tyr Ser Gly Phe Val Gln Ile Val Cys
145                 150                 155                 160

Ala Asn Tyr Ala Ser Met Leu Ala Asn Ala Arg Pro Asp Lys Ile Lys
                165                 170                 175

Phe Glu Glu Ile Thr Glu Ala Thr Asp Asp Gly Thr Lys Lys Met Gln
            180                 185                 190

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

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

Asp Lys Thr Ile Gln Arg Leu Arg Leu Leu Gln Pro Phe Phe Glu Lys
225                 230                 235                 240

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

Leu Glu His Ser Gly Gln Cys Thr Tyr Lys Gly Gly Arg Thr Ile Ser
            260                 265                 270

Ile Leu Glu Ile Gly Asp Ile Arg Ile Ser Arg Lys Glu Asn Ala Lys
        275                 280                 285
```

```
Gly Tyr Leu Leu Thr Ile Pro Ile Asn Arg Lys Ser Val Val Phe Asp
    290                 295                 300

Leu Tyr Gly Arg Lys Asp Thr Ile Gly Gly Asp Gly Arg Asp Leu Ile
305                 310                 315                 320

Asp Ile Met Asn Thr His Gly Ser Ser Leu Gln Phe Thr Ala Asp Gly
                325                 330                 335

Asn Asp Ile Tyr Leu Thr Ile Thr Ala Thr Lys Asn Phe Ile Lys Glu
            340                 345                 350

Lys Pro Thr Phe Asn Glu Asp Thr Val Leu Gly Gly Asp Val Asn Ile
        355                 360                 365

Lys His Ser Tyr Thr Val Phe Ser Thr Ser Pro Lys Asp Ile Pro Asp
    370                 375                 380

Phe Val Asn Phe Tyr Glu Tyr Phe Ala Lys Asp Gly Glu Ile Met Lys
385                 390                 395                 400

Leu Ala Pro Lys Pro Met Trp Asp Tyr Ile Val Ala Ala Ala Thr Lys
                405                 410                 415

Phe Leu Thr Ile Leu Pro Ile Glu Thr Pro Ala Ile Ser Ala Thr Val
            420                 425                 430

Tyr Gly Lys Arg Thr Glu Glu Gly Ile Ser Arg Ala Thr Phe Arg Glu
        435                 440                 445

Thr Gln Lys Leu Ile Ala Leu Glu Lys Ala Ile Glu Arg Val Met Lys
    450                 455                 460

Gln Val Phe Asp Lys Tyr Asn Asp Gly Lys His Pro Leu Glu Ala Ile
465                 470                 475                 480

Tyr Ile Gly Asn Ala Ile Lys Tyr Arg Arg Leu Ile Lys Gly Tyr Leu
                485                 490                 495
```

```
Ala Gln Lys Lys Lys Tyr Tyr Ser Ala His Ser Glu Tyr Asp Lys Ala
            500                 505                 510

Met Gly Tyr Thr Asp Asp Asp Thr Asp Arg Lys Glu Asn Met Asp Glu
        515                 520                 525

Arg Arg Phe Asp Asp Ser Lys Lys Phe Arg Tyr Thr Pro Glu Ala Gln
    530                 535                 540

Ala Leu Leu Asp Thr Met His Thr Ile Glu Lys Lys Ile Val Gly Cys
545                 550                 555                 560

Val Ser Asn Ala Ile Ser Tyr Ala Tyr His Lys Phe Asp Glu Asn Gly
                565                 570                 575

Phe Asn Val Ile Ala Leu Glu Asn Leu Thr Ser Ala Thr Phe Ala Lys
            580                 585                 590

Lys Tyr Lys Ser Asp Lys Pro Glu Ser Ile Lys Lys Leu Leu Asn Phe
        595                 600                 605

Asp Lys Leu Leu Gly Lys Thr Leu Asp Glu Ala Lys Ala Ser Lys Ser
    610                 615                 620

Ile Ser Lys His Pro Asn Trp Tyr Glu Leu Val Ala Asp Glu Asn Gly
625                 630                 635                 640

Cys Val Ser Asp Ile Arg Ile Thr Asp Glu Gly Gln Ser Ala Thr Tyr
                645                 650                 655

Arg Ser Leu Val Thr Glu Thr Ile Met Lys Val Ser His Phe Ala Glu
            660                 665                 670

Thr Lys Asp Arg Phe Ile Gly Leu Ala Asn Ser Gly Arg Leu Gln Val
        675                 680                 685

Gly Leu Val Pro Ser Gln Tyr Thr Ser Tyr Ile Asp Ser Thr Thr His
    690                 695                 700

Thr Leu Tyr Ala Val Ile Glu Asp Gly Lys Thr Val Leu Ala Pro Lys
705                 710                 715                 720
```

Glu Val Val Arg Ala Ser Gln Glu Arg His Ile Asn Gly Leu Asn Ala
725 730 735

Asp Tyr Asn Ser Ala Leu Asn Leu Lys Tyr Met Ile Thr Asp Glu Asn
740 745 750

Phe Arg Lys Thr Phe Thr Ser Glu Thr Ser Ala Asp Lys Phe Gly Trp
755 760 765

Gly Lys Pro Met Phe Ser Pro Thr Thr Arg Ser Gln Asp Glu Val Phe
770 775 780

Ser Ala Ile Lys Lys Ile Gly Ala Ile Thr Val Leu Glu Asp
785 790 795

<210> 38
<211> 781
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 38
Met Ala His Lys Asn Ser Asp Gly Glu Asn Thr Ile Asn Lys Thr Phe
1 5 10 15

Ile Phe Lys Val Lys Cys Glu Lys Asn Asp Ile Ile Ser Phe Trp Lys
20 25 30

Pro Ala Ala Glu Glu Tyr Cys Asn Tyr Tyr Asn Lys Leu Ser Glu Trp
35 40 45

Ile Gly Lys Asn Leu Ile Ser Met Lys Ile Gly Asp Leu Ala Lys Tyr
50 55 60

Ile Asp Asn Pro Lys Ser Lys Tyr Tyr Leu Ser Val Thr Asp Glu Asn
65 70 75 80

Lys Lys Asp Leu Pro Leu Tyr Lys Ile Phe Gln Lys Gly Phe Ser Ser
85 90 95

```
Ile Asp Ala Asp Asn Ala Leu Tyr Cys Ala Ile Asp Lys Leu Asn Pro
            100                 105                 110

Glu Gly Tyr Asn Gly Asn Ile Leu Gly Val Gly Lys Ser Asp Tyr Arg
        115                 120                 125

Arg Asn Gly Tyr Val Ser Ser Val Ile Gly Asn Phe Arg Thr Lys Met
    130                 135                 140

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

Val Asp Glu Glu Thr Leu Arg Arg Gln Thr Ile Cys Asp Val Glu Lys
                165                 170                 175

Tyr Arg Ile Glu Ser Glu Lys Asp Phe Arg Asp Leu Ile Asp Ile Leu
            180                 185                 190

Lys Ala Arg Glu Glu Thr Pro Arg Leu Lys Glu Lys Ile Ser Arg Leu
        195                 200                 205

Glu Leu Leu Tyr Asp Tyr Tyr Ser Lys Asn Thr Lys Thr Ile Lys Ser
    210                 215                 220

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

Val Arg Lys Ser Leu Asn Thr Ile Thr Ile His Lys Gln Asp Ser Lys
                245                 250                 255

Ile Glu Lys Glu Gly Asn Thr Ser Phe Arg Leu His Met Val Phe Asn
            260                 265                 270

Lys Lys Pro Tyr Thr Ile Thr Leu Leu Gly Asn Arg Gln Val Val Lys
        275                 280                 285

Tyr Ile Asp Gly Lys Arg Val Asp Ile Val Asn Ile Val Glu Lys His
    290                 295                 300
```

```
Gly Asp Trp Ile Thr Phe Asn Ile Lys Asn Gly Glu Leu Phe Val His
305                 310                 315                 320

Leu Thr Lys Cys Val Glu Phe Ser Lys Gly Gln Lys Glu Ile Lys Lys
                325                 330                 335

Ala Ala Gly Val Asp Val Asn Ile Lys His Ala Met Leu Ala Ala Ser
            340                 345                 350

Ile Val Asp Asp Gly Gln Leu Lys Gly Tyr Val Asn Leu Tyr Arg Glu
        355                 360                 365

Leu Ile Glu Asp Asp Asp Phe Val Ser Thr Phe Gly Asp Ser Asp Ser
    370                 375                 380

Gly Lys Thr Glu Leu Gly Met Tyr Gln Lys Met Ala Lys Thr Val Phe
385                 390                 395                 400

Phe Gly Val Leu Glu Val Glu Ser Leu Phe Glu Arg Val Val Asn Gln
                405                 410                 415

Gln Ser Gly Trp Lys Leu Asp Asn Gln Leu Ile Arg Arg Glu Arg Ala
            420                 425                 430

Met Glu Lys Val Phe Asp Arg Ile Val Lys Thr Thr Ser Asn Lys His
        435                 440                 445

Ile Ile Asp Tyr Val Asn Tyr Val Lys Met Leu Arg Ala Lys Tyr Lys
    450                 455                 460

Ala Tyr Phe Ile Leu Asp Glu Lys Tyr His Glu Lys Gln Arg Glu Tyr
465                 470                 475                 480

Asp Leu Ser Met Gly Phe Thr Asp Glu Ser Asp Glu Arg Arg Glu Leu
                485                 490                 495

Tyr Pro Phe Ile Asn Thr Glu Thr Ala Lys Glu Ile Leu Gly Lys Lys
            500                 505                 510

Arg Asn Val Glu Gln Asp Leu Ile Gly Cys Arg Asp Asn Ile Val Thr
        515                 520                 525
```

```
Tyr Ala Phe Asn Val Leu Arg Asn Asn Gly Tyr Asp Thr Ile Ser Val
    530                 535                 540

Glu Tyr Leu Asp Ser Ser Gln Phe Asp Lys Arg Arg Met Pro Thr Pro
545                 550                 555                 560

Lys Ser Leu Leu Glu Tyr His Lys Phe Lys Gly Lys Thr Gln Asp Glu
                565                 570                 575

Val Glu Arg Leu Met Ser Glu Lys Lys Phe Ala Lys Thr Asn Tyr Asp
            580                 585                 590

Ile His Tyr Asp Gly Glu Asn Lys Val Asp Gly Ile Val Tyr Ser Lys
        595                 600                 605

Glu Gly Glu Leu Arg Gln Lys Lys Leu Asn Phe Met Asn Leu Val Ile
    610                 615                 620

Lys Ala Ile His Phe Ala Asp Ile Lys Asp Lys Phe Ala Gln Leu Cys
625                 630                 635                 640

Asn Asn Asn Asp Val Asn Val Val Phe Gly Pro Ser Ala Phe Thr Ser
                645                 650                 655

Gln Met Asp Ser Glu Thr His Ser Leu Tyr Tyr Val Glu Lys Glu Thr
            660                 665                 670

Asn Gly Lys Asn Gly Lys Thr Gly Lys Lys Phe Val Leu Ala Asp Lys
        675                 680                 685

Lys Ser Val Arg Arg Arg Gln Glu Thr His Ile Asn Gly Leu Asn Ala
    690                 695                 700

Asp Phe Asn Ala Ala Arg Asn Leu Glu Tyr Ile Ala Ser Asn Pro Glu
705                 710                 715                 720

Leu Leu Glu Arg Met Thr Lys Arg Thr Lys Ser Gly Lys Asp Met Tyr
                725                 730                 735
```

```
Asn Thr Pro Ser Trp Asn Ile Arg Gln Glu Phe Lys Lys Asn Leu Ser
            740                 745                 750


Val Arg Thr Ile Asn Thr Phe Arg Glu Leu Gly Asn Val Lys Tyr Gly
        755                 760                 765


Lys Ile Asn Asn Glu Gly Leu Phe Val Glu Asp Asp Val
    770                 775                 780


<210> 39
<211> 786
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-bos taurus sequence

<400> 39
Met Ala Gln His Lys Ser Asn Asn Glu Glu Ser Ala Ile Asn Lys Thr
1               5                   10                  15


Phe Ile Phe Lys Ala Lys Cys Glu Lys Asn Asp Val Ile Ser Leu Trp
            20                  25                  30


Glu Pro Ala Ala Lys Glu Tyr Gly Asp Tyr Tyr Asn Lys Val Ser Lys
        35                  40                  45


Trp Ile Ala Asp Asn Leu Ile Thr Met Lys Ile Gly Asp Leu Ala Gln
    50                  55                  60


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


Lys Lys Lys Asp Leu Pro Leu Tyr Arg Ile Phe Gln Lys Gly Phe Ser
                85                  90                  95


Ser Gln Cys Ala Asp Asn Ala Leu Tyr Cys Ala Ile Lys Ser Ile Asn
            100                 105                 110


Pro Glu Asn Tyr Lys Gly Asn Ser Leu Gly Ile Gly Glu Ser Asp Tyr
        115                 120                 125
```

```
Arg Arg Phe Gly Tyr Ile Gln Ser Val Val Ser Asn Phe Arg Thr Lys
    130                 135                 140

Met Ser Ser Leu Lys Val Ser Val Lys Tyr Lys Lys Phe Asp Val Ser
145                 150                 155                 160

Asn Val Asp Asp Glu Thr Leu Lys Ile Gln Thr Ile Tyr Asp Val Asp
                165                 170                 175

Lys Tyr Gly Ile Glu Thr Ala Lys Glu Phe Lys Glu Leu Ile Glu Thr
            180                 185                 190

Leu Lys Thr Arg Val Glu Thr Pro Gln Leu Asn Asp Thr Ile Ala Arg
        195                 200                 205

Leu Lys Cys Leu Cys Asp Tyr Tyr Ser Lys Asn Glu Lys Ala Ile Asn
    210                 215                 220

Asn Glu Ile Glu Thr Met Ala Ile Ala Asp Leu Gln Lys Phe Gly Gly
225                 230                 235                 240

Cys Gln Arg Lys Ser Leu Asn Ala Phe Thr Ile His Lys Gln Asp Ser
                245                 250                 255

Leu Met Glu Lys Val Gly Asn Thr Ser Phe Arg Leu Gln Leu Ser Phe
            260                 265                 270

Arg Lys Lys Thr Tyr Val Ile Asn Leu Leu Gly Asn Arg Gln Val Val
        275                 280                 285

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

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

His Ile Thr Ser Pro Ile Val Phe Asp Lys Asp Val Arg Asp Ile Arg
                325                 330                 335

Asn Val Val Gly Ile Asp Val Asn Ile Lys His Ser Met Leu Ala Thr
            340                 345                 350
```

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

Glu Leu Leu Asn Asp Asp Val Phe Val Ser Thr Cys Asn Glu Ser Glu
    370                 375                 380

Leu Ala Leu Tyr Arg Gln Met Ser Glu Asn Val Asn Phe Gly Ile Leu
385                 390                 395                 400

Glu Thr Asp Ser Leu Phe Glu Arg Ile Val Asn Gln Ser Lys Gly Gly
                405                 410                 415

Cys Leu Lys Asn Lys Leu Ile Arg Arg Glu Leu Ala Met Gln Lys Val
            420                 425                 430

Phe Glu Arg Ile Thr Lys Thr Asn Lys Asp Gln Asn Ile Val Asp Tyr
        435                 440                 445

Val Asn Tyr Val Lys Met Met Arg Ala Lys Cys Lys Ala Ser Tyr Ile
    450                 455                 460

Leu Lys Glu Lys Tyr Asp Glu Lys Gln Lys Glu Tyr Tyr Val Lys Met
465                 470                 475                 480

Gly Phe Thr Asp Glu Ser Thr Glu Ser Lys Glu Thr Met Asp Lys Arg
                485                 490                 495

Arg Glu Glu Phe Pro Phe Val Asn Thr Asp Thr Ala Lys Glu Leu Leu
            500                 505                 510

Val Lys Gln Asn Asn Ile Arg Gln Asp Ile Ile Gly Cys Arg Asp Asn
        515                 520                 525

Ile Val Thr Tyr Ala Phe Asn Val Phe Lys Asn Asn Glu Tyr Asp Thr
    530                 535                 540

Leu Ser Val Glu Tyr Leu Asp Ser Ser Gln Phe Asp Lys Arg Arg Ile
545                 550                 555                 560
```

```
Pro Thr Pro Lys Ser Leu Leu Lys Tyr His Lys Phe Glu Gly Lys Thr
                565                 570                 575

Lys Asp Glu Val Glu Asn Met Met Lys Ser Glu Lys Leu Ser Asn Ala
            580                 585                 590

Tyr Tyr Thr Phe Lys Tyr Glu Asn Asp Val Val Ser Asp Ile Asp Tyr
        595                 600                 605

Ser Asp Glu Gly Asn Leu Arg Arg Ser Lys Leu Asn Phe Gly Asn Trp
    610                 615                 620

Ile Ile Lys Ala Ile His Phe Ala Asp Ile Lys Asp Lys Phe Val Gln
625                 630                 635                 640

Leu Ser Asn Asn Asn Lys Met Asn Ile Val Phe Cys Pro Ser Ala Phe
                645                 650                 655

Ser Ser Gln Met Asp Ser Ile Thr His Thr Leu Tyr Tyr Val Glu Lys
            660                 665                 670

Ile Thr Lys Asn Lys Lys Gly Lys Glu Lys Lys Lys Tyr Val Leu Ala
        675                 680                 685

Asn Lys Lys Met Val Arg Thr Gln Gln Glu Thr His Ile Asn Gly Leu
    690                 695                 700

Asn Ala Asp Tyr Asn Ser Ala Cys Asn Leu Lys Tyr Ile Ala Leu Asn
705                 710                 715                 720

Tyr Glu Leu Arg Asp Lys Met Thr Asp Arg Phe Lys Ala Ser Lys Lys
                725                 730                 735

Ile Lys Thr Met Tyr Asn Ile Pro Ala Tyr Asn Ile Lys Ser Asn Phe
            740                 745                 750

Lys Lys Asn Leu Ser Ala Lys Thr Ile Gln Thr Phe Arg Glu Leu Gly
        755                 760                 765

His Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Met Phe Val Glu Ile
    770                 775                 780
```

Leu Glu
785

<210> 40
<211> 798
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 40
Met Ala His Arg Lys Lys Lys Asp Asp Glu Ala Thr Leu Ser Tyr Lys
1 5 10 15

Phe Lys Val Lys Val Ile Glu Gly Asp Leu Thr Ala Asp Asp Ile Thr
20 25 30

Lys Cys Ile Ala Glu Asn Ala Glu Gln Gly Asn His Phe Ser Glu Phe
35 40 45

Ile His Lys Asn Leu Thr Ser Lys Thr Ile Gly Glu Phe Ala Ser Gln
50 55 60

Leu Pro Ala Glu Lys Arg Gln Phe Gly Tyr Tyr Gln Tyr Ala Ile Gly
65 70 75 80

Gly Thr Met Pro Ala Lys Lys Asn Ala Ser Asp Glu Asp Lys Pro Lys
85 90 95

Gly Glu Leu Ile Asp Trp Ser Lys Lys Pro Phe Tyr Val Leu Phe Ser
100 105 110

Lys Gly Tyr Ser Ala Thr His Ala Val Asn Leu Ile Phe Asn Val Tyr
115 120 125

Leu Asn Ser Glu Glu Gly Lys Ala Phe Ser Ala Lys Asn Ser Met Asn
130 135 140

Leu Ser Lys Ser Gln Phe Ala Tyr Ser Gly Phe Val Gln Ile Val Cys
145 150 155 160

```
Ala Asn Tyr Ala Ser Met Leu Ala Asn Ala Arg Pro Asp Lys Ile Lys
                165                 170                 175

Phe Glu Glu Ile Thr Glu Ala Thr Asp Asp Gly Thr Lys Lys Met Gln
            180                 185                 190

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

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

Asp Lys Thr Ile Gln Arg Leu Arg Leu Leu Gln Pro Phe Phe Glu Lys
225                 230                 235                 240

Asn Glu Glu Ser Ile Thr Glu Leu Tyr Tyr Asp Leu Ser Val Lys Ala
                245                 250                 255

Leu Glu His Ser Gly Gln Cys Thr Tyr Lys Gly Gly Arg Thr Ile Ser
            260                 265                 270

Ile Leu Glu Ile Gly Asp Ile Arg Ile Ser Arg Lys Glu Asn Ala Lys
        275                 280                 285

Gly Tyr Leu Leu Thr Ile Pro Ile Asn Arg Lys Ser Val Val Phe Asp
    290                 295                 300

Leu Tyr Gly Arg Lys Asp Thr Ile Gly Gly Asp Gly Arg Asp Leu Ile
305                 310                 315                 320

Asp Ile Met Asn Thr His Gly Ser Ser Leu Gln Phe Thr Ala Asp Glu
                325                 330                 335

Asn Asp Ile Tyr Leu Thr Ile Thr Ala Thr Lys Asn Phe Ile Lys Glu
            340                 345                 350

Lys Pro Thr Phe Asn Glu Asp Thr Val Leu Gly Gly Asp Val Asn Ile
        355                 360                 365
```

```
Lys His Ser Tyr Thr Val Phe Ser Ala Ser Pro Lys Asp Ile Pro Asp
    370                 375                 380

Phe Val Asn Phe Tyr Glu Tyr Phe Ala Lys Asp Gly Glu Ile Met Lys
385                 390                 395                 400

Leu Ala Pro Lys Pro Met Trp Asp Tyr Ile Val Ala Ala Ala Thr Lys
                405                 410                 415

Phe Leu Thr Ile Leu Pro Ile Glu Thr Pro Ala Ile Ser Ala Thr Val
            420                 425                 430

Tyr Gly Lys Arg Thr Glu Glu Gly Ile Ser Arg Ala Thr Phe Arg Glu
        435                 440                 445

Thr Gln Lys Leu Ile Ala Leu Glu Lys Ala Ile Glu Arg Val Met Lys
    450                 455                 460

Gln Val Phe Asp Lys Tyr Asn Asp Gly Lys His Pro Leu Glu Ala Ile
465                 470                 475                 480

Tyr Ile Gly Asn Ala Ile Lys Tyr Arg Arg Leu Ile Lys Gly Tyr Leu
                485                 490                 495

Ala Gln Lys Lys Lys Tyr Tyr Ser Ala His Ser Glu Tyr Asp Lys Ala
            500                 505                 510

Met Gly Tyr Thr Asp Asp Asp Thr Asp Arg Lys Glu Asn Met Asp Glu
        515                 520                 525

Arg Arg Phe Asp Asp Ser Lys Lys Phe Arg Tyr Thr Pro Glu Ala Gln
    530                 535                 540

Ala Leu Leu Asp Thr Met His Thr Ile Glu Lys Lys Ile Val Gly Cys
545                 550                 555                 560

Val Ser Asn Ala Ile Ser Tyr Ala Tyr His Lys Phe Asp Glu Asn Gly
                565                 570                 575

Phe Asn Val Ile Ala Leu Glu Asn Leu Thr Ser Ala Thr Phe Ala Lys
            580                 585                 590
```

```
Lys Tyr Lys Ser Asp Lys Pro Glu Ser Ile Lys Lys Leu Leu Asn Phe
        595                 600                 605

Asp Lys Leu Leu Gly Lys Thr Leu Asp Glu Ala Lys Ala Ser Lys Ser
    610                 615                 620

Ile Ser Lys His Pro Asn Trp Tyr Glu Leu Val Ala Asp Glu Asn Gly
625                 630                 635                 640

Cys Val Ser Asp Ile Arg Ile Thr Asp Glu Gly Gln Ser Ala Thr Tyr
                645                 650                 655

Arg Ser Leu Val Thr Glu Thr Ile Met Lys Val Ser His Phe Ala Glu
            660                 665                 670

Thr Lys Asp Arg Phe Ile Gly Leu Ala Asn Ser Gly Arg Leu Gln Val
        675                 680                 685

Gly Leu Val Pro Ser Gln Tyr Thr Ser Tyr Ile Asp Ser Thr Thr His
    690                 695                 700

Thr Leu Tyr Ala Val Ile Glu Asp Gly Lys Thr Val Leu Ala Pro Lys
705                 710                 715                 720

Glu Val Val Arg Ala Ser Gln Glu Arg His Ile Asn Gly Leu Asn Ala
                725                 730                 735

Asp Tyr Asn Ser Ala Leu Asn Leu Lys Tyr Met Ile Thr Asp Glu Asn
            740                 745                 750

Phe Arg Lys Thr Phe Thr Ser Glu Thr Ser Ala Asp Lys Phe Gly Trp
        755                 760                 765

Gly Lys Pro Met Phe Ser Pro Thr Thr Arg Ser Gln Asp Glu Val Phe
    770                 775                 780

Ser Ala Ile Lys Lys Ile Gly Ala Ile Thr Val Leu Glu Asp
785                 790                 795
```

<210> 41
<211> 771
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 41
Met Ala Asn Lys Arg Thr Asp Thr Thr Ile Asn Leu Asn Lys Thr Val
1 5 10 15

Ile Met Leu Thr Asn Met Leu Pro Glu Val Arg Ala Met Phe Gln Ala
20 25 30

Gly Ile Arg Gln Ala Gln Ala Tyr Ala Asp Leu Val Asn Lys Trp Ile
35 40 45

Cys Ser Asn Leu Thr Asn Lys Ile Gly Glu Val Leu Leu Pro Tyr Ile
50 55 60

Asp Asn Lys Asn Cys Val Tyr Tyr Glu Leu Cys Tyr Lys Tyr Lys Glu
65 70 75 80

Ala Pro Leu Tyr Thr Ile Phe Met Lys Gly Lys Phe Asp Leu Asn Ser
85 90 95

Arg Asn Asn Ala Leu Tyr Cys Ala Val Val Ala Gln Asn Ile Asp Asn
100 105 110

Tyr Ser Gly Asn Ile Phe Gly Phe Ser Gln Ser Asp Tyr Arg Arg Asn
115 120 125

Gly Tyr Cys Lys Val Val Phe Ser Asn Tyr Ala Thr Lys Met Ser Ser
130 135 140

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

Glu Thr Ile Gln Ser Gln Val Ile Tyr Glu Met Phe Thr Asn Gly Arg
165 170 175

```
Gln Trp Gly Lys Pro Glu Tyr Phe Ala Glu His Leu Lys Tyr Leu Glu
            180                 185                 190

Met Lys Asp Asn Val Ser Asp Lys Leu Met Phe Arg Met Lys Thr Leu
        195                 200                 205

Cys Glu Tyr Tyr Gln Thr His Thr Asp Leu Ile Asp Thr Met Ala Met
    210                 215                 220

Asn Ala Gly Val Glu Ala Leu Lys Gln Phe Glu Gly Leu Lys Leu Asn
225                 230                 235                 240

Arg Asp Lys Phe Ser Met Thr Ile Thr Thr Asn Ser Thr Ser Pro Tyr
                245                 250                 255

Thr Leu Thr Arg Val Ala Gly Thr Cys Ala Tyr Asn Leu His Ile Pro
            260                 265                 270

Cys Arg Lys Arg Ser Tyr Asp Ile Arg Leu Trp Gly Asn Arg Gln Thr
        275                 280                 285

Val Arg Trp Val Asn Gly Glu Leu Val Asp Ile Ala Asp Ile Ile Asn
    290                 295                 300

Gln His Gly Gln Thr Ile Ile Phe Thr Ile Lys Asn Gly Asn Val Tyr
305                 310                 315                 320

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

Lys Asn Val Val Gly Val Asp Val Asn Thr Lys His Met Leu Met Gln
            340                 345                 350

Thr Ser Ile Lys Asp Asn Gly Trp Val Lys Gly Tyr Val Asn Ile Tyr
        355                 360                 365

Lys Ala Leu Val Glu Asp Glu Glu Phe Val Lys Tyr Ile Ser Lys Ser
    370                 375                 380

Asp Leu Lys Leu Tyr Lys Asp Leu Ser Lys Tyr Val Ser Phe Cys Pro
385                 390                 395                 400
```

```
Leu Glu Leu Asn Leu Leu Tyr Thr Arg Tyr Leu Ser Lys Lys Gly Leu
                405                 410                 415

Pro Phe Asn Glu Ala Asp Asn Asn Ala Glu Lys Cys Val Glu Lys Val
            420                 425                 430

Leu Asn Asn Leu Val Lys Gln Tyr Glu Gly Asp Asp Val His Val Val
        435                 440                 445

Asn Tyr Ile His Asn Val Lys Lys Leu Arg Ala Leu Cys Lys Ala Ser
    450                 455                 460

Phe Val Leu Tyr Lys Lys Tyr Ala Glu Leu Gln Lys Ala Phe Asp Asp
465                 470                 475                 480

Ala Gln Gly Tyr Asn Asp Gln Ser Thr Glu Thr Lys Glu Thr Met Asp
                485                 490                 495

Lys Arg Arg Trp Glu Asn Pro Phe Ile Gln Thr Arg Glu Ala Gln Glu
            500                 505                 510

Leu Ile Ala Lys Met Asp Asn Ala Val Ala Gly Ile Ile Gly Cys Arg
        515                 520                 525

Asp Asn Ile Ile Thr Tyr Ala Tyr Lys Val Phe Gly Asp Asn Asn Tyr
    530                 535                 540

Asp Thr Val Gly Leu Glu Asn Leu Thr Thr Ser Gln Phe Asp Asn Tyr
545                 550                 555                 560

Ser Thr Val Lys Ser Pro Lys Ser Leu Leu Ser Tyr Tyr Gly Leu Leu
                565                 570                 575

Gly Gln Gln Val Asp Ser Asp Lys Tyr Asn Ala Val Met Thr Glu Ser
            580                 585                 590

Asn Lys Asp Trp Tyr Asp Phe Lys Thr Asp Gly Asp Gly Asn Ile Thr
        595                 600                 605
```

```
Asp Ile Thr Leu Thr Ala Ala Gly Glu Ala Gln Lys Ala Lys Ser Leu
    610                 615                 620

Phe Asn Asn Lys Val Leu Lys Asn Ile His Phe Ala Asp Val Lys Asp
625                 630                 635                 640

Lys Phe Ile Gln Leu Gly Asn Asn Gly Ser Ile Gln Thr Val Leu Val
                645                 650                 655

Pro Pro Ser Tyr Thr Ser Gln Met Asp Ser Lys Thr His Thr Ile Tyr
            660                 665                 670

Val Lys Glu Thr Val Asp Pro Lys Asn Lys Asn Lys Lys Lys Leu Lys
        675                 680                 685

Leu Val Asp Lys Lys Leu Val Arg His Gly Gln Glu Tyr His Lys Asn
    690                 695                 700

Gly Leu Asn Ala Asp Ile Asn Ala Ala Leu Asn Ile Ala Tyr Ile Val
705                 710                 715                 720

Glu Asn Gln Glu Met Arg Glu Val Met Cys Leu His Pro Ser Lys Lys
                725                 730                 735

Asp Gly Val Tyr Asp Gln Pro Phe Leu Lys Ala Thr Thr Lys Tyr Pro
            740                 745                 750

Ala Thr Val Ala Gly Ile Leu Leu Lys Met Gly Lys Thr Thr Asn Trp
        755                 760                 765

Gly Glu Lys
    770
```

<210> 42
<211> 764
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 42

```
Met Asn Lys Ser Tyr Val Phe Lys Ser Asn Val Ala Ile Asp Asp Ile
1               5                  10                  15

Met Ser Leu Phe Glu Pro Ala Ile Glu Glu Tyr Ile Asn Tyr Tyr Asn
            20                  25                  30

Arg Thr Ser Asp Phe Ile Cys Asp Asn Leu Thr Ser Met Lys Ile Gly
        35                  40                  45

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

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

Leu Asn Leu Asn Ser Ser Gln Lys Lys Asn Ala Asp Asn Ala Leu Tyr
                85                  90                  95

Glu Ala Ile Lys Val Leu Asn Ala Asp Gly Tyr Lys Gly Lys Asn Ile
            100                 105                 110

Leu Gly Leu Gly Asp Thr Tyr Phe Arg Arg Asn Gly Tyr Val Lys Asn
        115                 120                 125

Val Ile Ser Asn Tyr Arg Thr Lys Phe Val Thr Leu Lys Pro Asn Val
    130                 135                 140

Lys Tyr Ser Lys Ile Asp Ile Asn Ser Val Thr Glu Gln Leu Ile Lys
145                 150                 155                 160

Thr Gln Thr Ile Phe Glu Val Val Asn Lys Lys Ile Glu Ser Glu Thr
                165                 170                 175

Asp Phe Glu Asn Leu Ile Thr Tyr Phe Lys Asn Arg Glu Thr Pro Asn
            180                 185                 190

Asp Glu Lys Ile Lys Arg Leu Glu Leu Leu Phe Asp Tyr Tyr Thr Lys
        195                 200                 205

His Lys Asn Glu Ile Asn Glu Glu Ile Glu Lys His Ala Val Glu Ser
    210                 215                 220
```

```
Leu Lys Ser Phe Asn Gly Cys Arg Arg Asn Gly Asn Arg Lys Thr Met
225                 230                 235                 240

Thr Val Gln Met Gln Lys Met Leu Leu Lys Lys His Gly Leu Thr Ser
                245                 250                 255

Tyr Ile Leu His Leu Val Leu Asp Lys Lys Pro Tyr Asp Ile Asn Leu
            260                 265                 270

Met Gly Asn Arg Gln Thr Val Lys Val Asp Asn Asn Gly Asn Arg Val
        275                 280                 285

Asp Leu Val Asp Ile Ser Ser Lys His Gly Tyr Asp Leu Thr Phe Glu
    290                 295                 300

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

Ser Lys Lys Glu Gln Glu Ile Lys Asn Ile Leu Gly Ile Asp Ile Asn
                325                 330                 335

Thr Lys His Ser Met Leu Ala Thr Ser Ile Thr Asp Asn Gly Lys Val
            340                 345                 350

Lys Gly Tyr Ile Asn Ile Tyr Val Glu Leu Leu Lys Asn Lys Asp Phe
        355                 360                 365

Val Ser Thr Leu Asn Lys Glu Glu Leu Ala Tyr Tyr Thr Glu Met Ala
    370                 375                 380

Lys Phe Val Ser Phe Gly Leu Leu Glu Ile Pro Ser Leu Phe Glu Arg
385                 390                 395                 400

Val Ser Asn Gln Tyr Asp Lys Lys Asn Asn Val Ser Ile Thr Asp Glu
                405                 410                 415

Thr Leu Leu Lys Arg Glu Ile Ala Ile Ser Gln Thr Leu Asp Asn Leu
            420                 425                 430
```

```
Ala Lys Lys Tyr Arg Asp Lys Asn Cys Lys Ile Ala Ser Tyr Ile Asp
        435                 440                 445

Tyr Thr Lys Met Leu Arg Ser Lys Tyr Lys Ser Tyr Phe Ile Leu Lys
    450                 455                 460

Gln Lys Tyr Tyr Glu Lys Asn His Glu Tyr Asp Asp Lys Met Gly Phe
465                 470                 475                 480

Ser Asp Ile Ser Thr Asn Ser Lys Glu Thr Met Asp Pro Arg Arg Phe
                485                 490                 495

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

Leu Glu Asn Val Lys Cys Asp Ile Val Gly Cys Arg Asp Asn Ile Ile
        515                 520                 525

Lys Tyr Ala Tyr Asp Val Ile Val Leu Asn Gly Phe Asp Thr Ile Gly
    530                 535                 540

Leu Glu Tyr Leu Asp Ser Ser Asn Phe Glu Arg Asp Arg Leu Pro Phe
545                 550                 555                 560

Pro Thr Ala Lys Ser Leu Met Thr Tyr Tyr Gly Phe Glu Gly Lys Lys
                565                 570                 575

Tyr Ser Glu Ile Asp Lys Ser Val Phe Asn Thr Lys Tyr Tyr Asn Phe
            580                 585                 590

Ile Phe Asn Glu Asn Glu Thr Ile Lys Asp Ile Ser Tyr Ser Val Tyr
        595                 600                 605

Gly Leu Lys Glu Ile Gln Lys Lys Arg Phe Lys Asn Leu Val Ile Lys
    610                 615                 620

Ala Ile Gly Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu Ser Asn
625                 630                 635                 640

Asn Thr Asn Met Asn Val Ile Phe Val Pro Ala Ala Phe Thr Ser Gln
                645                 650                 655
```

```
Met Asp Ser Asn Thr His Lys Ile Tyr Val Lys Glu Ile Met Asp Lys
            660                 665                 670


Asn Asn Lys Lys Gln Leu Gln Leu Ile Asp Lys Arg Lys Val Arg Thr
        675                 680                 685


Lys Gln Glu Phe His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
    690                 695                 700


Asn Asn Ile Lys Tyr Ile Ala Glu Asn Asn Asp Leu Leu Leu Thr Met
705                 710                 715                 720


Cys Thr Lys Thr Lys Glu Asn Asn Arg Tyr Gly Asn Pro Leu Tyr Asn
                725                 730                 735


Ile Lys Asp Thr Phe Lys Lys Lys Ile Pro Ser Ser Ile Leu Asn Ile
            740                 745                 750


Phe Lys Lys Lys Asp Met Tyr Gln Ile Ile Cys Asp
        755                 760


<210> 43
<211> 768
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 43
Met Phe Arg Ile Phe Ala Ala Leu Lys Leu Thr Asn Met Gly His Val
1               5                   10                  15


Arg Leu Gln Lys Arg Glu Gly Glu Val Tyr Lys Thr Tyr Lys Leu Lys
            20                  25                  30


Val Lys Ser Phe Ser Gly Asn Val Asp Ile Lys Ala Gly Ile Val Glu
        35                  40                  45


Tyr Asp Gln Lys Phe Asn Asn Val Ser Gln Trp Ile Ala Asp His Leu
    50                  55                  60
```

```
Thr Ser Met Thr Ile Gly Glu Ala Ala Ser Arg Ile Ser Pro His Lys
65                  70                  75                  80

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

Gln Pro Leu Tyr Lys Ile Phe Thr Arg Gly Phe Gly Gly Met Asn Ala
            100                 105                 110

Asp Asn Leu Ile Ile Glu Cys Thr Lys Thr Glu Glu Asn Cys Lys Tyr
        115                 120                 125

Asp Lys Glu Lys Ser Leu Gly Phe Ser Glu Ser Val Phe Arg Thr Phe
    130                 135                 140

Gly Phe Ala Ala Asn Ala Ser Ser Asp Met Lys Ser Arg Met Thr Gln
145                 150                 155                 160

Ala Lys Val Lys Ile Gly Arg Lys Asn Ile Asp Glu Asp Ser Ala Asp
                165                 170                 175

Asp Glu Lys Cys Leu Gln Ala Ile Tyr Glu Ile Gln Lys Asn Glu Leu
            180                 185                 190

Leu Thr Asp Asp Asn Trp Lys Asp Arg Ile Gly Tyr Leu Glu Met Lys
        195                 200                 205

Gly Asp Gln Glu Arg Glu Leu Glu Arg Thr Thr Ile Leu Tyr Asp Tyr
    210                 215                 220

Tyr Arg Ala Asn Arg Thr Thr Val Leu Asp Lys Leu Asp Asn Leu Lys
225                 230                 235                 240

Val Glu Thr Leu Ser Lys Phe Arg Gly Ser Lys Arg Lys Ser Asp Arg
                245                 250                 255

Lys Ile Leu Thr Leu Asn Gly Ile Ser Tyr Asp Ile Lys Arg Lys Glu
            260                 265                 270
```

```
Gly Cys Gln Gly Phe Glu Leu Lys Phe Ser Val Asp Lys Asn His Met
        275                 280                 285

Glu Phe Asp Leu Leu Gly His Arg Ala Leu Ile Lys Asn Gly Glu Met
    290                 295                 300

Leu Val Asp Ile Glu Asn Cys His Gly Ser Gln Leu Ser Leu Glu Ile
305                 310                 315                 320

Asp Gly Asp Asp Met Tyr Ala Ile Ile Ser Met Arg Thr Phe Cys Glu
                325                 330                 335

Lys Asn Glu Ser Lys Leu Glu Lys Ile Ile Gly Ala Asp Val Asn Ile
            340                 345                 350

Lys His Met Phe Leu Met Thr Ser Glu Lys Asp Asp Gly Asn Thr Lys
        355                 360                 365

Cys Tyr Val Asn Leu Tyr Arg Glu Leu Leu Ser Asp Ser Asp Phe Thr
    370                 375                 380

Asp Val Leu Asn Lys Glu Glu Tyr Glu Ile Phe Ser Glu Leu Ser Lys
385                 390                 395                 400

Tyr Val Met Phe Gly Leu Ile Glu Thr Pro Tyr Leu Gly Ser Arg Val
                405                 410                 415

Ile Gly Thr Thr Gln His Glu Lys Ile Val Glu Asp Lys Ile Thr Ser
            420                 425                 430

Gly Met Lys Lys Ile Ala Ile Arg Leu Phe Gln Glu Gly Lys Val Arg
        435                 440                 445

Glu Arg Ile Tyr Val Gln Asn Val Leu Lys Ile Arg Ala Leu Leu Lys
    450                 455                 460

Ala Leu Phe Ser Thr Lys Leu Ala Tyr Ser Asn Glu Gln Lys Ile Tyr
465                 470                 475                 480

Asp Asn Leu Met Arg Phe Gly Glu Lys Asp Asp Arg Arg Lys Asp Glu
                485                 490                 495
```

```
Gly Phe His Thr Thr Cys Arg Gly Thr Ser Leu Arg Ser Glu Met Asp
            500                 505                 510

Met Leu Ser Lys Lys Ile Leu Ala Cys Arg Asp Asn Ile Val Glu Tyr
        515                 520                 525

Gly Tyr Tyr Val Ile Gly Leu Asn Gly Phe Asp Gly Ile Ser Leu Glu
    530                 535                 540

Asn Leu Glu Ser Ser Thr Phe Met Asp Val Lys Ile Ser Tyr Pro Ser
545                 550                 555                 560

Cys Asn Ser Met Leu Asp His Phe Lys Leu Lys Gly Lys Thr Ile Glu
                565                 570                 575

Glu Ala Glu Asn His Glu Thr Val Gly Lys Phe Ile Lys Lys Gly Tyr
            580                 585                 590

Tyr Val Met Thr Leu Val Asn Gly Lys Ile Asn Asp Ile Asn Tyr Ser
        595                 600                 605

Glu Lys Ala Val Met Leu His Lys Lys Asn Leu Leu Tyr Asp Thr Val
    610                 615                 620

Ile Lys Ser Thr His Phe Ala Asp Val Lys Asp Lys Phe Val Glu Leu
625                 630                 635                 640

Ser Asn Asn Gly Lys Val Ser Val Val Ile Val Pro Pro Tyr Phe Ser
                645                 650                 655

Ser Gln Met Asp Ser Val Thr His Lys Val Phe Thr Glu Glu Ile Val
            660                 665                 670

Val Gln Lys Lys Ser Ser Asn Gly Lys Val Arg Lys Thr Lys Lys Thr
        675                 680                 685

Val Leu Val Asp Lys Arg Lys Val Arg Lys Thr Gln Glu Ser His Ile
    690                 695                 700
```

```
Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Leu Asn Leu Lys Tyr Ile
705                 710                 715                 720


Ala Glu Thr Ile Asp Trp Arg Ser Thr Leu Cys Phe Lys Thr Trp Asn
                725                 730                 735


Thr Tyr Gly Ser Pro Gln Trp Asp Ser Lys Ile Lys Asn Gln Lys Thr
            740                 745                 750


Met Ile Asp Arg Leu Asp Ser Leu Gly Ala Ile Glu Leu Lys Asn Trp
        755                 760                 765


<210> 44
<211> 789
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 44
Met Ser His Glu Phe Asn Lys Asn Lys Gly Glu Asn Glu Ile Ser Lys
1               5                   10                  15


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


Trp Val Pro Ala Met Glu Glu Tyr Cys Thr Tyr Tyr Asn Arg Val Ser
        35                  40                  45


Lys Trp Ile Cys Asp Asn Leu Thr Glu Met Arg Ile Gly Asp Leu Ala
    50                  55                  60


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


Ile Thr Lys Lys Asp Leu Pro Leu Tyr Lys Ile Phe Lys Lys Gly Phe
                85                  90                  95


Ser Gly Leu Cys Ala Asp Asn Ala Leu Tyr Cys Ala Ile Ala Lys Leu
            100                 105                 110
```

```
Asn Pro Glu Gly Tyr Asp Gly Asn Met Phe Gly Leu Ser Glu Thr Tyr
        115                 120                 125

Tyr Arg Arg Gln Gly Tyr Ile Ala Asn Val Phe Gly Asn Tyr Arg Thr
    130                 135                 140

Lys Met Asn Ala Gly Leu Lys Val Gly Cys Ala Lys Trp Lys Lys Phe
145                 150                 155                 160

Asp Thr Asn Asp Val Asp Asp Glu Ile Leu Met Glu Gln Val Ile Val
                165                 170                 175

Asp Val Val Lys Tyr Asp Ile Asp Ser Lys Asn Glu Phe Lys Glu Tyr
            180                 185                 190

Ile Glu Val Leu Lys Cys Arg Glu Glu Asn Pro Lys Leu Leu Glu Thr
        195                 200                 205

Ile Glu Arg Leu Glu Cys Leu Tyr Gly Tyr Tyr Ser Gln His Glu Glu
    210                 215                 220

Asp Ile Lys Lys Lys Ile Glu Glu Leu Val Val Glu Glu Leu Lys Thr
225                 230                 235                 240

Phe Gly Gly Cys Val Arg Lys Ser Met Thr Ser Cys Thr Ile Thr Val
                245                 250                 255

Gln Asp Phe Val Met Glu Arg Ile Gly Asn Thr Gly Tyr Arg Ile Asn
            260                 265                 270

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

Gln Val Val Arg Tyr Val Asp Gly Asp Arg Val Glu Leu Val Asp Ile
    290                 295                 300

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

Leu Phe Val His Leu Thr Ser Gly Val Asp Phe Ser Lys Glu Glu Ser
                325                 330                 335
```

```
Ser Met Glu Asn Ile Val Gly Val Asp Val Asn Ile Lys His Ser Met
            340                 345                 350

Leu Ala Ser Ser Ile Val Asp Asp Gly Asn Val Asn Gly Tyr Ile Asn
        355                 360                 365

Ile Tyr Lys Glu Leu Val Asn Asp Asp Glu Phe Val Ser Thr Phe Gly
    370                 375                 380

Asp Ser Glu Ser Gly Leu Asn Glu Leu Glu Leu Tyr Arg Gln Met Ala
385                 390                 395                 400

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

Tyr Val Glu Gln Trp Lys Gly Ser Asp Ser Asp Ser Arg Leu Ala Arg
            420                 425                 430

Arg Glu Arg Val Val Gly Lys Val Phe Asp Arg Ile Val Lys Thr Asn
        435                 440                 445

Gly Asp Val His Val Val Asn Tyr Ile His Ala Val Lys Met Leu Arg
    450                 455                 460

Ala Lys Cys Lys Ala Tyr Phe Val Leu Lys Gln Lys Tyr Tyr Glu Lys
465                 470                 475                 480

Gln Lys Glu Tyr Asp Asp Ala His Gly Tyr Thr Asp Glu Ser Thr Ala
                485                 490                 495

Ser Lys Glu Thr Met Asp Lys Arg Arg Phe Glu Asn Pro Phe Val Glu
            500                 505                 510

Thr Asp Val Ala Lys Glu Leu Leu Gly Lys Leu Ala Cys Val Glu Gln
        515                 520                 525

Asp Ile Ile Gly Cys Arg Asp Asn Ile Val Thr Tyr Ala Phe Asn Val
    530                 535                 540
```

```
Phe Arg Arg Asn Gly Tyr Asp Thr Ile Ser Leu Glu Tyr Leu Asp Ser
545                 550                 555                 560

Ser Gln Phe Lys Lys Ile Gly Met Gly Ala Pro Thr Pro Lys Ser Leu
                565                 570                 575

Leu Lys Tyr His Lys Leu Glu Gly Lys Thr Val Glu Glu Val Glu Ser
            580                 585                 590

Ile Ile Ser Glu Lys Gly Leu Lys Lys Asn Leu Tyr Val Phe Lys Phe
        595                 600                 605

Gly Asp Asn Gly Leu Leu Ser Asp Ile Glu Tyr Ser Asp Glu Gly Leu
    610                 615                 620

Ile Arg Lys Lys Lys Ala Asp Phe Gly Asn Ile Ile Thr Lys Ala Ile
625                 630                 635                 640

His Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu Thr Asn Asn Ser
                645                 650                 655

Asp Met Gly Val Val Phe Cys Pro Ser Ala Phe Thr Ser Gln Met Asp
            660                 665                 670

Ser Lys Thr His Arg Leu Tyr Phe Val Glu Gly Leu Asp Gly Asn Gly
        675                 680                 685

Lys Asn Lys Tyr Val Leu Ala Asn Lys Trp Ser Val Arg Arg Gln Gln
    690                 695                 700

Glu Arg His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ser Ala Cys Asn
705                 710                 715                 720

Cys Gln His Ile Ala Tyr Asp Pro Ile Leu Arg Asp Ala Met Thr Ile
                725                 730                 735

Lys Val Glu Ala Gly Lys Gly Met Tyr Asn Lys Pro Ser Tyr Asp Ile
            740                 745                 750

Arg Lys Lys Phe Lys Lys Asn Leu Ser Ala Ala Thr Leu Lys Thr Phe
        755                 760                 765
```

Ile Lys Leu Gly Asn Thr Val Lys Gly Met Ile Val Asn Gly Gln Phe
    770   775   780

Val Glu Met Glu Ser
785

<210> 45
<211> 784
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 45
Met Tyr Asn Ser Lys Lys Lys Gly Glu Gly Asp Ile Gln Lys Ser Phe
1   5   10   15

Lys Phe Lys Val Lys Thr Asp Lys Glu Thr Val Glu Leu Phe Arg Lys
            20   25   30

Ala Ala Val Glu Tyr Ser Glu Tyr Tyr Lys Arg Leu Thr Thr Phe Leu
        35   40   45

Cys Glu Arg Leu Thr Asp Met Thr Trp Gly Glu Val Ala Ser Phe Ile
    50   55   60

Pro Glu Lys Tyr Arg Lys Asn Glu Tyr Tyr Lys Tyr Leu Ile Lys Glu
65   70   75   80

Glu Asn Lys Asp Leu Pro Leu Tyr Lys Met Phe Thr Lys Ala Ala Ser
                85   90   95

Ser Met Phe Ile Asp His Ser Ile Glu Arg Tyr Val Glu Ala Leu Asn
            100   105   110

Pro Glu Gly Asn Thr Gly Asn Ile Leu Gly Phe Cys Lys Ser Ser Tyr
        115   120   125

Val Arg Gly Gly Tyr Leu Lys Asn Val Val Ser Asn Ile Arg Thr Lys
    130   135   140

```
Phe Ala Thr Leu Lys Thr Gly Ile Lys Tyr Lys Lys Phe Asn Pro Ala
145                 150                 155                 160

Glu Asp Asp Glu Glu Thr Ile Leu Gly Gln Thr Val Phe Glu Met Glu
                165                 170                 175

Lys Arg Gly Leu Glu Phe Lys Cys Asp Phe Glu Lys Thr Ile Lys Tyr
            180                 185                 190

Leu Asn Glu Lys Gly Lys Thr Gln Glu Ala Glu Arg Leu Gln Cys Leu
        195                 200                 205

Met Glu Tyr Phe Ser Thr Asn Thr Asp Lys Ile Asn Glu Tyr Arg Glu
    210                 215                 220

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

Lys Ser Asn Ser Phe Ser Val Thr Leu Glu Lys Ala Asp Ile Lys Glu
                245                 250                 255

Asp Gly Leu Thr Gly Tyr Thr Met Lys Val Ser Lys Lys Leu Lys Glu
            260                 265                 270

Ile His Leu Leu Gly His Arg Arg Val Val Glu Val Val Asn Gly Arg
        275                 280                 285

Arg Val Asn Leu Val Asp Ile Cys Gly Asp Lys Ser Gly Asp Ser Lys
    290                 295                 300

Val Phe Val Val Asp Gly Asp Asn Leu Tyr Val Cys Ile Ser Ala Pro
305                 310                 315                 320

Val Lys Phe Ser Lys Asn Gly Met Glu Ala Lys Lys Tyr Ile Gly Val
                325                 330                 335

Asp Met Asn Met Lys His Ser Ile Ile Ser Val Ser Asp Asn Ala Ser
            340                 345                 350
```

```
Asp Met Lys Gly Phe Leu Asn Ile Tyr Lys Glu Leu Leu Lys Asp Glu
        355                 360                 365

Gly Phe Arg Lys Thr Leu Asn Ala Thr Glu Leu Glu Lys Tyr Glu Lys
    370                 375                 380

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

Glu Arg Ile Val Lys Gln Lys Lys Glu Asn Ser Val Asp Gly Leu Lys
                405                 410                 415

Val Gln Ala Glu Lys Lys Leu Ile Glu Arg Glu Ala Ala Ile Glu Arg
            420                 425                 430

Val Leu Asp Lys Leu Arg Lys Gly Thr Ser Asp Thr Asp Thr Glu Asn
        435                 440                 445

Tyr Ile Asn Tyr Asn Lys Ile Leu Arg Ala Lys Ile Lys Ser Ala Tyr
    450                 455                 460

Ile Leu Lys Asp Lys Tyr Tyr Glu Met Leu Gly Lys Tyr Asp Ser Glu
465                 470                 475                 480

Arg Ala Gly Ser Gly Asp Leu Ser Glu Glu Asn Lys Ile Lys Tyr Lys
                485                 490                 495

Asp Glu Phe Asn Glu Thr Glu Lys Gly Lys Glu Ile Leu Gly Lys Leu
            500                 505                 510

Asn Asn Val Tyr Lys Asp Ile Ile Gly Cys Arg Asp Asn Ile Val Thr
        515                 520                 525

Tyr Ala Val Asn Leu Phe Ile Arg Asn Gly Tyr Asp Thr Val Ala Leu
    530                 535                 540

Glu Tyr Leu Glu Ser Ser Gln Met Lys Ala Arg Arg Ile Pro Ser Thr
545                 550                 555                 560

Gly Gly Leu Leu Lys Gly His Lys Leu Glu Gly Lys Pro Glu Gly Glu
                565                 570                 575
```

```
Val Thr Ala Tyr Leu Lys Ala Asn Lys Ile Pro Lys Ser Tyr Tyr Ser
            580                 585                 590

Phe Glu Tyr Asp Gly Asn Gly Met Leu Thr Asp Val Lys Tyr Ser Asp
        595                 600                 605

Met Gly Glu Lys Ala Arg Gly Arg Asn Arg Phe Lys Asn Leu Val Pro
    610                 615                 620

Lys Phe Leu Arg Trp Ala Ser Ile Lys Asp Lys Phe Val Gln Leu Ser
625                 630                 635                 640

Asn Tyr Lys Asp Ile Gln Met Val Tyr Val Pro Ser Pro Tyr Thr Ser
                645                 650                 655

Gln Thr Asp Ser Arg Thr His Ser Leu Tyr Tyr Ile Glu Thr Val Lys
            660                 665                 670

Val Asp Glu Lys Thr Gly Lys Glu Lys Lys Glu His Ile Val Ala Pro
        675                 680                 685

Lys Glu Ser Val Arg Thr Glu Gln Glu Ser Phe Val Asn Gly Met Asn
    690                 695                 700

Ala Asp Thr Asn Ser Ala Asn Asn Ile Lys Tyr Ile Phe Glu Asn Glu
705                 710                 715                 720

Thr Leu Arg Asp Lys Phe Leu Lys Arg Thr Lys Asp Gly Thr Glu Met
                725                 730                 735

Tyr Asn Arg Pro Ala Phe Asp Leu Lys Glu Cys Tyr Lys Lys Asn Ser
            740                 745                 750

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

Gly Lys Leu Asp Glu Asn Gly Asn Phe Ile Glu Asn Glu Cys Asn Lys
    770                 775                 780
```

<210> 46
<211> 764
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 46
Met Asn Lys Ser Tyr Val Phe Lys Ser Asn Val Ala Ile Asp Asp Ile
1 5 10 15

Met Ser Leu Phe Glu Pro Ala Ile Glu Glu Tyr Ile Asn Tyr Tyr Asn
20 25 30

Arg Thr Ser Asp Phe Ile Cys Asp Asn Leu Thr Ser Met Lys Ile Gly
35 40 45

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

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

Leu Asn Leu Asn Ser Ser Gln Lys Lys Asn Ala Asp Asn Ala Leu Tyr
85 90 95

Glu Ala Ile Lys Val Leu Asn Ala Asp Gly Tyr Lys Gly Lys Asn Ile
100 105 110

Leu Gly Leu Gly Asp Thr Tyr Phe Arg Arg Asn Gly Tyr Val Lys Asn
115 120 125

Val Ile Ser Asn Tyr Arg Thr Lys Phe Val Thr Leu Lys Pro Asn Val
130 135 140

Lys Tyr Ser Lys Ile Asp Ile Asn Ser Val Thr Glu Gln Leu Ile Lys
145 150 155 160

Thr Gln Thr Ile Phe Glu Val Val Asn Lys Lys Ile Glu Ser Glu Thr
165 170 175

```
Asp Phe Glu Asn Leu Ile Thr Tyr Phe Lys Asn Arg Glu Thr Pro Asn
            180                 185                 190

Asp Glu Lys Ile Lys Arg Leu Glu Leu Leu Phe Asp Tyr Tyr Thr Lys
        195                 200                 205

His Lys Asn Glu Ile Asn Glu Glu Ile Glu Lys His Ala Val Glu Ser
    210                 215                 220

Leu Lys Ser Phe Asn Gly Cys Arg Arg Asn Gly Asn Arg Lys Thr Met
225                 230                 235                 240

Thr Val Gln Met Gln Lys Met Leu Leu Lys Lys His Gly Leu Thr Ser
                245                 250                 255

Tyr Ile Leu His Leu Val Leu Asp Lys Lys Pro Tyr Asp Ile Asn Leu
            260                 265                 270

Met Gly Asn Arg Gln Thr Val Lys Val Asp Asn Asn Gly Asn Arg Val
        275                 280                 285

Asp Leu Val Asp Ile Ser Ser Lys His Gly Tyr Asp Leu Thr Phe Glu
    290                 295                 300

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

Ser Lys Lys Glu Gln Glu Ile Lys Asn Ile Leu Gly Ile Asp Ile Asn
                325                 330                 335

Thr Lys His Ser Met Leu Ala Thr Ser Ile Thr Asp Asn Gly Lys Val
            340                 345                 350

Lys Gly Tyr Ile Asn Ile Tyr Val Glu Leu Leu Lys Asn Lys Asp Phe
        355                 360                 365

Val Ser Thr Leu Asn Lys Glu Glu Leu Ala Tyr Tyr Thr Glu Met Ala
    370                 375                 380

Lys Phe Val Ser Phe Gly Leu Leu Glu Ile Pro Ser Leu Phe Glu Arg
385                 390                 395                 400
```

```
Val Ser Asn Gln Tyr Asp Lys Lys Asn Asn Val Ser Ile Thr Asp Glu
                405                 410                 415

Thr Leu Leu Lys Arg Glu Ile Ala Ile Ser Gln Thr Leu Asp Asn Leu
            420                 425                 430

Ala Lys Lys Tyr Arg Asp Lys Asn Cys Lys Ile Ala Ser Tyr Ile Asp
        435                 440                 445

Tyr Thr Lys Met Leu Arg Ser Lys Tyr Lys Ser Tyr Phe Ile Leu Lys
    450                 455                 460

Gln Lys Tyr Tyr Glu Lys Asn His Glu Tyr Asp Asp Lys Met Gly Phe
465                 470                 475                 480

Ser Asp Ile Ser Thr Asn Ser Lys Glu Thr Met Asp Pro Arg Arg Phe
                485                 490                 495

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

Leu Glu Asn Val Lys Cys Asp Ile Val Gly Cys Arg Asp Asn Ile Ile
        515                 520                 525

Lys Tyr Ala Tyr Asp Val Ile Val Leu Asn Gly Phe Asp Thr Ile Gly
    530                 535                 540

Leu Glu Tyr Leu Asp Ser Ser Asn Phe Glu Arg Asp Arg Leu Pro Phe
545                 550                 555                 560

Pro Thr Ala Lys Ser Leu Met Thr Tyr Tyr Gly Phe Glu Gly Lys Lys
                565                 570                 575

Tyr Ser Glu Ile Asp Lys Ser Val Phe Asn Thr Lys Tyr Tyr Asn Phe
            580                 585                 590

Ile Phe Asn Glu Asn Glu Thr Ile Lys Asp Ile Ser Tyr Ser Val Tyr
        595                 600                 605
```

```
Gly Leu Lys Glu Ile Gln Lys Lys Arg Phe Lys Asn Leu Val Ile Lys
    610                 615                 620

Ala Ile Gly Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu Ser Asn
625                 630                 635                 640

Asn Thr Asn Met Asn Val Ile Phe Val Pro Ala Ala Phe Thr Ser Gln
                645                 650                 655

Met Asp Ser Asn Thr His Lys Ile Tyr Val Lys Glu Ile Met Asp Lys
            660                 665                 670

Asn Asn Lys Lys Gln Leu Gln Leu Ile Asp Lys Arg Lys Val Arg Thr
        675                 680                 685

Lys Gln Glu Phe His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
    690                 695                 700

Asn Asn Ile Lys Tyr Ile Ala Glu Asn Asn Asp Leu Leu Leu Thr Met
705                 710                 715                 720

Cys Thr Lys Thr Lys Glu Asn Asn Arg Tyr Gly Asn Pro Leu Tyr Asn
                725                 730                 735

Ile Lys Asp Thr Phe Lys Lys Lys Ile Pro Ser Ser Ile Leu Asn Ile
            740                 745                 750

Phe Lys Lys Lys Asp Met Tyr Gln Ile Ile Cys Asp
        755                 760
```

<210> 47
<211> 758
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 47

```
Met Ala His Lys Thr Lys Glu Ser Glu Lys Leu Val Lys Ser Phe Lys
1               5                   10                  15
```

```
Leu Lys Val Asp Ile Ser Asn Cys Glu Ile Glu Lys Lys Trp Ile Pro
            20                  25                  30

Ser Phe Glu Glu Tyr Thr Asn Tyr Tyr Asn Gly Val Ser Asn Trp Ile
        35                  40                  45

Cys Glu Asn Leu Ile Ser Met Lys Ile Gly Asp Leu Gly Gln Tyr Ile
    50                  55                  60

Lys Asn Thr Glu Ser Val Tyr Tyr Lys Phe Ile Thr Asp Glu Ser Ile
65                  70                  75                  80

Ser Asn Leu Pro Leu Tyr Lys Ile Phe Thr Leu Lys Gln Thr Gln Asn
                85                  90                  95

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

Tyr Asn Gly Asn Ser Ile Gly Leu Gly Glu Thr Asp Tyr Arg Arg Phe
        115                 120                 125

Gly Tyr Val Gln Cys Val Ile Ser Asn Tyr Arg Thr Lys Ile Gly Thr
    130                 135                 140

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

Asp Val Ile Phe Glu Gln Thr Met Tyr Glu Met Ile Asp Lys Ser Leu
                165                 170                 175

Glu Lys Lys Glu Asp Trp Glu Asn Ile Ile Ser Asn Tyr Lys Ala Lys
            180                 185                 190

Gln Thr Glu Asn Thr Ser Lys Ile Asn Arg Met Glu Thr Leu Tyr Ser
        195                 200                 205

Phe Phe Ile Glu His Ser Glu Glu Ile Ile Glu Lys Ser Asn Leu Val
    210                 215                 220

Ala Ile Glu Gln Leu Ala Leu Phe Asn Gly Cys Lys Arg Lys Ser Leu
225                 230                 235                 240
```

```
Ser Thr Met Thr Ile His Ser Gln His Ser Lys Leu Gln Lys Asn Gly
                245                 250                 255

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

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

Asn Asp Ile Ile Asp Ile Cys Asn Asn Tyr Gly Asp Phe Ile Thr Phe
    290                 295                 300

Gln Ile Lys Asn Gly Lys Met Phe Ile Ile Leu Thr Ala Lys Val Asp
305                 310                 315                 320

Phe Asp Lys Glu Asn Ile Glu Ile Lys Asn Val Val Gly Ala Asp Val
                325                 330                 335

Asn Ile Lys His Asn Met Ile Ala Ser Ser Ile Ile Asp Asn Gly Asn
            340                 345                 350

Val Phe Gly Tyr Ile Asn Ile Tyr Lys Glu Leu Leu Asn Asp Glu Asp
        355                 360                 365

Phe Cys Ser Ser Cys Thr Asn Glu Glu Leu Asp Ile Tyr Lys Glu Ile
    370                 375                 380

Ser Lys Ser Val Asn Phe Gly Leu Leu Glu Cys Glu Ser Leu Phe Ser
385                 390                 395                 400

Arg Val Ser Ala Gln Ile Tyr Lys Glu Asn Glu Ser Ile Ser Lys Leu
                405                 410                 415

Asp Asp Arg Phe Leu Arg Arg Glu Lys Ser Ile Glu Asn Val Leu Asn
            420                 425                 430

Arg Leu Ser Lys Gln Tyr Arg Tyr Lys Asp Cys Lys Ile Ala Thr Tyr
        435                 440                 445
```

```
Ile Asp Tyr Thr Lys Ile Met Arg Asp Ser Tyr Lys Ser Tyr Phe Ile
    450                 455                 460

Ile Lys Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Ser Met
465                 470                 475                 480

Gly Tyr Val Asp Glu Ser Thr Asn Ser Lys Lys Thr Met Asp Lys Arg
                485                 490                 495

Arg Phe Glu Asn Pro Phe Ile Glu Thr Glu Thr Ala Lys Asn Ile Leu
            500                 505                 510

Ser Lys Leu Asn Arg Ile Glu Ser Arg Leu Ile Gly Cys Arg Asn Asn
        515                 520                 525

Ile Thr Asn Tyr Ala Phe Asp Val Phe Lys Asn Asn Gly Phe Asp Thr
    530                 535                 540

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

Leu Thr Pro Ile Ser Met Leu Lys Tyr His Lys Phe Glu Gly Lys Ser
                565                 570                 575

Ile Glu Glu Val Lys Thr Leu Asn Val Lys Phe Ser Met Asp Asn Tyr
            580                 585                 590

Glu Phe Glu Phe Asp Asn Asn Gly Lys Ile Thr Asn Ile Ser Phe Ser
        595                 600                 605

Gln Leu Gly Lys Arg Glu Val Met Lys Thr Asn Phe Phe Asn Leu Ile
    610                 615                 620

Ile Lys Ala Ile His Phe Ala Glu Ile Lys Asp Lys Phe Ile Gln Leu
625                 630                 635                 640

Ser Asn Asn Lys Pro Ile Asn Ile Val Leu Val Pro Ser Ala Phe Ser
                645                 650                 655

Ser Gln Met Asp Ser Lys Asp His Lys Leu Tyr Val Asp Glu Asn Gly
            660                 665                 670
```

```
Lys Leu Ile Asn Lys Arg Lys Val Arg Lys Gln Gln Glu Arg His Ile
        675                 680                 685

Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala Cys Asn Leu Ser Tyr Leu
    690                 695                 700

Ala Lys Asn Asn Glu Leu Leu Glu Lys Val Cys Leu Lys Arg Lys Lys
705                 710                 715                 720

Phe Gly Lys Ala Ser Tyr Ser Val Pro Tyr Trp Asn Val Lys Asp Ala
                725                 730                 735

Phe Lys Lys Asn Val Ser Ser Asn Met Ile Ala Thr Ile Lys Lys Met
            740                 745                 750

Asn Met Val Lys Val Phe
        755


<210> 48
<211> 785
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 48
Met Ala His Lys Thr Asn Asn Gly Glu Asn Thr Ile Asn Lys Thr Phe
1               5                   10                  15

Ile Phe Lys Ala Lys Cys Glu Lys Asn Asp Ile Ile Ser Leu Trp Lys
            20                  25                  30

Pro Ala Ala Glu Glu Tyr Cys Asn Tyr Tyr Asn Lys Leu Ser Lys Trp
        35                  40                  45

Ile Gly Asp Ser Leu Thr Thr Met Lys Ile Gly Asp Leu Ala Gln Tyr
    50                  55                  60

Ile Thr Asn Gln Asn Ser Ala Tyr Tyr Leu Ala Val Thr Asn Asp Ser
65                  70                  75                  80
```

```
Lys Lys Asp Leu Pro Leu Tyr Lys Ile Phe Gln Lys Gly Phe Ser Ser
                85                  90                  95

Gln Cys Ala Asp Asn Ala Leu Tyr Ser Ala Ile Lys Ala Ile Asn Pro
            100                 105                 110

Glu Asn Tyr Asn Gly Asn Ser Leu Glu Ile Gly Glu Thr Asp Tyr Arg
        115                 120                 125

Arg Phe Gly Tyr Val Gln Ser Val Ile Gly Asn Phe Arg Thr Lys Met
    130                 135                 140

Ser Ser Leu Lys Val Ser Val Lys Tyr Lys Lys Phe Asp Val Asn Asp
145                 150                 155                 160

Val Asp Glu Glu Thr Leu Lys Thr Gln Thr Ile Tyr Asp Val Asp Lys
                165                 170                 175

Tyr Gly Ile Glu Ser Ile Lys Asp Phe Asn Glu Phe Ile Glu Val Leu
            180                 185                 190

Lys Leu Arg Glu Glu Thr Pro Gln Leu Asn Glu Lys Ile Thr Arg Leu
        195                 200                 205

Glu Cys Leu Cys Gly Tyr Tyr Ser Lys Asn Glu Glu Asn Ile Lys Asn
    210                 215                 220

Glu Ile Glu Thr Met Ala Ile Ser Asp Leu Gln Lys Phe Gly Gly Cys
225                 230                 235                 240

Gln Arg Lys Ser Leu Asn Thr Leu Thr Ile His Lys Gln Asn Ser Leu
                245                 250                 255

Met Glu Lys Val Gly Asn Thr Ser Phe Thr Leu Gln Leu Ser Phe Asn
            260                 265                 270

Lys Lys Pro Tyr Thr Ile Asn Leu Leu Gly Asn Arg Gln Val Val Lys
        275                 280                 285
```

```
Phe Val Asp Gly Lys Arg Val Asp Leu Ile Asp Ile Thr Glu Lys His
    290                 295                 300

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

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

Ala Val Gly Val Asp Val Asn Ile Lys His Asn Met Leu Ala Thr Ser
            340                 345                 350

Ile Lys Asp Asp Gly Asn Val Lys Gly Tyr Ile Asn Leu Tyr Lys Glu
        355                 360                 365

Leu Val Asn Asp Cys Asp Phe Ile Ser Thr Cys Asn Glu Asp Glu Phe
    370                 375                 380

Asp Leu Tyr Arg Gln Met Ser Glu Ser Val Asn Phe Gly Ile Leu Glu
385                 390                 395                 400

Thr Asp Ser Leu Phe Glu Arg Val Val Asn Gln Ser Lys Gly Gly Cys
                405                 410                 415

Leu Asn Asn Lys Phe Ile Arg Arg Glu Leu Ala Met Gln Lys Val Phe
            420                 425                 430

Asp Asn Ile Thr Lys Thr Asn Lys Asp Gln Asn Ile Val Asp Tyr Val
        435                 440                 445

Asn Tyr Val Lys Met Leu Arg Ala Lys Tyr Lys Ala Tyr Phe Ile Leu
    450                 455                 460

Lys Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Lys Met Gly
465                 470                 475                 480

Phe Thr Asp Val Ser Thr Glu Ser Lys Glu Thr Met Asp Lys Arg Arg
                485                 490                 495

Met Glu Phe Pro Phe Val Asn Thr Asp Thr Ala Lys Glu Leu Leu Ala
            500                 505                 510
```

```
Lys Leu Asn Asn Ile Glu Gln Asp Leu Ile Gly Cys Arg Asp Asn Ile
        515                 520                 525

Val Thr Tyr Ala Phe Asn Ile Phe Lys Asn Asn Gly Tyr Asp Thr Leu
    530                 535                 540

Ala Val Glu Tyr Leu Asp Ser Ala Gln Phe Asp Lys Arg Arg Met Pro
545                 550                 555                 560

Thr Pro Thr Ser Leu Leu Lys Tyr His Lys Phe Glu Gly Lys Thr Lys
                565                 570                 575

Asp Glu Val Glu Asp Met Met Lys Ser Lys Lys Phe Ser Asn Ala Tyr
            580                 585                 590

Tyr Thr Phe Lys Phe Glu Asn Asp Val Val Ser Asn Ile Glu Tyr Ser
        595                 600                 605

Asn Asp Gly Ile Trp Lys Gln Lys Gln Leu Asn Phe Gly Asn Leu Ile
    610                 615                 620

Ile Lys Ala Ile His Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu
625                 630                 635                 640

Cys Asn Asn Asn Lys Met Asn Ile Val Phe Cys Pro Ser Ala Phe Thr
                645                 650                 655

Ser Gln Met Asp Ser Ile Thr His Thr Leu Tyr Tyr Val Glu Lys Ile
            660                 665                 670

Thr Lys Lys Lys Asn Gly Lys Glu Glu Lys Lys Tyr Val Leu Ala Asn
        675                 680                 685

Lys Lys Met Val Arg Thr Gln Gln Glu Thr His Ile Asn Gly Leu Asn
    690                 695                 700

Ala Asp Tyr Asn Ser Ala Cys Asn Leu Lys Tyr Ile Ala Leu Asn Asp
705                 710                 715                 720
```

```
Glu Leu Arg Asn Glu Met Thr Asp Thr Phe Lys Val Thr Asn Arg Gln
                725                 730                 735

Lys Thr Met Tyr Gly Ile Pro Ala Tyr Asn Ile Lys Arg Gly Phe Lys
            740                 745                 750

Lys Asn Leu Ser Ala Lys Thr Ile Asn Thr Phe Arg Lys Leu Gly His
        755                 760                 765

Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Met Phe Val Glu Thr Leu
    770                 775                 780

Ala
785
```

<210> 49
<211> 805
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 49

```
Met Ala His Lys Thr Asn Asn Gly Glu Asn Thr Ile Asn Lys Thr Phe
1               5                   10                  15

Ile Phe Lys Ala Lys Cys Asp Asn Asn Asp Ile Ile Ser Leu Trp Lys
            20                  25                  30

Pro Ala Met Glu Glu Tyr Cys Thr Tyr Tyr Asn Lys Leu Ser Gln Trp
        35                  40                  45

Ile Cys Asn Asn Leu Thr Ser Met Lys Val Lys Asp Leu Phe Ala Tyr
    50                  55                  60

Leu Asp Asp Lys Gln Lys Thr Lys Pro Cys Val Asp Lys Lys Thr Gly
65                  70                  75                  80

Glu Thr Lys Ile Gly Val Gly Tyr Tyr Arg Tyr Phe Ile Glu Asn Asn
                85                  90                  95
```

```
Lys Glu Asp Met Pro Leu Tyr Trp Leu Phe Thr Lys Asn Cys Ser Ser
            100                 105                 110

Ser His Ala Asp Asn Leu Leu Phe Glu Phe Val Arg Lys Val Asn His
        115                 120                 125

Glu Glu Tyr Asn Gly Asn Ser Leu Gly Met Gly Glu Thr Asp Tyr Arg
    130                 135                 140

Arg Phe Gly Tyr Phe Gln Asn Val Ile Ser Asn Phe Arg Thr Lys Met
145                 150                 155                 160

Ser Ser Leu Lys Ala Thr Thr Lys Trp Lys Lys Phe Asp Val Asn Asp
                165                 170                 175

Val Asp Glu Asp Thr Leu Lys Asn Gln Thr Ile Tyr Asp Val Asp Lys
            180                 185                 190

Tyr Gly Ile Glu Ser Val Asn Asp Phe Asn Glu Arg Ile Asp Ile Leu
        195                 200                 205

Lys Ile Arg Glu Glu Thr Glu Gln Thr Lys Asp Lys Ile Ala Arg Leu
    210                 215                 220

Glu Cys Leu Cys Lys Tyr Tyr Lys Glu His Glu Glu Asp Ile Lys Asn
225                 230                 235                 240

Glu Ile Ala Thr Met Ala Ile Ala Asp Leu Gln Lys Phe Gly Gly Cys
                245                 250                 255

Gln Arg Lys Ser Met Asn Thr Leu Thr Ile His Lys Gln Asp Ser Pro
            260                 265                 270

Met Glu Lys Val Gly Asn Thr Ser Phe Asn Leu Arg Leu Thr Phe Asn
        275                 280                 285

Lys Lys Pro Tyr Thr Leu Asn Leu Leu Gly Asn Arg Gln Val Val Lys
    290                 295                 300

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

```
Gly Asp Trp Ile Thr Phe Asn Ile Lys Asn Asn Glu Leu Phe Val His
                325                 330                 335

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

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

Ile Val Asp Asp Gly Asn Val Lys Gly Tyr Ile Asn Leu Tyr Arg Glu
    370                 375                 380

Leu Val Asn Asn Asn Asp Phe Ile Ala Thr Phe Gly Asn Ser Lys Asn
385                 390                 395                 400

Gly His Gln Gly Leu Glu Ile Tyr Glu Gln Met Ala Glu Asn Val Asn
                405                 410                 415

Phe Gly Ile Leu Glu Thr Glu Ser Leu Phe Glu Arg Val Val Asn Gln
            420                 425                 430

Ser Asn Gly Gly Glu Leu Asn Asn Gln Leu Ile Arg Arg Glu Ile Ala
        435                 440                 445

Met Gln Lys Val Phe Asp Asn Ile Thr Lys Thr Asn Asn Asp Lys Asn
    450                 455                 460

Ile Val Asn Tyr Val Asn Tyr Val Lys Met Leu Arg Ala Lys Tyr Lys
465                 470                 475                 480

Ala Tyr Phe Ile Leu Lys Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr
                485                 490                 495

Asp Asp Met Met Gly Phe Asn Asp Glu Ser Thr Glu Asn Lys Glu Met
            500                 505                 510

Met Asp Lys Arg Arg Phe Glu Phe Ser Phe Ile Asn Thr Asp Thr Ala
        515                 520                 525
```

```
Gln Glu Leu Leu Ile Lys Leu Asn Lys Val Glu Gln Asp Leu Ile Gly
    530                 535                 540

Cys Arg Asp Asn Ile Val Thr Tyr Ala Phe Asn Val Phe Lys Thr Asn
545                 550                 555                 560

Gly Tyr Asp Thr Leu Ala Val Glu Tyr Leu Asp Ser Ala Gln Phe Asp
                565                 570                 575

Lys Ala Lys Met Pro Thr Pro Lys Ser Leu Leu Lys Tyr His Lys Phe
            580                 585                 590

Glu Gly Lys Thr Ile Asp Glu Val Lys Glu Met Met Asn Asn Lys Asn
        595                 600                 605

Phe Thr Asn Ala Tyr Tyr Asn Phe Lys Phe Glu Asn Glu Ile Val Lys
    610                 615                 620

Asp Ile Glu Tyr Ser Thr Asp Gly Ile Trp Arg Gln Lys Lys Leu Asn
625                 630                 635                 640

Phe Met Asn Leu Ile Ile Lys Ala Ile His Phe Ala Asp Ile Lys Asp
                645                 650                 655

Lys Phe Val Gln Leu Cys Asn Asn Asn Ser Met Asn Val Val Phe Cys
            660                 665                 670

Pro Ser Ala Phe Thr Ser Gln Met Asp Ser Ile Thr His Ser Leu Tyr
        675                 680                 685

Tyr Ile Glu Lys Thr Ser Lys Thr Lys Asn Gly Lys Glu Lys Lys Gln
    690                 695                 700

Tyr Val Leu Ala Asn Lys Lys Met Val Arg Thr Gln Gln Glu Lys His
705                 710                 715                 720

Ile Asn Gly Leu Asn Ala Asp Phe Asn Ser Ala Cys Asn Leu Lys Tyr
                725                 730                 735

Ile Ala Leu Asp Glu Glu Leu Arg Asn Ala Met Thr Asp Glu Phe Asn
            740                 745                 750
```

```
Pro Lys Lys Gln Lys Thr Met Tyr Gly Val Pro Ala Tyr Asn Ile Lys
        755                 760                 765


Asn Gly Phe Lys Lys Asn Leu Ser Thr Lys Thr Ile Asn Thr Phe Arg
    770                 775                 780


Thr Leu Gly His Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Val Phe
785                 790                 795                 800


Val Glu Asn Leu Ala
                805


<210> 50
<211> 784
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 50
Met Tyr Asn Ser Lys Lys Lys Gly Glu Gly Asp Ile Gln Lys Ser Phe
1               5                   10                  15


Lys Phe Lys Val Lys Thr Asp Lys Glu Thr Val Glu Leu Phe Arg Lys
            20                  25                  30


Ala Ala Val Glu Tyr Ser Glu Tyr Tyr Lys Arg Leu Thr Thr Phe Leu
        35                  40                  45


Cys Glu Arg Leu Thr Asp Met Thr Trp Gly Glu Val Ala Ser Phe Ile
    50                  55                  60


Pro Glu Lys Tyr Arg Lys Asn Glu Tyr Tyr Lys Tyr Leu Ile Lys Glu
65                  70                  75                  80


Glu Asn Lys Asp Leu Pro Leu Tyr Lys Met Phe Thr Lys Ala Ala Ser
                85                  90                  95


Ser Met Phe Ile Asp His Ser Ile Glu Arg Tyr Val Glu Ala Leu Asn
            100                 105                 110
```

```
Pro Glu Gly Asn Thr Gly Asn Ile Leu Gly Phe Cys Lys Ser Ser Tyr
        115                 120                 125

Val Arg Gly Gly Tyr Leu Lys Asn Val Val Ser Asn Ile Arg Thr Lys
    130                 135                 140

Phe Ala Thr Leu Lys Thr Gly Ile Lys Tyr Lys Lys Phe Asn Pro Ala
145                 150                 155                 160

Glu Asp Asp Glu Glu Thr Ile Leu Gly Gln Thr Val Phe Glu Met Glu
                165                 170                 175

Lys Arg Gly Leu Glu Phe Lys Cys Asp Phe Glu Lys Thr Ile Lys Tyr
            180                 185                 190

Leu Asn Glu Lys Gly Lys Thr Gln Glu Ala Glu Arg Leu Gln Cys Leu
        195                 200                 205

Met Glu Tyr Phe Ser Thr Asn Thr Asp Lys Ile Asn Glu Tyr Arg Glu
    210                 215                 220

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

Lys Ser Asn Ser Phe Ser Val Thr Leu Glu Lys Ala Asp Ile Lys Glu
                245                 250                 255

Asp Gly Leu Thr Gly Tyr Thr Met Lys Val Ser Lys Lys Leu Lys Glu
            260                 265                 270

Ile His Leu Leu Gly His Arg Arg Val Val Glu Val Val Asn Gly Arg
        275                 280                 285

Arg Val Asn Leu Val Asp Ile Cys Gly Asp Lys Ser Gly Asp Ser Lys
    290                 295                 300

Val Phe Val Val Asp Gly Asp Asn Leu Tyr Val Cys Ile Ser Ala Pro
305                 310                 315                 320
```

```
Val Lys Phe Ser Lys Asn Gly Met Glu Ala Lys Lys Tyr Ile Gly Val
                325                 330                 335

Asp Met Asn Met Lys His Ser Ile Ile Ser Val Ser Asp Asn Ala Ser
            340                 345                 350

Asp Met Lys Gly Phe Leu Asn Ile Tyr Lys Glu Leu Leu Lys Asp Glu
        355                 360                 365

Gly Phe Arg Lys Thr Leu Asn Ala Thr Glu Leu Glu Lys Tyr Glu Lys
    370                 375                 380

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

Glu Arg Ile Val Lys Gln Lys Lys Glu Asn Ser Val Asp Gly Leu Lys
                405                 410                 415

Val Gln Ala Glu Lys Lys Leu Ile Glu Arg Glu Ala Ala Ile Glu Arg
            420                 425                 430

Val Leu Asp Lys Leu Arg Lys Gly Thr Ser Asp Thr Asp Thr Glu Asn
        435                 440                 445

Tyr Ile Asn Tyr Asn Lys Ile Leu Arg Ala Lys Ile Lys Ser Ala Tyr
    450                 455                 460

Ile Leu Lys Asp Lys Tyr Tyr Glu Met Leu Gly Lys Tyr Asp Ser Glu
465                 470                 475                 480

Arg Ala Gly Ser Gly Asp Leu Ser Glu Glu Asn Lys Ile Lys Tyr Lys
                485                 490                 495

Asp Glu Phe Asn Glu Thr Glu Lys Gly Lys Glu Ile Leu Gly Lys Leu
            500                 505                 510

Asn Asn Val Tyr Lys Asp Ile Ile Gly Cys Arg Asp Asn Ile Val Thr
        515                 520                 525

Tyr Ala Val Asn Leu Phe Ile Arg Asn Gly Tyr Asp Thr Val Ala Leu
    530                 535                 540
```

```
Glu Tyr Leu Glu Ser Ser Gln Met Lys Ala Arg Arg Ile Pro Ser Thr
545                 550                 555                 560

Gly Gly Leu Leu Lys Gly His Lys Leu Glu Gly Lys Pro Glu Gly Glu
                565                 570                 575

Val Thr Ala Tyr Leu Lys Ala Asn Lys Ile Pro Lys Ser Tyr Tyr Ser
            580                 585                 590

Phe Glu Tyr Asp Gly Asn Gly Met Leu Thr Asp Val Lys Tyr Ser Asp
        595                 600                 605

Met Gly Glu Lys Ala Arg Gly Arg Asn Arg Phe Lys Asn Leu Val Pro
    610                 615                 620

Lys Phe Leu Arg Trp Ala Ser Ile Lys Asp Lys Phe Val Gln Leu Ser
625                 630                 635                 640

Asn Tyr Lys Asp Ile Gln Met Val Tyr Val Pro Ser Pro Tyr Thr Ser
                645                 650                 655

Gln Thr Asp Ser Arg Thr His Ser Leu Tyr Tyr Ile Glu Thr Val Lys
            660                 665                 670

Val Asp Glu Lys Thr Gly Lys Glu Lys Lys Glu His Ile Val Ala Pro
        675                 680                 685

Lys Glu Ser Val Arg Thr Glu Gln Glu Ser Phe Val Asn Gly Met Asn
    690                 695                 700

Ala Asp Thr Asn Ser Ala Asn Asn Ile Lys Tyr Ile Phe Glu Asn Glu
705                 710                 715                 720

Thr Leu Arg Asp Lys Phe Leu Lys Arg Thr Lys Asp Gly Thr Glu Met
                725                 730                 735

Tyr Asn Arg Pro Ala Phe Asp Leu Lys Glu Cys Tyr Lys Lys Asn Ser
            740                 745                 750
```

```
Asn Val Ser Val Phe Asn Thr Leu Lys Lys Thr Leu Gly Ala Ile Tyr
        755                 760                 765


Gly Lys Leu Asp Glu Asn Gly Asn Phe Ile Glu Asn Glu Cys Asn Lys
    770                 775                 780


<210> 51
<211> 764
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 51
Met Asn Lys Ser Tyr Val Phe Lys Ser Asn Val Ala Ile Asp Asp Ile
1               5                   10                  15


Met Ser Leu Phe Glu Pro Ala Ile Glu Glu Tyr Ile Asn Tyr Tyr Asn
            20                  25                  30


Arg Thr Ser Asp Phe Ile Cys Asp Asn Leu Thr Ser Met Lys Ile Gly
        35                  40                  45


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


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


Leu Asn Leu Asn Ser Ser Gln Lys Lys Asn Ala Asp Asn Ala Leu Tyr
                85                  90                  95


Glu Ala Ile Lys Val Leu Asn Ala Asp Gly Tyr Lys Gly Lys Asn Ile
            100                 105                 110


Leu Gly Leu Gly Asp Thr Tyr Phe Arg Arg Asn Gly Tyr Val Lys Asn
        115                 120                 125


Val Ile Ser Asn Tyr Arg Thr Lys Phe Val Thr Leu Lys Pro Asn Val
    130                 135                 140
```

```
Lys Tyr Ser Lys Ile Asp Ile Asn Ser Val Thr Glu Gln Leu Ile Lys
145                 150                 155                 160

Thr Gln Thr Ile Phe Glu Val Val Asn Lys Lys Ile Glu Ser Glu Thr
                165                 170                 175

Asp Phe Glu Asn Leu Ile Thr Tyr Phe Lys Asn Arg Glu Thr Pro Asn
            180                 185                 190

Asp Glu Lys Ile Lys Arg Leu Glu Leu Leu Phe Asp Tyr Tyr Thr Lys
        195                 200                 205

His Lys Asn Glu Ile Asn Glu Glu Ile Glu Lys His Ala Val Glu Ser
    210                 215                 220

Leu Lys Ser Phe Asn Gly Cys Arg Arg Asn Gly Asn Arg Lys Thr Met
225                 230                 235                 240

Thr Val Gln Met Gln Lys Met Leu Leu Lys Lys His Gly Leu Thr Ser
                245                 250                 255

Tyr Ile Leu His Leu Val Leu Asp Lys Lys Pro Tyr Asp Ile Asn Leu
            260                 265                 270

Met Gly Asn Arg Gln Thr Val Lys Val Asp Asn Asn Gly Asn Arg Val
        275                 280                 285

Asp Leu Val Asp Ile Ser Ser Lys His Gly Tyr Asp Leu Thr Phe Glu
    290                 295                 300

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

Ser Lys Lys Glu Gln Glu Ile Lys Asn Ile Leu Gly Ile Asp Ile Asn
                325                 330                 335

Thr Lys His Ser Met Leu Ala Thr Ser Ile Thr Asp Asn Gly Lys Val
            340                 345                 350

Lys Gly Tyr Ile Asn Ile Tyr Val Glu Leu Leu Lys Asn Lys Asp Phe
        355                 360                 365
```

```
Val Ser Thr Leu Asn Lys Glu Glu Leu Ala Tyr Tyr Thr Glu Met Ala
    370                 375                 380

Lys Phe Val Ser Phe Gly Leu Leu Glu Ile Pro Ser Leu Phe Glu Arg
385                 390                 395                 400

Val Ser Asn Gln Tyr Asp Lys Lys Asn Asn Val Ser Ile Thr Asp Glu
                405                 410                 415

Thr Leu Leu Lys Arg Glu Ile Ala Ile Ser Gln Thr Leu Asp Asn Leu
            420                 425                 430

Ala Lys Lys Tyr Arg Asp Lys Asn Cys Lys Ile Ala Ser Tyr Ile Asp
        435                 440                 445

Tyr Thr Lys Met Leu Arg Ser Lys Tyr Lys Ser Tyr Phe Ile Leu Lys
    450                 455                 460

Gln Lys Tyr Tyr Glu Lys Asn His Glu Tyr Asp Asp Lys Met Gly Phe
465                 470                 475                 480

Ser Asp Ile Ser Thr Asn Ser Lys Glu Thr Met Asp Pro Arg Arg Phe
                485                 490                 495

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

Leu Glu Asn Val Lys Cys Asp Ile Val Gly Cys Arg Asp Asn Ile Ile
        515                 520                 525

Lys Tyr Ala Tyr Asp Val Ile Val Leu Asn Gly Phe Asp Thr Ile Gly
    530                 535                 540

Leu Glu Tyr Leu Asp Ser Ser Asn Phe Glu Arg Asp Arg Leu Pro Phe
545                 550                 555                 560

Pro Thr Ala Lys Ser Leu Met Thr Tyr Tyr Gly Phe Glu Gly Lys Lys
                565                 570                 575
```

```
Tyr Ser Glu Ile Asp Lys Ser Val Phe Asn Thr Lys Tyr Tyr Asn Phe
            580                 585                 590

Ile Phe Asn Glu Asn Glu Thr Ile Lys Asp Ile Ser Tyr Ser Val Tyr
        595                 600                 605

Gly Leu Lys Glu Ile Gln Lys Lys Arg Phe Lys Asn Leu Val Ile Lys
    610                 615                 620

Ala Ile Gly Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu Ser Asn
625                 630                 635                 640

Asn Thr Asn Met Asn Val Ile Phe Val Pro Ala Ala Phe Thr Ser Gln
                645                 650                 655

Met Asp Ser Asn Thr His Lys Ile Tyr Val Lys Glu Ile Met Asp Lys
            660                 665                 670

Asn Asn Lys Lys Gln Leu Gln Leu Ile Asp Lys Arg Lys Val Arg Thr
        675                 680                 685

Lys Gln Glu Phe His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
    690                 695                 700

Asn Asn Ile Lys Tyr Ile Ala Glu Asn Asn Asp Leu Leu Leu Thr Met
705                 710                 715                 720

Cys Thr Lys Thr Lys Glu Asn Asn Arg Tyr Gly Asn Pro Leu Tyr Asn
                725                 730                 735

Ile Lys Asp Thr Phe Lys Lys Lys Ile Pro Ser Ser Ile Leu Asn Ile
            740                 745                 750

Phe Lys Lys Lys Asp Met Tyr Gln Ile Ile Cys Asp
        755                 760
```

<210> 52
<211> 768
<212> PRT
<213> Unknown

<220>

<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 52

```
Met Phe Arg Ile Phe Ala Ala Leu Lys Leu Thr Asn Met Gly His Val
1               5                   10                  15


Arg Leu Gln Lys Arg Glu Gly Glu Val Tyr Lys Thr Tyr Lys Leu Lys
            20                  25                  30


Val Lys Ser Phe Ser Gly Asn Val Asp Ile Lys Ala Gly Ile Val Glu
        35                  40                  45


Tyr Asp Gln Lys Phe Asn Asn Val Ser Gln Trp Ile Ala Asp His Leu
    50                  55                  60


Thr Ser Met Thr Ile Gly Glu Ala Ala Ser Arg Ile Ser Pro His Lys
65                  70                  75                  80


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


Gln Pro Leu Tyr Lys Ile Phe Thr Arg Gly Phe Gly Gly Met Asn Ala
            100                 105                 110


Asp Asn Leu Ile Ile Glu Cys Thr Lys Thr Glu Glu Asn Cys Lys Tyr
        115                 120                 125


Asp Lys Glu Lys Ser Leu Gly Phe Ser Glu Ser Val Phe Arg Thr Phe
    130                 135                 140


Gly Phe Ala Ala Asn Ala Ser Ser Asp Met Lys Ser Arg Met Thr Gln
145                 150                 155                 160


Ala Lys Val Lys Ile Gly Arg Lys Asn Ile Asp Glu Asp Ser Ala Asp
                165                 170                 175


Asp Glu Lys Cys Leu Gln Ala Ile Tyr Glu Ile Gln Lys Asn Glu Leu
            180                 185                 190


Leu Thr Asp Asp Asn Trp Lys Asp Arg Ile Gly Tyr Leu Glu Met Lys
        195                 200                 205
```

```
Gly Asp Gln Glu Arg Glu Leu Glu Arg Thr Thr Ile Leu Tyr Asp Tyr
    210                 215                 220

Tyr Arg Ala Asn Arg Thr Thr Val Leu Asp Lys Leu Asp Asn Leu Lys
225                 230                 235                 240

Val Glu Thr Leu Ser Lys Phe Arg Gly Ser Lys Arg Lys Ser Asp Arg
                245                 250                 255

Lys Ile Leu Thr Leu Asn Gly Ile Ser Tyr Asp Ile Lys Arg Lys Glu
            260                 265                 270

Gly Cys Gln Gly Phe Glu Leu Lys Phe Ser Val Asp Lys Asn His Met
        275                 280                 285

Glu Phe Asp Leu Leu Gly His Arg Ala Leu Ile Lys Asn Gly Glu Met
    290                 295                 300

Leu Val Asp Ile Glu Asn Cys His Gly Ser Gln Leu Ser Leu Glu Ile
305                 310                 315                 320

Asp Gly Asp Asp Met Tyr Ala Ile Ile Ser Met Arg Thr Phe Cys Glu
                325                 330                 335

Lys Asn Glu Ser Lys Leu Glu Lys Ile Ile Gly Ala Asp Val Asn Ile
            340                 345                 350

Lys His Met Phe Leu Met Thr Ser Glu Lys Asp Asp Gly Asn Thr Lys
        355                 360                 365

Cys Tyr Val Asn Leu Tyr Arg Glu Leu Leu Ser Asp Ser Asp Phe Thr
    370                 375                 380

Asp Val Leu Asn Lys Glu Glu Tyr Glu Ile Phe Ser Glu Leu Ser Lys
385                 390                 395                 400

Tyr Val Met Phe Gly Leu Ile Glu Thr Pro Tyr Leu Gly Ser Arg Val
                405                 410                 415
```

```
Ile Gly Thr Thr Gln His Glu Lys Ile Val Glu Asp Lys Ile Thr Ser
            420                 425                 430

Gly Met Lys Lys Ile Ala Ile Arg Leu Phe Gln Glu Gly Lys Val Arg
        435                 440                 445

Glu Arg Ile Tyr Val Gln Asn Val Leu Lys Ile Arg Ala Leu Leu Lys
    450                 455                 460

Ala Leu Phe Ser Thr Lys Leu Ala Tyr Ser Asn Glu Gln Lys Ile Tyr
465                 470                 475                 480

Asp Asn Leu Met Arg Phe Gly Glu Lys Asp Asp Arg Arg Lys Asp Glu
                485                 490                 495

Gly Phe His Thr Thr Cys Arg Gly Thr Ser Leu Arg Ser Glu Met Asp
            500                 505                 510

Met Leu Ser Lys Lys Ile Leu Ala Cys Arg Asp Asn Ile Val Glu Tyr
        515                 520                 525

Gly Tyr Tyr Val Ile Gly Leu Asn Gly Phe Asp Gly Ile Ser Leu Glu
    530                 535                 540

Asn Leu Glu Ser Ser Thr Phe Met Asp Val Lys Ile Ser Tyr Pro Ser
545                 550                 555                 560

Cys Asn Ser Met Leu Asp His Phe Lys Leu Lys Gly Lys Thr Ile Glu
                565                 570                 575

Glu Ala Glu Asn His Glu Thr Val Gly Lys Phe Ile Lys Lys Gly Tyr
            580                 585                 590

Tyr Val Met Thr Leu Val Asn Gly Lys Ile Asn Asp Ile Asn Tyr Ser
        595                 600                 605

Glu Lys Ala Val Met Leu His Lys Lys Asn Leu Leu Tyr Asp Thr Val
    610                 615                 620

Ile Lys Ser Thr His Phe Ala Asp Val Lys Asp Lys Phe Val Glu Leu
625                 630                 635                 640
```

```
Ser Asn Asn Gly Lys Val Ser Val Val Ile Val Pro Pro Tyr Phe Ser
                645                 650                 655


Ser Gln Met Asp Ser Val Thr His Lys Val Phe Thr Glu Glu Ile Val
            660                 665                 670


Val Gln Lys Lys Ser Ser Asn Gly Lys Val Arg Lys Thr Lys Lys Thr
        675                 680                 685


Val Leu Val Asp Lys Arg Lys Val Arg Lys Thr Gln Glu Ser His Ile
    690                 695                 700


Asn Gly Leu Asn Ala Asp Tyr Asn Ala Ala Leu Asn Leu Lys Tyr Ile
705                 710                 715                 720


Ala Glu Thr Ile Asp Trp Arg Ser Thr Leu Cys Phe Lys Thr Trp Asn
                725                 730                 735


Thr Tyr Gly Ser Pro Gln Trp Asp Ser Lys Ile Lys Asn Gln Lys Thr
            740                 745                 750


Met Ile Asp Arg Leu Asp Ser Leu Gly Ala Ile Glu Leu Lys Asn Trp
        755                 760                 765


<210> 53
<211> 764
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 53
Met Asn Lys Ser Tyr Val Phe Lys Ser Asn Val Ala Ile Asp Asp Ile
1               5                   10                  15


Met Ser Leu Phe Glu Pro Ala Ile Glu Glu Tyr Ile Asn Tyr Tyr Asn
            20                  25                  30


Arg Thr Ser Asp Phe Ile Cys Asp Asn Leu Thr Ser Met Lys Ile Gly
        35                  40                  45
```

```
Asp Leu Ala Asn Tyr Ile Lys Asn Lys Glu Asn Val Tyr Cys Lys Phe
    50                  55                  60

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

Leu Asn Leu Asn Ser Ser Gln Lys Lys Asn Ala Asp Asn Ala Leu Tyr
                85                  90                  95

Glu Ala Ile Lys Val Leu Asn Ala Asp Gly Tyr Lys Gly Lys Asn Ile
            100                 105                 110

Leu Gly Leu Gly Asp Thr Tyr Phe Arg Arg Asn Gly Tyr Val Lys Asn
        115                 120                 125

Val Ile Ser Asn Tyr Arg Thr Lys Phe Val Thr Leu Lys Pro Asn Val
    130                 135                 140

Lys Tyr Ser Lys Ile Asp Ile Asn Ser Val Thr Glu Gln Leu Ile Lys
145                 150                 155                 160

Thr Gln Thr Ile Phe Glu Val Val Asn Lys Lys Ile Glu Ser Glu Thr
                165                 170                 175

Asp Phe Glu Asn Leu Ile Thr Tyr Phe Lys Asn Arg Glu Thr Pro Asn
            180                 185                 190

Asp Glu Lys Ile Lys Arg Leu Glu Leu Leu Phe Asp Tyr Tyr Thr Lys
        195                 200                 205

His Lys Asn Glu Ile Asn Glu Glu Ile Glu Lys His Ala Val Glu Ser
    210                 215                 220

Leu Lys Ser Phe Asn Gly Cys Arg Arg Asn Gly Asn Arg Lys Thr Met
225                 230                 235                 240

Thr Val Gln Met Gln Lys Met Leu Leu Lys Lys His Gly Leu Thr Ser
                245                 250                 255
```

```
Tyr Ile Leu His Leu Val Leu Asp Lys Lys Pro Tyr Asp Ile Asn Leu
            260                 265                 270

Met Gly Asn Arg Gln Thr Val Lys Val Asp Asn Asn Gly Asn Arg Val
        275                 280                 285

Asp Leu Val Asp Ile Ser Ser Lys His Gly Tyr Asp Leu Thr Phe Glu
    290                 295                 300

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

Ser Lys Lys Glu Gln Glu Ile Lys Asn Ile Leu Gly Ile Asp Ile Asn
                325                 330                 335

Thr Lys His Ser Met Leu Ala Thr Ser Ile Thr Asp Asn Gly Lys Val
            340                 345                 350

Lys Gly Tyr Ile Asn Ile Tyr Val Glu Leu Leu Lys Asn Lys Asp Phe
        355                 360                 365

Val Ser Thr Leu Asn Lys Glu Glu Leu Ala Tyr Tyr Thr Glu Met Ala
    370                 375                 380

Lys Phe Val Ser Phe Gly Leu Leu Glu Ile Pro Ser Leu Phe Glu Arg
385                 390                 395                 400

Val Ser Asn Gln Tyr Asp Lys Lys Asn Asn Val Ser Ile Thr Asp Glu
                405                 410                 415

Thr Leu Leu Lys Arg Glu Ile Ala Ile Ser Gln Thr Leu Asp Asn Leu
            420                 425                 430

Ala Lys Lys Tyr Arg Asp Lys Asn Cys Lys Ile Ala Ser Tyr Ile Asp
        435                 440                 445

Tyr Thr Lys Met Leu Arg Ser Lys Tyr Lys Ser Tyr Phe Ile Leu Lys
    450                 455                 460

Gln Lys Tyr Tyr Glu Lys Asn His Glu Tyr Asp Asp Lys Met Gly Phe
465                 470                 475                 480
```

```
Ser Asp Ile Ser Thr Asn Ser Lys Glu Thr Met Asp Pro Arg Arg Phe
                485                 490                 495

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

Leu Glu Asn Val Lys Cys Asp Ile Val Gly Cys Arg Asp Asn Ile Ile
        515                 520                 525

Lys Tyr Ala Tyr Asp Val Ile Val Leu Asn Gly Phe Asp Thr Ile Gly
    530                 535                 540

Leu Glu Tyr Leu Asp Ser Ser Asn Phe Glu Arg Asp Arg Leu Pro Phe
545                 550                 555                 560

Pro Thr Ala Lys Ser Leu Met Thr Tyr Tyr Gly Phe Glu Gly Lys Lys
                565                 570                 575

Tyr Ser Glu Ile Asp Lys Ser Val Phe Asn Thr Lys Tyr Tyr Asn Phe
            580                 585                 590

Ile Phe Asn Glu Asn Glu Thr Ile Lys Asp Ile Ser Tyr Ser Val Tyr
        595                 600                 605

Gly Leu Lys Glu Ile Gln Lys Lys Arg Phe Lys Asn Leu Val Ile Lys
    610                 615                 620

Ala Ile Gly Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu Ser Asn
625                 630                 635                 640

Asn Thr Asn Met Asn Val Ile Phe Val Pro Ala Ala Phe Thr Ser Gln
                645                 650                 655

Met Asp Ser Asn Thr His Lys Ile Tyr Val Lys Glu Ile Met Asp Lys
            660                 665                 670

Asn Asn Lys Lys Gln Leu Gln Leu Ile Asp Lys Arg Lys Val Arg Thr
        675                 680                 685
```

```
Lys Gln Glu Phe His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala
    690                 695                 700

Asn Asn Ile Lys Tyr Ile Ala Glu Asn Asn Asp Leu Leu Leu Thr Met
705                 710                 715                 720

Cys Thr Lys Thr Lys Glu Asn Asn Arg Tyr Gly Asn Pro Leu Tyr Asn
                725                 730                 735

Ile Lys Asp Thr Phe Lys Lys Lys Ile Pro Ser Ser Ile Leu Asn Ile
            740                 745                 750

Phe Lys Lys Lys Asp Met Tyr Gln Ile Ile Cys Asp
        755                 760
```

<210> 54
<211> 805
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 54

```
Met Ala His Lys Thr Asn Asn Gly Glu Asn Thr Ile Asn Lys Thr Phe
1               5                   10                  15

Ile Phe Lys Ala Lys Cys Asp Asn Asn Asp Ile Ile Ser Leu Trp Lys
            20                  25                  30

Pro Ala Met Glu Glu Tyr Cys Thr Tyr Tyr Asn Lys Leu Ser Gln Trp
        35                  40                  45

Ile Cys Asn Asn Leu Thr Ser Met Lys Val Lys Asp Leu Phe Ala Tyr
    50                  55                  60

Leu Asp Asp Lys Gln Lys Thr Lys Pro Cys Val Asp Lys Lys Thr Gly
65                  70                  75                  80

Glu Thr Lys Ile Gly Val Gly Tyr Tyr Arg Tyr Phe Ile Glu Asn Asn
                85                  90                  95
```

```
Lys Glu Asp Met Pro Leu Tyr Trp Leu Phe Thr Lys Asn Cys Ser Ser
            100                 105                 110

Ser His Ala Asp Asn Leu Leu Phe Glu Phe Val Arg Lys Val Asn His
        115                 120                 125

Glu Glu Tyr Asn Gly Asn Ser Leu Gly Met Gly Glu Thr Asp Tyr Arg
    130                 135                 140

Arg Phe Gly Tyr Phe Gln Asn Val Ile Ser Asn Phe Arg Thr Lys Met
145                 150                 155                 160

Ser Ser Leu Lys Ala Thr Thr Lys Trp Lys Lys Phe Asp Val Asn Asp
                165                 170                 175

Val Asp Glu Asp Thr Leu Lys Asn Gln Thr Ile Tyr Asp Val Asp Lys
            180                 185                 190

Tyr Gly Ile Glu Ser Val Asn Asp Phe Asn Glu Arg Ile Asp Ile Leu
        195                 200                 205

Lys Ile Arg Glu Glu Thr Glu Gln Thr Lys Asp Lys Ile Ala Arg Leu
    210                 215                 220

Glu Cys Leu Cys Lys Tyr Tyr Lys Glu His Glu Glu Asp Ile Lys Asn
225                 230                 235                 240

Glu Ile Ala Thr Met Ala Ile Ala Asp Leu Gln Lys Phe Gly Gly Cys
                245                 250                 255

Gln Arg Lys Ser Met Asn Thr Leu Thr Ile His Lys Gln Asp Ser Pro
            260                 265                 270

Met Glu Lys Val Gly Asn Thr Ser Phe Asn Leu Arg Leu Thr Phe Asn
        275                 280                 285

Lys Lys Pro Tyr Thr Leu Asn Leu Leu Gly Asn Arg Gln Val Val Lys
    290                 295                 300

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

```
Gly Asp Trp Ile Thr Phe Asn Ile Lys Asn Asn Glu Leu Phe Val His
                325                 330                 335

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

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

Ile Val Asp Asp Gly Asn Val Lys Gly Tyr Ile Asn Leu Tyr Arg Glu
    370                 375                 380

Leu Val Asn Asn Asn Asp Phe Ile Ala Thr Phe Gly Asn Ser Lys Asn
385                 390                 395                 400

Gly His Gln Gly Leu Glu Ile Tyr Glu Gln Met Ala Glu Asn Val Asn
                405                 410                 415

Phe Gly Ile Leu Glu Thr Glu Ser Leu Phe Glu Arg Val Val Asn Gln
            420                 425                 430

Ser Asn Gly Gly Glu Leu Asn Asn Gln Leu Ile Arg Arg Glu Ile Ala
        435                 440                 445

Met Gln Lys Val Phe Asp Asn Ile Thr Lys Thr Asn Asn Asp Lys Asn
    450                 455                 460

Ile Val Asn Tyr Val Asn Tyr Val Lys Met Leu Arg Ala Lys Tyr Lys
465                 470                 475                 480

Ala Tyr Phe Ile Leu Lys Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr
                485                 490                 495

Asp Asp Met Met Gly Phe Asn Asp Glu Ser Thr Glu Asn Lys Glu Met
            500                 505                 510

Met Asp Lys Arg Arg Phe Glu Phe Ser Phe Ile Asn Thr Asp Thr Ala
        515                 520                 525
```

```
Gln Glu Leu Leu Ile Lys Leu Asn Lys Val Glu Gln Asp Leu Ile Gly
    530                 535                 540

Cys Arg Asp Asn Ile Val Thr Tyr Ala Phe Asn Val Phe Lys Thr Asn
545                 550                 555                 560

Gly Tyr Asp Thr Leu Ala Val Glu Tyr Leu Asp Ser Ala Gln Phe Asp
                565                 570                 575

Lys Ala Lys Met Pro Thr Pro Lys Ser Leu Leu Lys Tyr His Lys Phe
            580                 585                 590

Glu Gly Lys Thr Ile Asp Glu Val Lys Glu Met Met Asn Asn Lys Asn
        595                 600                 605

Phe Thr Asn Ala Tyr Tyr Asn Phe Lys Phe Glu Asn Glu Ile Val Lys
    610                 615                 620

Asp Ile Glu Tyr Ser Thr Asp Gly Ile Trp Arg Gln Lys Lys Leu Asn
625                 630                 635                 640

Phe Met Asn Leu Ile Ile Lys Ala Ile His Phe Ala Asp Ile Lys Asp
                645                 650                 655

Lys Phe Val Gln Leu Cys Asn Asn Asn Ser Met Asn Val Val Phe Cys
            660                 665                 670

Pro Ser Ala Phe Thr Ser Gln Met Asp Ser Ile Thr His Ser Leu Tyr
        675                 680                 685

Tyr Ile Glu Lys Thr Ser Lys Thr Lys Asn Gly Lys Glu Lys Lys Gln
    690                 695                 700

Tyr Val Leu Ala Asn Lys Lys Met Val Arg Thr Gln Gln Glu Lys His
705                 710                 715                 720

Ile Asn Gly Leu Asn Ala Asp Phe Asn Ser Ala Cys Asn Leu Lys Tyr
                725                 730                 735

Ile Ala Leu Asp Glu Glu Leu Arg Asn Ala Met Thr Asp Glu Phe Asn
            740                 745                 750
```

```
Pro Lys Lys Gln Lys Thr Met Tyr Gly Val Pro Ala Tyr Asn Ile Lys
        755                 760                 765


Asn Gly Phe Lys Lys Asn Leu Ser Thr Lys Thr Ile Asn Thr Phe Arg
    770                 775                 780


Thr Leu Gly His Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Val Phe
785                 790                 795                 800


Val Glu Asn Leu Ala
                805


<210> 55
<211> 785
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      mammals-digestive system-rumen-ovis aries sequence

<400> 55
Met Ala His Lys Thr Asn Asn Gly Glu Asn Thr Ile Asn Lys Thr Phe
1               5                   10                  15


Ile Phe Lys Ala Lys Cys Glu Lys Asn Asp Ile Ile Ser Leu Trp Lys
            20                  25                  30


Pro Ala Ala Glu Glu Tyr Cys Asn Tyr Tyr Asn Lys Leu Ser Lys Trp
        35                  40                  45


Ile Gly Asp Ser Leu Thr Thr Met Lys Ile Gly Asp Leu Ala Gln Tyr
    50                  55                  60


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


Lys Lys Asp Leu Pro Leu Tyr Lys Ile Phe Gln Lys Gly Phe Ser Ser
                85                  90                  95


Gln Cys Ala Asp Asn Ala Leu Tyr Ser Ala Ile Lys Ala Ile Asn Pro
            100                 105                 110
```

```
Glu Asn Tyr Asn Gly Asn Ser Leu Glu Ile Gly Glu Thr Asp Tyr Arg
        115                 120                 125

Arg Phe Gly Tyr Val Gln Ser Val Ile Gly Asn Phe Arg Thr Lys Met
    130                 135                 140

Ser Ser Leu Lys Val Ser Val Lys Tyr Lys Lys Phe Asp Val Asn Asp
145                 150                 155                 160

Val Asp Glu Glu Thr Leu Lys Thr Gln Thr Ile Tyr Asp Val Asp Lys
                165                 170                 175

Tyr Gly Ile Glu Ser Ile Lys Asp Phe Asn Glu Phe Ile Glu Val Leu
            180                 185                 190

Lys Leu Arg Glu Glu Thr Pro Gln Leu Asn Glu Lys Ile Thr Arg Leu
        195                 200                 205

Glu Cys Leu Cys Gly Tyr Tyr Ser Lys Asn Glu Glu Asn Ile Lys Asn
    210                 215                 220

Glu Ile Glu Thr Met Ala Ile Ser Asp Leu Gln Lys Phe Gly Gly Cys
225                 230                 235                 240

Gln Arg Lys Ser Leu Asn Thr Leu Thr Ile His Lys Gln Asn Ser Leu
                245                 250                 255

Met Glu Lys Val Gly Asn Thr Ser Phe Thr Leu Gln Leu Ser Phe Asn
            260                 265                 270

Lys Lys Pro Tyr Thr Ile Asn Leu Leu Gly Asn Arg Gln Val Val Lys
        275                 280                 285

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

Gly Asp Trp Val Thr Phe Asn Ile Lys Asn Asp Glu Leu Phe Val His
305                 310                 315                 320
```

```
Leu Thr Ser Pro Ile Asp Phe Glu Lys Glu Val Cys Glu Ile Lys Asn
                325                 330                 335

Ala Val Gly Val Asp Val Asn Ile Lys His Asn Met Leu Ala Thr Ser
            340                 345                 350

Ile Lys Asp Asp Gly Asn Val Lys Gly Tyr Ile Asn Leu Tyr Lys Glu
        355                 360                 365

Leu Val Asn Asp Cys Asp Phe Ile Ser Thr Cys Asn Glu Asp Glu Phe
    370                 375                 380

Asp Leu Tyr Arg Gln Met Ser Glu Ser Val Asn Phe Gly Ile Leu Glu
385                 390                 395                 400

Thr Asp Ser Leu Phe Glu Arg Val Val Asn Gln Ser Lys Gly Gly Cys
                405                 410                 415

Leu Asn Asn Lys Phe Ile Arg Arg Glu Leu Ala Met Gln Lys Val Phe
            420                 425                 430

Asp Asn Ile Thr Lys Thr Asn Lys Asp Gln Asn Ile Val Asp Tyr Val
        435                 440                 445

Asn Tyr Val Lys Met Leu Arg Ala Lys Tyr Lys Ala Tyr Phe Ile Leu
    450                 455                 460

Lys Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr Asp Ile Lys Met Gly
465                 470                 475                 480

Phe Thr Asp Val Ser Thr Glu Ser Lys Glu Thr Met Asp Lys Arg Arg
                485                 490                 495

Met Glu Phe Pro Phe Val Asn Thr Asp Thr Ala Lys Glu Leu Leu Ala
            500                 505                 510

Lys Leu Asn Asn Ile Glu Gln Asp Leu Ile Gly Cys Arg Asp Asn Ile
        515                 520                 525

Val Thr Tyr Ala Phe Asn Ile Phe Lys Asn Asn Gly Tyr Asp Thr Leu
    530                 535                 540
```

```
Ala Val Glu Tyr Leu Asp Ser Ala Gln Phe Asp Lys Arg Arg Met Pro
545                 550                 555                 560

Thr Pro Thr Ser Leu Leu Lys Tyr His Lys Phe Glu Gly Lys Thr Lys
                565                 570                 575

Asp Glu Val Glu Asp Met Met Lys Ser Lys Lys Phe Ser Asn Ala Tyr
            580                 585                 590

Tyr Thr Phe Lys Phe Glu Asn Asp Val Val Ser Asn Ile Glu Tyr Ser
        595                 600                 605

Asn Asp Gly Ile Trp Lys Gln Lys Gln Leu Asn Phe Gly Asn Leu Ile
    610                 615                 620

Ile Lys Ala Ile His Phe Ala Asp Ile Lys Asp Lys Phe Val Gln Leu
625                 630                 635                 640

Cys Asn Asn Asn Lys Met Asn Ile Val Phe Cys Pro Ser Ala Phe Thr
                645                 650                 655

Ser Gln Met Asp Ser Ile Thr His Thr Leu Tyr Tyr Val Glu Lys Ile
            660                 665                 670

Thr Lys Lys Lys Asn Gly Lys Glu Glu Lys Lys Tyr Val Leu Ala Asn
        675                 680                 685

Lys Lys Met Val Arg Thr Gln Gln Glu Thr His Ile Asn Gly Leu Asn
    690                 695                 700

Ala Asp Tyr Asn Ser Ala Cys Asn Leu Lys Tyr Ile Ala Leu Asn Asp
705                 710                 715                 720

Glu Leu Arg Asn Glu Met Thr Asp Thr Phe Lys Val Thr Asn Arg Gln
                725                 730                 735

Lys Thr Met Tyr Gly Ile Pro Ala Tyr Asn Ile Lys Arg Gly Phe Lys
            740                 745                 750
```

Lys Asn Leu Ser Ala Lys Thr Ile Asn Thr Phe Arg Lys Leu Gly His
        755   760   765

Tyr Arg Asp Gly Lys Ile Asn Glu Asp Gly Met Phe Val Glu Thr Leu
    770   775   780

Ala
785

<210> 56
<211> 735
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown:
      pig gut metagenome sequence

<400> 56
Met Ala His Lys Lys Asn Ile Gly Ala Glu Ile Val Lys Thr Tyr Ser
1   5   10   15

Phe Lys Val Lys Asn Thr Asn Gly Ile Thr Met Glu Lys Leu Met Ala
            20   25   30

Ala Ile Asp Glu Tyr Gln Ser Tyr Tyr Asn Leu Cys Ser Asp Trp Ile
        35   40   45

Cys Lys Asn Leu Thr Thr Met Thr Ile Gly Asp Leu Asp Arg Tyr Ile
    50   55   60

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

Val Trp Lys Asn Gln Pro Leu Tyr Lys Ile Phe Gly Lys Lys Tyr Ser
                85   90   95

Ala Asn Asn Arg Asn Asn Ala Leu Tyr Cys Ala Leu Ser Ser Val Ile
            100   105   110

Asp Met Asn Lys Glu Asn Val Leu Gly Phe Ser Lys Thr His Tyr Val
        115   120   125

```
Arg Asn Gly Tyr Ile Leu Asn Val Ile Ser Asn Tyr Ala Ser Lys Leu
    130                 135                 140

Ser Lys Leu Asn Thr Gly Val Lys Ser Arg Ala Ile Lys Glu Thr Ser
145                 150                 155                 160

Asp Glu Ala Thr Ile Ile Glu Gln Val Ile Tyr Glu Met Glu His Asn
                165                 170                 175

Lys Trp Glu Ser Ile Glu Asp Trp Lys Asn Gln Ile Glu Tyr Leu Asn
            180                 185                 190

Ser Lys Thr Asp Tyr Asn Pro Thr Tyr Met Glu Arg Met Lys Thr Leu
        195                 200                 205

Ser Ala Tyr Tyr Ser Glu His Lys Ser Glu Ile Asp Ala Lys Met Gln
    210                 215                 220

Glu Met Ala Val Glu Asn Leu Val Lys Phe Gly Gly Cys Arg Arg Asn
225                 230                 235                 240

Asn Ser Lys Lys Ser Met Phe Ile Met Gly Ser Asn His Thr Asn Tyr
                245                 250                 255

Thr Ile Ser Tyr Ile Gly Glu Asn Cys Phe Asn Ile Asn Phe Ala Asn
            260                 265                 270

Ile Leu Asn Phe Asp Val Tyr Gly Arg Arg Asp Val Val Lys Asn Gly
        275                 280                 285

Glu Val Leu Val Asp Ile Met Ala Asn His Gly Asp Ser Ile Val Leu
    290                 295                 300

Lys Ile Val Asn Gly Glu Leu Tyr Ala Asp Val Pro Cys Ser Val Thr
305                 310                 315                 320

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

Asn Met Lys His Met Leu Leu Ser Thr Ser Val Thr Asp Asn Gly Ser
            340                 345                 350
```

```
Leu Asp Phe Leu Asn Ile Tyr Lys Glu Met Ser Asn Asn Ala Glu Phe
        355                 360                 365

Met Ala Leu Cys Pro Glu Lys Asp Arg Lys Tyr Tyr Lys Asp Ile Ser
    370                 375                 380

Gln Tyr Val Thr Phe Ala Pro Leu Glu Leu Asp Leu Leu Phe Ser Arg
385                 390                 395                 400

Ile Ser Lys Gln Asp Lys Val Lys Met Glu Lys Ala Tyr Ser Glu Ile
                405                 410                 415

Leu Glu Ala Leu Lys Trp Lys Phe Phe Ala Asn Gly Asp Asn Lys Asn
            420                 425                 430

Arg Ile Tyr Val Glu Ser Ile Gln Lys Ile Arg Gln Gln Ile Lys Ala
        435                 440                 445

Leu Cys Val Ile Lys Asn Ala Tyr Tyr Glu Gln Gln Ser Ala Tyr Asp
    450                 455                 460

Ile Asp Lys Thr Gln Glu Tyr Ile Glu Thr His Pro Phe Ser Leu Thr
465                 470                 475                 480

Glu Lys Gly Met Ser Ile Lys Ser Lys Met Asp Lys Ile Cys Gln Thr
                485                 490                 495

Ile Ile Gly Cys Arg Asn Asn Ile Ile Asp Tyr Ala Tyr Ser Phe Phe
            500                 505                 510

Glu Arg Asn Gly Tyr Thr Ile Ile Gly Leu Glu Lys Leu Thr Ser Ser
        515                 520                 525

Gln Phe Glu Lys Thr Lys Ser Met Pro Thr Cys Lys Ser Leu Leu Asn
    530                 535                 540

Phe His Lys Val Leu Gly His Thr Leu Ser Glu Leu Glu Thr Leu Pro
545                 550                 555                 560
```

```
Ile Asn Asp Val Val Lys Lys Gly Tyr Tyr Ala Phe Thr Thr Asp Asn
                565                 570                 575

Glu Gly Arg Ile Thr Asp Ala Ser Leu Ser Glu Lys Gly Lys Val Arg
            580                 585                 590

Lys Met Lys Asp Asp Phe Phe Asn Gln Ala Ile Lys Ala Ile His Phe
        595                 600                 605

Ala Asp Val Lys Asp Tyr Phe Ala Thr Leu Ser Asn Asn Gly Gln Thr
    610                 615                 620

Gly Ile Phe Phe Val Pro Ser Gln Phe Thr Ser Gln Met Asp Ser Asn
625                 630                 635                 640

Thr His Asn Leu Tyr Phe Glu Asn Ala Lys Asn Gly Gly Leu Lys Leu
                645                 650                 655

Ala Ser Lys Ser Lys Val Arg Lys Ser Gln Glu Tyr His Leu Asn Gly
            660                 665                 670

Leu Pro Ala Asp Tyr Asn Ala Ala Arg Asn Ile Ala Tyr Ile Gly Leu
        675                 680                 685

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

Ser Leu Tyr Asn Gln Pro Ile Tyr Asp Thr Gly Ile Lys Lys Thr Ala
705                 710                 715                 720

Gly Val Phe Ser Arg Met Lys Lys Leu Lys Lys Tyr Lys Val Ile
                725                 730                 735
```

<210> 57
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 57

actatgttgg aatacatttt tataggtatt tacaact 37

<210> 58
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 58
attgttggaa tatcactttt gtagggtatt cacaac 36

<210> 59
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 59
aatgttgttc acccttttt 19

<210> 60
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 60
cctgttgtga atactctttt ataggtatca aacaac 36

<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 61
attgttgtaa ctcttatttt gtatggagta aacaac 36

<210> 62
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 62
attgttgtag acacctttt ataaggattg aacaac 36

<210> 63
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 63
cttgttgtat atactctttt ataggtatta aacaac 36

<210> 64
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 64
cttgttgtat atgtcctttt ataggtatt 29

<210> 65
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 65
cttgttgtat atgtcttttt ataggtattg aacaac 36

<210> 66

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 66
tactcttttt taggtaatga acaac 25

<210> 67
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 67
cttgttgtat atattctttt ataggtatta aacaac 36

<210> 68
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 68
catgttgtac atactatttt ttaagtatta aacaac 36

<210> 69
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 69
gatgttggac actatgtttt atacggtgga tacaac 36

<210> 70
<211> 36
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 70
gatgttgtta tgctgttttt gtaagtaata aacaac 36

<210> 71
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 71
attgttgtag acctcttttt ataaggattg aacaac 36

<210> 72
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 72
attgttgtac gaaccatttt atatggtaat aacaac 36

<210> 73
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 73
actgtaaaac ccctgcagat gaaaggaaag tacaacagt 39

<210> 74
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 74
atcatgttgt acatactatt ttttaagtat taaacaacta 40

<210> 75
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 75
attgttgaat ggctatgttt gtatgctatt tacaac 36

<210> 76
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 76
attgttgggg tacttctttt atagggtact cacaac 36

<210> 77
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 77
attgttgtag accttgtgtt ttaggggtct aacaacg 37

<210> 78
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 78
actgtgttgg aatacaatat gagatgtatt tacaac 36

<210> 79
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 79
attgttgtgg cataccgcaa ggcggatgct gacaac 36

<210> 80
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 80
aattgttgag ataccgtttt ttatggtatt ggcaac 36

<210> 81
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 81
attgttgtgg cataccgtat tacgggtgct gacaa 35

<210> 82
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 82
attgttgtgg cataccgtat tacgggtgct gacaac 36

<210> 83
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 83
attgtgttgg gatacacttt tataggtatt tacaac 36

<210> 84
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 84
tattgttgaa tacctttctt ataaaggtaa ttacaac 37

<210> 85
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 85
tgttgtaaat ggctttttat gggcaacgaa caactc 36

<210> 86
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 86
attgttgaat gtattctttt ttaggacaga tacaac 36

<210> 87
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 87
attgttgaat ggtatctttt atagactgat tacaact 37

<210> 88
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 88
attgttggat aataggtttt ttatcttaat tacaac 36

<210> 89
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 89
actgttgaat agttgatttt atatcctatt tacaac 36

<210> 90
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 90
attgttgtag atacctttt gtaaggattg aacaac 36

<210> 91
<211> 644
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 91
tatatcgtgg ccgaatatgt taacgcggac gacgtccgtc ttgtgaagtt tcaggacgag 60

gatttcgaca ggcttcttga caaggttaga gaatggaaca agaaacatct tgttgttgga 120

aatcggaact tcgaagaaaa atttgcgtaa tccaaaaatt ttccgtatat ttgcggcgtg 180

aaattaaaaa tatgtttaac taaaaacaaa gattatggca cacaagaatc ctgatgggga 240

gaacaccatc aacaaaactt ttattttcaa agtgaaatgc gagaagaatg atattatatc 300

gttctggaaa cccgcagctg aagagtattg caactattac aacaaactta gcgaatggat 360

tggcaaagat atgtataaca cgccgtcatg gaacatccgg caagagttca agaagaattt 420

aagtgttaga accataaaca cgtttcgtga gcttggcaat gtgaaatacg gcaaaatcaa 480

caatgaaggg ctttttgtcg aagacgatgt gtaaacatta agatttccat acgacaggat 540

tcaaaaaaac gttctttgaa atattggatt ggtggcaaga ggctgttttt tttaggctaa 600

aaagttgtgt aaatagcaga aacacagaac ataacataaa atct 644

<210> 92
<211> 264
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 92
aactgctaca attctgccga gtttatgatt cagacaaaat tcaaaaaaag acttccgcaa 60

gcaaccgttt ttggtgaatt gaacagaaac gggtatgtta aagtattgac ccaagaagaa 120

tatgacgaac tcacaaaatc agcaaaataa tttattactg attgaaaaat aaagcgttct 180

ttgacatatt gtataacaaa caagcatttt tgtaagagat aacccatttc attttattga 240

tatacaatga aatgaaaaga atat 264

<210> 93
<211> 614
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 93
gataaatttg cccgtaatgt tatcgggttc aagtcatatc acgaactgct tgataatgct 60

atcataaaag aaaaattaca acgggaattt ggttatgaag atgctccgaa aacgtggttg 120

ttcggacaac aaaaaaatga atgtttctaa tgtattaaaa caataattca attacaattt 180

taagattatg gcacaacaca aatcaaacaa cgaagaatca gcaatcaaca agactttcat 240

tttcaaggca aaatgcgata agaacgatgt catatcgtta tgggaaccag cggcaaagga 300

atactgcgac tattataaca aagtgagcaa gtggattaaa actatgtata acatacccgc 360

atataacatt aagtccaatt tcaagaaaaa tttgagcgcc aaaacaattc aaacttttag 420

agaacttgga cactaccgtg acggaaaaat aaatgaggat ggtatgtttg ttgaaaactt 480

ggaataattc tgtatatacc aattagaatt gaaaaaaaaa cgctctttga catattgttt 540

tctacataaa aacaagattt tacacaacgc aatacatcat aaagtgttgc gttataacaa 600

ataacaaaaa ttct 614

<210> 94
<211> 1041
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-cattle and sheep rumen sequence

<400> 94
tttattcaat gcgaaccaga ggtcttgacg catgaatctg gctatacata tcgttatgcg 60

accgacgaag agaaaatatt gattaaaaga tgcaaatatt gaataggcaa ttttaaattg 120

tgaaaaaaaa aatgattgaa tataagttta cgtttgaact ggatggacat ctatcggcgt 180

acgattttgt tacgttgcaa gaacggtttg aaagggaatt gaatccttat tttgatgatg 240

ggagcatatc tggtactctt tcttatgcaa atgatgatta atatgcaaat aatatggcac 300

atgtaagaac aaaaaatgaa ggaaacatgg caaaaacata ttcttttaag gtcagagaaa 360

caaaccttaa aaaggatgtg atgattgaat ataacgaata ttataacagg ttatccgatt 420

ggatatgtgg caatttaacc aaaatctcgg aaaatgaaga atggaggaat gccttatgca 480

aaccaacaga aaacatgtac aacgaaccga tttacgttcc cttggttaaa tcacagaacg 540

gaatgttcaa ggcaattaaa aaattgggcg caacgaagat atggcaagaa tagaaagacc 600

gatttttaaa tctgaaatca cttctaacga attgtatact aaagaaatat aaagaatata 660

catcttttat gacattatga tattgttgta tgcatcattt cacatggtaa taacaacgaa 720

gagaaacacc gagcgaccca caaacctatt gtcgtacgca tcatttcaca tgataataac 780

aacgaatatt cctgcaagca tgatttaaca atttttaaga acctggtggt ttctccgttg 840

ggttcttttt agtatctttg ccttgttgaa acaaataaaa caaattgaat tatgatttat 900

aaaggcaaag aaatagacga aagttaccac atcaataaat gggaagatga agagatttac 960

tctggtccaa cccattatga atcattcgaa gccgatgaaa taaaagagtt ctacctcaag 1020

gcacttgcaa aggaaaagga a 1041

<210> 95
<211> 1545
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
gut metagenome sequence

<400> 95
gtgcgcatat acactcaatt cgccgatgac cgtgtgtacg cgaaggattg tatcgacgga 60

ttctttagta taagacaaga taccgaaatg cgcctcgtgt ataaaaatga gatagcacgc 120

gggcttgagt gtatcaatat tgtaagatag tagttttctg ttattttaca tattgatgtg 180

ttttggcatg gtttttgtta aaatataatc tagcagtatt gagactgcgg agtaacgtgt 240

ctaactgttt cattataagc agtaaagact aatattttta tatcttaaac ttatttttat 300

tatggctggt cacagcaaaa tcaaagaaaa tcacattatg aaggcgtttc ttatgaaagt 360

aaaagaaacg cgaaaaaaac agtggcaatc aaattttatt agaagtgaga ttgctaagtt 420

tacaaattat tacaatgggc tgtcaaagtt ccttcttgga agcccgactg gagggacata 480

tgacactgca tattttgata caaagattca aggctccaag ggggtatatg ataagattaa 540

agaaaacgga gaaacttata ttgcagtatt aagtgatgac gttattacgg cagaggtgta 600

aaatcctctg ccaacatcgc aagtaactca ttgaaaatta gttaaatgcg aatgccaaca 660

aaagtgaacg aactgacttg taaagcagga tgttgttata tctttttgta gataataagc 720

aacaagatac aatcaatcgc gagtttatac tgaaatgttg ttacactgtt tttgtaagtg 780

ttaaacaacc ttgcacaaat gtcatctacc agtacaatag atgttgttat actgttttgt 840

aggtattaaa caaccattgc gcagactgac agagtaacct ttcctgatat gttgttacac 900

atttttgtaa gtgttaaaca actgacgcat tgatattgcc ttgtctatta agaatgttgt 960

tatgctcttt ttattggtat aaacaaccga gcaactggta ctcaaatttt aaatactgtc 1020

gcgctatgtt atgtacatcg aacagctacc actcaatggc tttgtttgca accgtgatta 1080

attcaatcgc ggttgcattt gttttatgat gtgtttttgt atatattatg tatatatgga 1140

aaaggaaaac agggtatcgg agttatggag caagttctct gatattgact tgcgccgaag 1200

ccaaatgaca tatatgccaa taagaggtag taaaagatac ggcagaagaa taaaacgtag 1260

tgacatcgag tacgagtaca gatatctgta tagagcaaac aaacattggt aatatgaccg 1320

tagctaaatt atcaagtaat cataagccag cgtgccttgg acgaatctca gctttaaaca 1380

ccccgattag atttgagtgt cgggctggta atagtataag gcctggcaac atagagtata 1440

gctataaaag atggaaaacg tcgtaatttc aactatgcac aacccgcata cgctggctta 1500

ttaccaaggt aagctggctc ctatgcattt cagacaagat acagg 1545

<210> 96
<211> 1380
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-cattle and sheep rumen sequence

<400> 96
agcctgtata cagggacaag gttaagtaca acaccaaggc tgaggcaaag aagagggctg 60

atgatatgaa caaacagaat agggtcatac accagctgtc tgtttatttg tgtcctaaat 120

gtcataagtg gcatataggt aggagcagtg tggagagtgt gcgcagggaa gggtacttta 180

gtcagatttg aaattaattg ttatatggcg catagaaata aaaacctagc agaaaactgc 240

attaacaaaa cattcagttt taaagtcaaa gccgaaaaag aggagataaa ttcaaaatgg 300

attccagcca ttaaagaata tactgcttat tataacagga taagtgactg gataaacctg 360

tattcacagc ctacttatga tattaaggaa gtttataaga aaaacgctgg ttgcaaagtg 420

ataaacgact tcattaaaaa cggtaacgcc gttatatgtt gtatcgaaaa taacaaacta 480

attgagacaa atggaagaca atagttcaaa ttttaaatgt aaaacagtca ttaatgtatt 540

aatatataat acatagcaaa aatccagatg ttgaatacat ttcttttaag tgtacttaca 600

acgcggtggc attgctaaaa tatagtcctg tggatgttga atacatttct tttaagtgta 660

cttacaacca acgctgtaca cattgctaat ggatgatgac gatatagagg tgttgaacta 720

ccttaatgaa aactacacca atgaaaacat tgagtatata cgcggttggt ggatggatga 780

cgacgataaa ctccagacac ttgacaggtt tttgaaaaat ttttcaatat agacctgtca 840

ctgttgcggc tataagaaga ccgatttgac actgaaagac cgatactggg tttgccccga 900

atgcggtgca aaactagacc gcgataccaa tgcaggaata aacattaaga atgagacaat 960

tagactgata aacaaagaat aatgagaact ataataggga ggtgtacccc cgaatttaag 1020

ccagtggaga accatacaaa cctatcatat aggggttcaa tgaatctgga atttctgaca 1080

aaaacagggt ttaacagcca gtgtaccaat gactaacaca ggacatataa agacaaatct 1140

aacaataaaa aaaaatattg accaattctg cagaaaaaac aggttggttt cggttatgtt 1200

ggtgaataaa gacagttaga ttaattttat atggaaatga aaatagagac aaaagacgag 1260

aacatctacg tattcatcta tgccaagtcc gcctacttcg gcaatacatt tgaatatggc 1320

ggcacatttt ccgtcggcaa ggacgacaac tggaacgatg tgagaggcca cgttaccgaa 1380

<210> 97
<211> 853
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 97
gacaacatcc tggtcaagac cgaggttaac agaaggtact gccgccttat gaccgacgag 60

aacggagtgt ggctcctgag gaaaaacgac aaacatccaa catattttat ctaccagaac 120

ggaacactct atcaatatga ggaagattga ttagttgatg ttttcataat aattttatct 180

ggaatttgaa aagattccag attttttttt tatttcgact gtacaaaaaa caggttccgt 240

tgcgttatat aggtgtaaat taaaaattca gtcaaacaaa aattggaata aaatatggct 300

aacaagagaa cagacacaac aatcaacctt aacaaaaccg ttataatgtt aacgaacatg 360

ctgccagaag tacgggcaat gtttcaggcg ggaatacgcc aggctcaagt ttatgcagac 420

ttggtgaaca agtggatatg ttcacaggaa atgagagagg ttatgtgtct ccatccgtca 480

aaaaaggacg gggtgtacga ccaaccgttc ctgaaagcta caaccaaata cccagccacg 540

gtagctggta tcctgcttaa gatgggaaaa acaaccaatt ggggtgagaa ataataccca 600

cccgccccat ttttttacac tgattagttc tttgacttat tgatttatat tggtttacac 660

aaattatcga cacaataaat aaaaaaaatt gtatattagt agtatgatga cagaagaaac 720

acggaagaca atagagagcg tcatagtggt tctcggcata gcaatcatgc tggcagccgc 780

cgtccgaata atgacgcaga acaaagcaat tgtgaaatat gatgaacagg ttgaaaccat 840

gcaaacttgc ata 853

<210> 98
<211> 795
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
gut metagenome sequence

<400> 98
atggaagttg tacgtggtgg aaatcaatgg gaggtttatg acaattacga tgagactatg 60

aaagcatcaa aaaatgtaag gtctgtattg ggacttccgg aagtaaaata tccacctgag 120

gattttagga catataattt ctaataaaaa tgaacggaaa aatttccgtt catttttttt 180

ttgtttattg gtgaaaaaat agtatctttg taaaaaataa atgttaaaat atttttatg 240

ggaaatacta caaaaaaagg aaatttgacg aagacttatt tattcaaagc caatctttca 300

gaacaagact ttaaattatg gaggtctatt gttgaagagt atcaaagata taaggaagtg 360

ttgagtaaat gggtatgtga ccatcttaga aatgcaatgt gtacgaaccc gaaaagtgag 420

actggatatt ctgtaccgtt cttgacttca agaatcaaga aacagaacat tatggttgta 480

gaattgaaaa aaatgggcat ggttgaagtc ttgaatgaaa aatcaacaga aatttaagaa 540

aaaaatattt atataatgta ctgaaaataa gtaaataata aatattgtgt aaaaaacttg 600

atatttttt tttgttatct ttataatata aaataaaatg taaatatgaa aaatctgtta 660

aaactcaaag aacaaatcaa ggattacaaa catcttcagt ttgtgttgga gaaagaagat 720

gaatctgaac tccattatag atgtatgact gaagattttt cgttcaaggt atctgaagaa 780

aaagacggaa cactt 795

<210> 99
<211> 420
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
bovine gut metagenome sequence

<400> 99
ttataaacat ctaaaaagaa agacttatga caacaaaaca agttaaatca atcgttttaa 60

aagtaaaaaa cactaatgaa tgccctatta caaaagatgt aataaatgaa tataaaaaat 120

attataatat atgtagtgaa tggattaaag ataatctaac aagtattact attggaaacg 180

aaaatttacg aaaattattt tgtggtaaac ttaaagtaag tggatataat acaccaatat 240

tagacgcaac aaaaaaaggt caatttaata tattggcaga attaaaaaaa cagaataaaa 300

ttaaaatatt tgaaatagaa aaataagtct tatgattaca aaaataatag atttcaaaca 360

ttttttttaa ttctatttta ttgactaatt cattgaaata taaataatta caaataaccc 420

<210> 100
<211> 1058
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 100
gatagatata gtattgcagc atttctggct tgcgaatcat cagcaatgca aaaatgtgac 60

tattggaaca atgatgatgc ccaagattac ataagaaact acaaagaggc ttatagtaat 120

gcagtaagac ttgcgttttt taatgattaa gcaacacgct taacattgtc aaatgtaacg 180

acattaagtg cgtgtttcat aagggcagcg aacctttcgc cgcccttctt tttttgttgc 240

tgtaacggaa ttatgtttac ttttgtgcca tcaagtatat agttccctta ataaattgta 300

tattaattaa aagtttggca caatatttga tgcgtacaaa ttaaaataaa aacattttga 360

attttaaaat ttaatttgta attttaaata agaaagtttt atttaactaa aataaaaaaa 420

atgaataaat cttatgtttt taagtcgaat gtggctattg atgacattat gtctttattt 480

gaaccggcaa ttgaagagta cataaactat tacaatagaa ccagcgattt catttgtgat 540

aatcttacat caatgaaaat cggagatttg ttgcttctaa caatgtgtac taagacaaaa 600

gaaaataata gatacggtaa ccccctctat aatatcaaag atacttttaa aaagaaaata 660

ccatcttcaa tacttaatat attcaaaaaa aaggatatgt atcaaataat atgtgattaa 720

ttatgccttt ttttaataaa aaattgttaa ataatacttt gtttattaat aaattataaa 780

tatcacagta aactattagg gatttgtaaa atttatggaa attatataca tgatggcact 840

aagatttggt tattaagaaa tttttctgta taagtataat aacctattta taattataat 900

tgaataaaat gtataatatg gaaaacacag gcttttatac agtttcaaat attgaaactt 960

ctcataagcc aaccgaaaat tctaatgacg aaattcttag gattttcaat aaaagaaggc 1020

cttattgccc ttcagacttt aagaagcaac attttatt 1058

<210> 101
<211> 554
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 101
aggctcaacc tcctcaaccc gatttatctt gagatcgcca agtacggaca cttcgggagg 60

aagagctatg tgaaggacgg catcaagtac ttcccgtggg aggatttgga tttggttgaa 120

gacatcagaa aaattttcga aatggaatag agggaaccgg aatttttcc ggtttttctt 180

tgtcctttcg aaaataaata gtatctttgt aaaaaaacaa cagattatgt acaatagtaa 240

gaagaagggg gagggtgaca ttcagaagtc gttcaagttc aaggtcaaaa cggacaagga 300

gacggtcgaa ttattcagaa aggccgcagt cgaatactcg gaatactaca agaggctgac 360

aacattcctc tgtgagatgt ataacagacc agcgtttgac ttgaaggagt gctacaagaa 420

aaattccaat gtaagtgtct tcaacacatt gaagaaaact ctcggtgcaa tatatggaaa 480

gctcgatgaa aacggaaatt ttattgagaa tgaatgtaat aagtaactgg aataaaagaa 540

attagacaga gtaa 554

<210> 102
<211> 1039
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 102
ttgtattggt tgctgtatgg cgacggaagt gacatatatg atgacgggtg gtttgactgt 60

gttcataatt ttgcccgtaa tgttatcggg tttcagtcat atcacgaact gcttgataat 120

gctattataa aagaaaaatt acaacggtaa tttggttatg aagatgctcc gaaaacgtgg 180

ttgttcggac aacaaaaaaa tgaatgtttc taatgtatta aaacaataat tcaattacaa 240

ttttaagatt atggcacaac acaaatcaaa caacgaagaa tcagcaatca acaagacttt 300

cattttcaag gcaaaatgcg agaagaacga tgtcatatcg ttatgggaac cagcagcaaa 360

ggaatacggc gactattata acaaagtgag caagtggatt aaaactatgt ataacatacc 420

cgcatataac attaagtcca atttcaagaa aaatttgagc gccaaaacaa ttcaaacttt 480

tagagaactt ggacactacc gtgacggaaa aataaatgag gatggtatgt ttgttgaaat 540

tttggaataa ttctgtatat accaattaga attgaaaaaa aaacgctctt tgacatattg 600

ttttctacat aaaaacaaga ttttacacaa cgcaatacat cataaagtgt tgcgttataa 660

caaataacaa aaattctgga cgggaaagga agatgtcaga cgtttttatt gttggaatac 720

tcgtttttta cggtatttac aactgccccg tagcggaatc aaaataccac cgcattgttg 780

gagtacaagt tttacacggt attcacagta cgaacaccga atgaactgaa aaaaataaac 840

ccgaccttgc aaccgtagat ataaataaag caatacaaaa tttgaaacta tggcacacat 900

taaaaaaatt gacgaaatgg caagtcaaac tgtttcactc cgttctgacg cattgttcaa 960

aaaagcgttt gaggaatttg aaaaggagtt gaaagaagtt ctcaaatcgc acaacaatat 1020

catttattgt ggaggtgat 1039

<210> 103
<211> 1252

<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 103
ctcatcaaat tgtacaagtc gttgacggac actgaatttg acaagaagaa aatcatcaat 60

gatgtctacg acggcacttt tgagataatc ctcaaatacc caaagaagaa gaacgggaca 120

ttcgtgttct ggaaacatta caagaagtaa cacaatgata cacagtatgt tgtaagaaat 180

aagatttagg ctttaatttt aatatatgaa aatatggcac acaaaggaga aaaggaaggc 240

taccaaatca agacactgaa gttcaaggta cgctcgcatg acatcgggaa atcactttat 300

gatattgtca acgaatacac caactactat aacaaagtaa gcaaatggat atgtgacaac 360

cttggttaca acgagccatt ctacaagtca agggtgaaaa gcgccgcctc catgatgtca 420

ggattgaaaa aactgggcgc caccatgcca ttgacggatg aaaatgccat tttttcaaca 480

ccaaaaccga agaaaaacat tggaaaacaa taatttacac aaagtctacg gcgggaatcg 540

tgataaaaat gaacgagatt gttgggatat acctttttata ggattttcac aacatctgag 600

ttgtttgatg ttaaaaactt taactaataa ggcaagaagt cccattcctt caggtggggg 660

tagttcattt gttgggatac tcgtttcaca cggtattcac aacttccaac caaccattaa 720

aaaaccttca aatattgttg gagtacccgt tttatacggt gcaaagcctc cccgacgatt 780

tcaagttcct gtacgaagat gtcaattttg gatagcaact gttaccaata aacatattca 840

aaagtaatca aatatattca aaaacaactc gtataaatat ataaagttcg tgatatttat 900

tataaagaag ccgaaggaga gagcggtttc cgaacaataa agatatacag aggttttatt 960

cttgacggca ctctctcctt tagccgcaag tttaattcct ctttttttatt gcactatggt 1020

catcgacagc aaatatacca agacattcaa gtcaaacgga ctgacccatc agaaatatga 1080

cgagttgctc tcgtttgctt ctatgctgcg tgaccataag aacaccatct ccgaatatgt 1140

caatgccaac cttgaacact acctcgaata ctcaaaactc gacttcctta aggaaatgcg 1200

tgcgaggtac aaggatgtcg ttccgagttc gtttgacgct caactctaca cg 1252

<210> 104
<211> 1131
<212> DNA

<213> Unknown

<220>
<223> Description of Unknown:
pig gut metagenome sequence

<400> 104
agaatctgtc ctatatgtgg gaaacattgc gaatatgagg aaatggaggg cgaccacatt 60

gttccatggt caaagggcgg taaaaccgat ataggcaacc tccaaatgct atgcaagaag 120

tgcaatcacg aaaagtccaa tagatattag tggcgtaatc aaaaatttgt ttgtgttgag 180

gaaaagcagt gaaaaaaaac attgtttttc ctcaattttt atttgcataa ttcaaataat 240

tttttatttt ataggataat agagctaaca agcattaaca attattaaaa cgatttatat 300

tgaaaataaa ttttgtggga atatttattt ttactacctt tgcatcgtaa tacaattaaa 360

caaatttttg attatggcac acaaaaagaa cataggagca gagatagtaa aaacttactc 420

ttttaaggtg aagaatacca atggtatcac aatggaaaaa ttaatggccg ccattgatga 480

gtatcagtcg tactataacc tttgcagtga ttggatatgc aagggtcttg acgaaataat 540

gaggaatact tttctgaaaa aagcaaatag caataaatca ttgtataatc agccaatcta 600

cgatacgggt atcaagaaaa ccgcaggtgt gtttcctaga atgaaaaaat taaagaaata 660

taaagttatc tgaaataaaa tatgtatttt tctttgtgga aatacctatt aatagactga 720

tttctaataa gttataagaa atactgtatg tagtaaataa gatatcatat ttttgcggag 780

aggcacatgg agtatgctat agggtttttg ctaccgagca gaaagcaaaa gaaaaaatgc 840

agggatgata tcatttcatt cttgcatttt gcttatacat attcaatcaa gtatcatttt 900

ctgtttttac tattatccta taaaataaaa ttttcctcaa catttccaaa tttaatttgc 960

aataattttt tttgataaaa agtgcaaata aattttatag attcaaaact tttgattaac 1020

tttgtaacaa gaaaaacatt aaggattatg ggttacacat attttagggt tactgatgaa 1080

agggcaaggg atgttatgcc aaaggcggct gaaatcataa aggatatttt c 1131

<210> 105
<211> 3677
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 105
cttcacctcg tacagccgac aataagtttc gcttggactg aacttatgtg cgcctgcgca 60

ttcatagcgg gtggcgtatc aggctatctc atcaagggca agatgccaaa cgacgggaac 120

aagtaccagt cggtagaggg aaaggaatag gacaaaaaaa aacacatcac ccccagcgca 180

tcgggcgcgg aggtcgggtg tgcatataac ggtgtctgtg gcgcaactgg tagcgcagtg 240

gattgtggtt ccaaaggttg cgagttcgag cctcgccaga cacccattat cacacggaag 300

cattggatgg aagtgcaagt acctactggg aacttcctga aagcgcaagc aaagtcgagg 360

tctaacggta cttatgaccg aggtaatggc ggggcgttgg ttcgagtcca acacaatgtt 420

tccatttaca cggagagttg caggagtggt aactggtcag attgctaatc tgaagcccac 480

ctcgttgtgg caggggtccg aatcccttac tctccgccaa gcaacatacc cgcagagtag 540

tcgcgtatat tctgtcggtg tggtcagaaa gaagtgaatg tgatgcgaac gcgcgaaacc 600

atcgcattta gagtccgaat ctcctctgcg gtagccagtc cgcatagttt aatcaggtta 660

aaacattctg acgctttttt aaatcgcggg agtagttcag tggtagaaca tcggcttccc 720

aagccgaggg tcgcgggttc gagtcccgtt tcccgctcaa cacataggct gtggacaagg 780

tgggcgaaag tatttttttcc atagttttac accaacgccc gccttttcct aaacgcattg 840

gagagataga ggacttgcct tctaaacaag cagtacgggg gaacttgcat ccgacctccg 900

tttcaatgcg gtagaactcc gctcccgtga cagcgacgaa tgatgcaata gcggttcacg 960

agatacctca agaaacttca tttttcaaaa gccacaatag ttcaactggt agaacggcgg 1020

tatcgtaaac cgcaggttgc tggttcaatt cctgcttgtg gctcaacaat ttcgggggct 1080

tgcaacgctg ccactgcggg tggaagccag cgacaagaac ttgtgtgaag ccgaaacgca 1140

gtccttcggg agaggggcga aggggcaagc gagatgtgtc ccacttttt aaagtaacag 1200

gctttaataa atatttatca ttcccgaaag gctgtgcgga acagcctctc ggcttttacg 1260

gggatttagt tcagttggta gaacatctgg ttcgcaatca gaaggtcgcg ggttcgactc 1320

ccgcaatctc cacaaatata aatatagtat tgccctgtgg tgcaatcggt aacacaccag 1380

attctgaatc tggaatttcg agttcgagcc tcggtggggc aacacaatag gcagccgtac 1440

tgccgaatac aagcctgtgg agaacccaac cgtggatgac cgttgcctat gcaacctaaa 1500

aagcggtggt tctgtgaagc aggaagcgga aatacaatat tccgcatacg gtggtggtgt 1560

aatcggtaac ataacaatat ccgaaaagtt taaaccatac acccgacgat tatttttatt 1620

cattgttagc gaccgccgtg aggcggacgc aggctggcgg tcggataatg acgcataatg 1680

gcggttgtga aagccgacgg aaagcactac atcgttaagt gccagccacc ataataggca 1740

gccgtactgc cgaatttaag cctgtggaga acccaaccgt ggatgaccgt tgcgtaagca 1800

acctaaaaag cgatggttct gcgaagcagg aaggaaatgc ccaatttatt aggtttttcc 1860

atacggtatg acagcctcta actgtagcgc attacaaaac aaacgctacc attacataaa 1920

tggtcagagg cataacgccg agcgcaggta tggtatgcgt tcaagtcgca gtcacggaag 1980

ccccagataa aaatgggagg tgcttgcggt caagcgagtg gtcagcgggc ttgcactcgg 2040

tgtggcaaca atggtcgttt ccgaacttac gaccattcaa aaagataagg tagtggcttg 2100

tgagtgaaaa gaaactctcg atacgctcct ttcgtctaac ggtcaggacg cgagattctc 2160

aatctcgtaa tgcgggttcg attcccgcag ggagtacaat ggcgaacaca cgacaatcca 2220

aactgaaggg gaactggaaa accctcgctc cgagataaca tcagcgcaga gaggttggtg 2280

aggcaaccgt aaaagtaatc ctgtgtgcaa gcaagaagga agttcgggtt caagtcccga 2340

tgaggattat tgttgaagag ggatatgatt caaccatagc acttatggtg ctgtgcaagg 2400

gttataggca gccgtactgc cgaatacaag cctgtggaga acccaacagt ggatgaccgt 2460

tgcctatgca acctaaaaag cggtggttct gcgaagcagg aaggaaatgc ccaatttatt 2520

aggtttttcc atacggtatc actactcgcg gtggatgtgg aaataaccgc gatttggtca 2580

gttggtgaag ttggttatca tacctgcctg tcacgcaggt gttcacgagt tcgagcctcg 2640

tactgaccgc agacaaagac aaagaacgag aggacttgta tgacttgcaa atgtcacgga 2700

ctcaaacaag aaaagtttat aggctattag aggatgactg tttctttaat ttgttttctt 2760

gtactgaagg tcatcactgc cgtgccacca agccgtgcaa gtccaaatgg tgcgttagtt 2820

cagttggtta gaatgccagc ctgtcacgct ggaggtcgcg ggttcgattc ccgcacgcac 2880

cgcaataatc tggatatagg caaattacac atatcatatg tcgccccgcg taatcataga 2940

cgacactgcg gacgacagcg gcgagaatgt cgaaaggctc gacagcataa tgacattcga 3000

catcaccgac accccgatat acgaaggcgg ggaggaactt gagataaacg caaaattcaa 3060

cagatagaaa taattaaaac aaacggcaat ggcacacaga aaaaagaaag atgacgaagc 3120

aacgctatcg tacaagttca aggtaaaggt catagagggc gacctgacgg cagacgacat 3180

aacgaagtgt atcgcggaaa acgcggagca gggcaaccat ttctccgagt tcatacacga 3240

tgagaatttc aggaagacct tcacatccga gatcagcgcg gacaagttcg gatggggcaa 3300

gccgatgttc agcccgacca ccagaagtca ggacgaagtg ttctccgcga taaagaaaat 3360

cggggcgata accgtgctgg aagattagcg catattattc tcatatctaa aattggaagg 3420

acacctgcgg acgcgggtgt ccttttttct taaaatgcca atttataaat aatatataac 3480

ttatatttat tgtacttttt ttgtttaact aaaacacata gacaaatatg gaaattcaac 3540

agattaggtt tataaaccca gttgattttg aagaaacaat cgttaatgta cccacggaga 3600

agggcgaaag attcctgaga acaaaaatct atacggacga gtattcaccc gaaacattca 3660

taaaactctg cgagaag 3677

<210> 106
<211> 831
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 106
tggcgattat tcttacggca aaggccttat ccatgcatac ataaatcgag acatcaaaag 60

tttttgcttg ccaaacactt taatatgtga atgccatata ccaaaacata ccagatatat 120

tactgattac tcaggtacaa atatagccgc aaagaaaatc atcatcgaca aagttgtctg 180

ggagaaggta tgtataaaaa cataatggta ttaggggaga aattttcttg gacggaatga 240

atataatttc ataccaacac cgtgcattga ttaaactaaa ttaaattatc aagcataaaa 300

agtttggcac ggtttttgat atagtaaatt tgtatttaaa atttttaata tggcacacaa 360

aactaaagaa tcagaaaaat tagtaaagtc tttcaaatta aaagtagaca ttagcaattg 420

cgaaattgaa aagaaatgga ttccttcttt tgaagaatac acaaattatt ataatggagt 480

aagtaattgg atttgtgaac tattagaaaa agtttgcctg aaaagaaaaa aatttggaaa 540

ggcttcttat tcagtaccat attggaacgt taaagacgca tttaagaaaa acgttagctc 600

aaacatgatt gctacaatta aaaaaatgaa tatggtaaag gttttttaat gcgtgattat 660

ggcgtttttt aaacataaaa tcatttataa tatattgaaa aacattttat tatataaaat 720

atgcatctta gtgaaaccgt gttttcgtat agattgctgg attatacttt tttataggat 780

aattacagct cgaacttctt tgatggcatt aataagatat tgttggatta t 831

<210> 107
<211> 634
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 107
atcatggctg aaagcgtccg cctgattgca gagcaaaccg caagcccgaa ggttgtcatc 60

aagagccgtt acgctctggt cgacgcaggt ttctatcctg agttgaacta tgtgaccttc 120

ttcgtgaaca ctccagatca actggtttaa tcactgcggg tagcaagcga ttgactacgg 180

aaggccgatt cgatagagtc ggtcttcttt ttttttgta tattttcttt ttttggtttg 240

gaaatgttcc gtatatttgc agcactaaaa ctaaccaata tgggacatgt acgtttgcaa 300

aaaagagagg gagaggttta taagacctac aaacttaaag taaagagctt ttctggcaat 360

gtagacatta aagctggtat cgttgaatac gatatcgccg aaacaattga ttggagaagt 420

acgctttgtt tcaagacatg gaatacgtat ggttctcctc aatgggactc gaagatcaag 480

aaccagaaaa cgatgatcga tcgactggat tcgttgggtg caatagaatt gaaaaactgg 540

tgattttgat catggttttg aaacaaaata ttgatttttc gttctttgac atgcttgtta 600

aaaattgagt atcagtttaa tataaagaat atat 634

<210> 108
<211> 1154
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
human gut metagenome sequence

<400> 108
ggaaacaatt ataacgatgc ctacaaaacg ttaattcaaa tgagagacaa aggaatttta 60

acgcaggaag ttgtaaatgt atttacccta ttgaaagggc ggtatattaa agaaaaagaa 120

tacggaacac aatataatac tatcaattaa atttttggt agtttcattt ggaattgcca 180

attatttttt tattttatag aataatagag ccaacaagca ttagcaatta ttaaatcgat 240

ttatattgaa aataaatttt gtgggaatat ttatttttac tatctttgca tcgtaagata 300

attacaaaac attaacaaca tttattaaac aattaaacaa attttaatta tggcgcacaa 360

aaagaacgta ggagcagaga tagtaaaaac ttactctttt aaggtaaaga ataccaatgg 420

tatcacaatg gaaaaattga tgaacgccat tgacgagttt cagtcatact ataacctttg 480

tagcgattgg atatgcaagg gtcttgacga aacaatgagg aacacttttc tgaaaaaagc 540

aaatagcaat aaatcattgt ataatcagcc aatctacgat acgggtatca agaagaccgc 600

aggtgtgttt tccagaatga aaaaattaaa gagatatgaa attatctaaa ataaaatatg 660

aatttttctt tgcggaaata ccttttaata gattgatttc taataagtta taagaaatac 720

aatagatact gaaggaaaat caaagtgtaa tcaaaaattt gtttgtgttg aggaagcagt 780

gaagaaattt cattgtttcc tcaattttta tttgcataat ccaaaaagtt ttttatttta 840

taggataata agactaacaa atctcaacga ctattaaaac gatttatata aaaaaagttt 900

tgcagttcca atctttttg ctatctttgc agtgttgaaa gacaacaaag atttaagttt 960

aacaaacaaa tacttttat tacatatttt aatttttttg tattatgaca atagaagaaa 1020

aagcaaggga agaataccct tatataaccc catctgatgg gtatgaatgc catgattata 1080

atgaagccgc taaagacggt tttattgagg gggcaaaatg gatgcttgaa aaagccgctg 1140

aatggtttaa gaat 1154

<210> 109
<211> 1048
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 109
atatgggcaa agcgtgataa aattgaaaac aaatatgtca aagaaccatt aaaacgagtc 60

aatgaagata tgtggtggat gtactatgtt tatgaatgga atgtgtttta tgtgcttgaa 120

gaaaatgtcc atccatatat gaaaaaataa attttaccac acatattatt attcgtgtca 180

tgccgatgag gtttggcacg atttttgttt atatggagag acataatgtc agtcaataca 240

tgacaacttg tcacaataac tgacattaaa agtttggcac aatatttgct tataagaaaa 300

acgaacaagt aaaattaaaa ttttatagat tatggcacac aaaacaaaca acggagaaaa 360

caccatcaac aaaactttca tcttcaaagc aaaatgcgag aagaacgata ttatatcgtt 420

atggaaaccc gcagcagaag agtattgcaa ctattataac aaattgagca aatggattgg 480

taaaacaatg tacggcattc ctgcatataa catcaaaaga ggttttaaga agaatttaag 540

tgccaaaact ataaacacat ttagaaaact tggacactat cgtgatggaa aaataaatga 600

ggatggcatg tttgttgaaa ctttggcata gaatttgcat ataccaatta gaattgaaaa 660

aatcgctctt tgacacactg aaacatacaa aaacaccaca atttttaat ccttttctat 720

ttgtatttta ttgaaataaa atgtattata gtaatatatc tgctaaggtc atatttttca 780

ttgttctcaa attgttggat aatgttttgt gtgtttcatt tttgtcattg tgtcacctta 840

actgacaagg tggcacattt tttatgtcaa tatgtcagtt gaggttttgg cataattttt 900

gtataatggt aaatggataa gaattgaaat tacaatgaca acaaaacaaa ggttaataaa 960

gagaataaac aaggcattcg gatttgaatt aacggatgca acaccttgtt tccaccatca 1020

aggtagaaga tggggaagcg gtggtttc 1048

<210> 110
<211> 968
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 110
gaaggcggcg cgtttgaaat cgctaacgta attgaaaatg ccaagaagca gaatctcggg 60

gagggtggat acaaggaatt gtgcaatgat ttcctgaaac atgcgaggga aacgtttttc 120

agtgggaaat acgaacacca ttcttggtag tggatttgtt attttggtaa atataattaa 180

cgcggcattg tcgtcagtga atataatatt gcatttcgac agtattttat aagtattttg 240

acttataaac agtatttata agttattcgg cttataggtt aattagccta tagatgttgt 300

ttataggttg gatgacctat agtgccaagt tttgaagaaa tcgttatagt catcgttctg 360

ccctattaga tattccgtat ttctttaaga ctgttataat acaaatatac tacaaatcat 420

gcaatttttg atttttaaca aaaattaaga aatagggtat tattgtgtat tgtttttttgt 480

tatatatttg tcctgttagg ttaaatcacc gcgcctgatg acgaagtcgg tggtagaatt 540

agactaatat taaatatgtc tcatgaattt aacaagaata aaggtgagaa tgagattagc 600

aagaccttta ttttcaaaac aaaatgcggg aagaatgata ttacatcatt atgggttccc 660

gcgatggagg agtattgcac gtattacaac agggtaagca aatgggggaa aggtatgtac 720

aacaagccgt catatgacat acggaagaaa ttcaagaaga acttgagtgc ggctactttg 780

aaaactttca ttaagttggg aaacacggtg aaagggatga ttgtcaacgg acagtttgtt 840

gaaatggaat cataggttga cagaaacgga aaatcggttt gtttgttaga agaatatttg 900

ttgaaattca tttttctttt gctaacgtat atacaaataa ctgtaataga atatcttata 960

taagatat 968

<210> 111
<211> 1542
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-fecal sequence

<400> 111
acaaatgaaa ttatgggaca agtaaaactt aataaacctc ttctgtatat caaaatattg 60

actatcttta gacataacct tgtcaaataa taaatctaaa ttactctttt ccttttcttt 120

tttaaataat ttcatattaa atattcccat aatttattaa tatatttttt tttcattact 180

tatttctctg ttatataaat agttacataa aaaaattaaa actatttttt aaaaagtctt 240

gtgtatataa aaaaaatata gtacctttgc acccgaaatc aagatttaat cctgttttca 300

tattatattt atcaatttta tactaattaa taaacttatg gcaaataaaa aatttaaact 360

tacaaaaaat gaagtcgtga aatcattcgt actcaaagtt gctaaccaaa aaaaatgtgc 420

tatcactaac gaaacacttc aagaatataa aaactattat aataaggtaa gtcagtggat 480

taataacatc gtacaaaatg aaacgtggag aaatctattt actaacaaaa ccaataatac 540

atatggatta cctatactaa caccttcaaa aaaaggacaa tctaatatca ttacacaatt 600

aatgaaaatt aatgcaacac aagaacttgt tgtataatat aatctatttt taaatttata 660

atactaatat aattcattga taattaaata attatataaa attcctatat acaatagaaa 720

gactttccac agacatgttg tacatacatt tttttaagta ttaaacaacg catacccacc 780

aatggtacac gaaaattttc atgttgtaca tactattttt aggtattaaa caactcactg 840

ttttgacgat taatataggc atgttgtaca tactcttttt agatattaac aacctgtaaa 900

caataacaat atttacaaca ataatccatt tttgaaataa tgaaaaattt tctggaaaaa 960

ttttttaaca agtctgtttt tgaaataatg aaaaaatttc tggaaaaatt tttttaacaa 1020

acccattttt gattggttca ttttttattg gaaaattagt gtgtggaact acccacccgt 1080

atatgagcaa gtgttatggg gtgtaacgtg gggagggtta catagggggg tctttggtag 1140

ggggtacata ggtagggtaa taatggggtc tttggtaggg ggtacatagg tagtccccat 1200

atattattat aaaaagtaaa ataaatgata tatgcaagag tttttgaaaa tttatttta 1260

ttttgctact tagactttac aaaaagtaga tatatagtat tttcttttca aaatattttg 1320

tagtttggaa aaaaagcagt acctttgcac acggaaacga aaaacaagtt taacctatta 1380

aatttttagt ttatggcaat aaacattttg acttattctg ctatggcaga aaaatcttgg 1440

gaaaatttta tgcgtgaaaa ttgcggttac gagcgcatta gtacatttta tagtgatttc 1500

actattgcag accattgtgg tggtgtaaac gcaataaaag ac 1542

<210> 112
<211> 920
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-fecal sequence

<400> 112
gatgtgaatg aagaatttct tggtggcttg cgaagcacta tgacatatct tggagcaaag 60

agattgaaag atattccgaa atgttgcgtt ttctatcgtg taaatcatca gttgaataca 120

atttatgaga atacaacgat aggaaaataa tataaatttt atattatttt gagaaaaaga 180

gtctaaattt gggctctttt ttcgtttttt atgaaaaaat atgaaaaaag tttgtaaaaa 240

atttgtaata ttgaaaaaat agtattatat ttgtatcaaa tttaaaaata aaatataaat 300

atggcaaaat caataatgaa aaaatcaatt aaattcaaag taaaaggaaa tagtccaata 360

aacgaagata ttataaatga gtataaaggt tattataata cctgtagtaa ttggattaat 420

aataatttaa caagcataac tattggtgaa aatgaagact ggagaaaagt gttttgtatc 480

aaaccaaaaa aagaagatta caatacacct ttattggatg ctacgaaaaa tggtcaattt 540

agaatacttg acaagttgaa aaaattaaat gctactaaat tattagaaat ggaaaaataa 600

taaatatata caataaattt atataatttt gtctattttt aattttagtt cattagataa 660

tatgttcata aattcattga catataatta taaataaata tatatgcaat aaaattcgag 720

agacatttca tcagagatgt ctcttttta ttttttgtta tatttatatt atgaatatta 780

gattggaact cataaagaca aaggataaac agaacattgc aaagcgtata gtggaaagca 840

atcactcata tgttccaacc tggcgtagtg taggacgaag gatagattat cttatttatt 900

tggataatga tgttgtcgga 920

<210> 113
<211> 1217
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-ovis aries sequence

<400> 113
gtgaactata tctacgaatc aatcgaagga atattgacaa aaacaatgaa tccaaccact 60

ttacaggata tcatccttaa cggaatcaca tatacaccag tggaagacaa cacaacaaca 120

tgcgacggat gtgaatttaa agacacataa ggccaatgta tgctaacaca cctattcgat 180

aacgacatgg tccaaaactg cctcaaggaa aaaaacggcg ttgcagatat catatatgtc 240

aaaaaagaaa attaatcgga atcttgattt ggattttaat attatttgtt gtataattac 300

aatagaaaga aaattttgta tattttaaaa tttgtaaatt aaaatttaga aaaatggcac 360

acaaaacaaa caacggagaa aatacaatca ataaaacttt tattttcaaa gcaaagtgcg 420

ataataacga tattatatcg ttatggaaac ccgcaatgga agagtattgt acttattaca 480

ataaattaag ccaatggatt tgcaagacaa tgtatggagt accagcttac aacattaaaa 540

acggtttcaa aaaaaatctg agcacaaaga caatcaatac gtttagaacg cttggccact 600

atcgtgacgg aaaaataaac gaagacggcg tattcgttga aaacctggca taataaggag 660

taaaaaaatg ttctttgata ttctgacaca aatgaaaaaa caatcaaaaa tttatttctg 720

ttttgcttgt aatttattga aataaaatgt attatataga aatatgtcgg tggataatag 780

tcaaatagtc tgttgactgt tgaatagtaa gttttttact ctattgacaa caggtgatgt 840

ggatggaaca tacaaagttt attgttgagt aataggtttt acacttttac cacaacttta 900

gtgattttat gtataaaata attaaaatca tatataaaaa tttttccaga aagtagtact 960

tattgaatta aaattatatt gtgaaaaatg gtttttgatt ttaattttat ttgttgtata 1020

attgaaatgt aatttaattt agaattgtat aaataaaaaa cgtaaaaatg agactgccaa 1080

cagaaattta tgagtcaggc acaatggtta gtaagatatc ggaaaaacca tttaaatcag 1140

gtttaagggt taatactgta aagtctgtag ttgaacatcc acataagatt gacccgaata 1200

ctaataaggg tgttcca 1217

<210> 114
<211> 930
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 114
gactacgact ggttctcaaa tgtgtacggc gccatcaggg aggaacgtga gaaaatgaga 60

agggaagagg aggaacgcag gaagaacgaa cccaagacgg tgaaaaccaa agaggttgac 120

ttgttcgggg atgatgacct gccgttctaa taaaaaaaaa aacaaacctc tccgaaattg 180

aacgtatcaa cttcggagag gttatatagg gtgatggaaa tgttaaataa aaagtttaaa 240

aataactatg ggaaacaaag tacaaagtaa tgaaacaata gttaagactt atacatttaa 300

agtgcgtgga ttcataagtg gtgctaccca cgaaataatg aaatcagcca taaaacaata 360

tatagaagat tctaacaatc tatcagattg gattaatgta gagaatgaaa tacttaggaa 420

ctctttcctt aaagaagaga ctaaaaaata cacttataat acaccattat tcactcccag 480

acttaagtca tcggaaaaaa taataacaga attgaaaaaa ttgggtatga ctacggttat 540

agaataacca ttacacattt ttttcataac aaacgttctt taacatattg gaaaataaga 600

aaatacgata ttcatataaa aatccgtccc acacaaaatt aatgtaatat cttagttttg 660

ttacatcaac actatataat taaaaaaata aaaaaatatt ttgtggattc aaaaaatcat 720

tatatatttg cgtccgaaaa ttaacactta tgtcaaacaa atttaaaatg taaaagaact 780

atgcaaacag aaacacagaa tttcacaggc gagttgagag caatcaacac aacaatgggt 840

tcaagcaaga gctacaagac aatctgccgt tgcgcacttg acatcctcaa gggatatatc 900

gttacgcacg acattaggga caacttctca 930

<210> 115
<211> 1087
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
mammals-digestive system-rumen-bos taurus sequence

<400> 115
acagagggtg tatggatagg catgaaccac caaggcaaaa tactgatggc ttgcagggag 60

gctttgtgta acaactgtga acccccgatt gattacaagg cactgaacga tgccgagata 120

tatttttatg gaaaagaagt taaattttaa aaattaaaag atatggcgaa caaaagcaca 180

aaaggaaacc tgcccaagac aatcataatg aaggcaaacc ttagccccga tggtttcact 240

caatgggaaa gggttgtaaa agaataccaa gcctacaaag acacgttgag taaatgggta 300

gcccaaaatc tcagacaaat aatgtgcaag acaccgcaga caaagaacgg ctactcatca 360

cctgtgctca cctcaaaggt taaaagccaa gtggaaatgg taagagaatt gaaaaaaatg 420

ggaaaaacca ttctttattc caatgattca cttccttttt gaaactaaaa tgtcttatgt 480

gtatttgaat tataggctaa tataaagatt gtactgtgtt gagatacact tttagaggta 540

tttacaacaa aatgcgtgat atggaaatga agaaataact gtgttgagat acacttttag 600

aggtatttac aacaccatat aaacctgacc atctcctgaa tctcgcccga cacggataat 660

gttagatatg ttcacaatac aactgcatgt gctattcaag aaaaaatagt atatttacaa 720

tatgttggtg cataatatta gatgtgctta cacaacgcag acctgaaaag ccaggataaa 780

agtatgcggg attgtgtttt tagaacactg ttcaatccgc tgtatgtcgc ttgaagcgtc 840

agtaacctat gtcgaaacaa tccttttaga ggtgtttacg accgaccaga aacagcaaga 900

cctgtattta tgttggtata cggttctttt taggggatta gtagttgaat ccctttcac 960

ccttggtgtt cacgggttgt gagacattct tcatacccat gcgtgtcttc tcagccatct 1020

taccgaaagt tataggcaca atatgttcaa tgcctgcctg ctgagcattg tagcatatat 1080

cagacag 1087

<210> 116

<211> 1064
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
gut metagenome sequence

<400> 116
agaatgcttt ccccaattga atgtgaaaga ctacagacac tgccagataa ctataccgaa 60

ggtgttagca aatgcgcaag atataaggca atcggaaacg gatggacagt tgatgtaatt 120

tcacatattt ttaagaattt gaaaaattaa tttggtattt tgaaatattt gacttatttt 180

tgcaacataa aatttaaaac aaatttatat ggcacacgcg aaaaaaaaat tttgacaaag 240

gaaagcaaat aacaaaaacg ttctctttca aggtgttaaa tattaagaac aatggcgaat 300

cagttgatat gaatactata gaattagcca tgaaagagta caataggtat tataacattt 360

gtagtgattg gatttgcaac aatctaatga cgccaattgg ttccctatat caatacatag 420

atgatgagaa atggagaaaa aaatttgttc gcccaacaaa cactaataaa ccgttgtata 480

actctccagt tttctcccct gctgtaaaat ctgaaggtgg tactattaaa aatctccaaa 540

ttttaagcgc aacaaagacc ataattcttt gatttaatta ttaatacata tatcgttcgt 600

aaatttaata caaccacaac caaatatgat aatttgcata attaaaaaaa ttcacatatc 660

tttgtagcat aaaaacaaat agagaaaaaa tgacacttta cagatttaca cttttaggca 720

atacacaaat ttatgtatat gctggcacgt ttgaagatgc tctcaggaca tttcgtaaat 780

catatggaga tacgggattc aagtcaattg aagagcttcc tgaatttaga gataacatac 840

ttatacaact agattgattg aaacaaacgt caattaccca ccactgaagt agtgggtttc 900

tttgcagtga ttttatgaaa acgatagaag acagagcaga catagcaagc gatattgcta 960

aaagagaatt tgaagaagat agttattgga gtcattacgc agacgatatg gtaacatctg 1020

cttttgttga aggatgctat aaaggctata tttcaggtgc gaca 1064

<210> 117
<211> 1617
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
terrestrial metagenome sequence

<400> 117
aaggagatag attatgacag ggaaggtaat atcacaaata tatatcttta ctatgagtca 60

gatagtttat ggaatgaaaa atttgaattt atattaacat tagatggtta tgaattaaag 120

atacctattt ttatagtaag tgtaagatag ttttggcacg gaaattgcag taatgttttc 180

ctgtcaagaa caaataaaat aaaaaatatg aaaaaatcaa ttaaattcaa agtaaaagga 240

aattgtccaa taaccaaaga tgttataaat gaatataaag aatattataa taaatgcagt 300

gattggatta agaataattt aacaagcata actattgggg aaatggcaaa atttctcaat 360

gaagtgtgga gagaaatatt ttgtacaagg cctaaaaagg cagaatataa cgttccatcg 420

ttggatacaa caaaaaaagg accatctgca atattgcata tgttgaaaaa aatcgaggca 480

attaaaatat tagaaacaga aaagtagtga ctatagatat aaacttctat gatagatatc 540

tgtttttaa ttctattatg caatataata tattgaaata taaacaatta taaataaaac 600

gggtgtatac aacaagtttt ttgtttttct tattcattat ctgtatattt gtattataaa 660

caaatacaaa tatgtataat gaatcaggaa tatattgcta taaaaacaaa ataaacggaa 720

aattatatat tggacaggcg ctaaatctta aaagaagata tttaaacttt ttaaatatca 780

accacagata tgcgggtcaa gtaatagaaa acgcacgtaa aaaatatggt gtagataact 840

ttgaatattc aatccttact cactgtccag tagacgaatt aaattattgg gaagcatttt 900

atgtagaaag attaaattgt gtcacacccc acggttataa tatgactaat gggggcgatt 960

cagtatatac ttctacacaa gcatttaaag atgcacaaac tgaaaagttg aagcaaacta 1020

ttctatctaa gaatcctaat cttaatgtca gcaaagtaaa atatgaaggt aatagaattt 1080

cagttataat tacttgccca atacatggca catttaaaaa aacgcctgat tactttagaa 1140

atccagaaat aaatgatttg tgttgtccta aatgtgtgag ggaagatata agacaaaaga 1200

ctgaagatag tttctttaaa caagcaacaa agaaatgggg agataagtat gattattcta 1260

aaactataat agtagataga attaccccag ttacaattac ttgccctata cacggagatt 1320

ttacagtatt accagggaac catgtgtgta aagataaaaa tactggagga tgccaacaat 1380

gtagtgaaga aagacaacat attgaatcat tagaaaaagg tagcgtgaag gtcattaaga 1440

tgataaagaa aaagtttgga aacaaatatt cattagataa attcgaatat aggggagata 1500

aagaaaaagt aattcttatt tgccctattc atggagaatt ttcaatgacg ccaggtaatt 1560

taagatatag caacggttgt ccacaatgca ctttagaaaa tgcttatcgt ataaaat 1617

<210> 118
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 118
agttgtaaat acctataaaa atgtattcca acatagt 37

<210> 119
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 119
gttgtgaata ccctacaaaa gtgatattcc aacaat 36

<210> 120
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 120
aaaaagggtg aacaacatt 19

<210> 121
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 121
gttgtttgat acctataaaa gagtattcac aacagg 36

<210> 122
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 122
gttgtttact ccatacaaaa taagagttac aacaat 36

<210> 123
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 123
gttgttcaat ccttataaaa aggtgtctac aacaat 36

<210> 124
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 124
gttgtttaat acctataaaa gagtatatac aacaag 36

<210> 125
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 125
aatacctata aaaggacata tacaacaag 29

<210> 126

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

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 126
gttgttcaat acctataaaa agacatatac aacaag 36

<210> 127
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 127
gttgttcatt acctaaaaaa gagta 25

<210> 128
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 128
gttgtttaat acctataaaa gaatatatac aacaag 36

<210> 129
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 129
gttgtttaat acttaaaaaa tagtatgtac aacatg 36

<210> 130
<211> 36
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 130
gttgtatcca ccgtataaaa catagtgtcc aacatc 36

<210> 131
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 131
gttgtttatt acttacaaaa acagcataac aacatc 36

<210> 132
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 132
gttgttcaat ccttataaaa agaggtctac aacaat 36

<210> 133
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 133
gttgttatta ccatataaaa tggttcgtac aacaat 36

<210> 134
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 134
actgttgtac tttcctttca tctgcagggg ttttacagt 39

<210> 135
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 135
tagttgttta atacttaaaa aatagtatgt acaacatgat 40

<210> 136
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 136
gttgtaaata gcatacaaac atagccattc aacaat 36

<210> 137
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 137
gttgtgagta ccctataaaa gaagtacccc aacaat 36

<210> 138
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 138
cgttgttaga cccctaaaac acaaggtcta caacaat 37

<210> 139
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 139
gttgtaaata catctcatat tgtattccaa cacagt 36

<210> 140
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 140
gttgtcagca tccgccttgc ggtatgccac aacaat 36

<210> 141
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 141
gttgccaata ccataaaaaa cggtatctca acaatt 36

<210> 142
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 142
ttgtcagcac ccgtaatacg gtatgccaca acaat 35

<210> 143
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 143
gttgtcagca cccgtaatac ggtatgccac aacaat 36

<210> 144
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 144
gttgtaaata cctataaaag tgtatcccaa cacaat 36

<210> 145
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 145
gttgtaatta cctttataag aaaggtattc aacaata 37

<210> 146
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 146
gagttgttcg ttgcccataa aaagccattt acaaca 36

<210> 147
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 147
gttgtatctg tcctaaaaaa gaatacattc aacaat 36

<210> 148
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 148
agttgtaatc agtctataaa agataccatt caacaat 37

<210> 149
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 149
gttgtaatta agataaaaaa cctattatcc aacaat 36

<210> 150
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 150
gttgtaaata ggatataaaa tcaactattc aacagt 36

<210> 151
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 151
gttgttcaat ccttacaaaa aggtatctac aacaat 36

<210> 152
<211> 103
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 152
attgggactt ccggaagtaa aatatccacc tgaggatttt aggacatata atttctaata 60

aaaatgaacg gaaaaatttc cgttcatttt ttttttgttt att 103

<210> 153
<211> 105
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 153
tattgggact tccggaagta aaatatccac ctgaggattt taggacatat aatttctaat 60

aaaaatgaac ggaaaaattt ccgttcattt ttttttgttt tattg 105

<210> 154
<211> 163
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 154
gacgagaacg gagtgtggct cctgaggaaa aacgacaaac atccaacata ttttatctac 60

cagaacggaa cactctatca atatgaggaa gattgattag ttgatgtttt cataataatt 120

ttatctggaa tttgaaaaga ttccagattt ttttttttatt tcg 163

<210> 155
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 155
gcaatcaaca agactttcat tttcaaggca aaatgcgata agaacgatgt catatcgtta 60

tgggaa 66

<210> 156
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 156
gatgctccga aaacgtggtt gttcggacaa caaaaaaatg aatgtttcta atgtattaa 59

<210> 157
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 157
gacggaaaaa taaatgagga tggtatgttt gttgaaaact tggaataatt ctgtatatac 60

caattagaat 70

<210> 158
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 158
tgttgattgc tgattcttcg ttgtttgatt tgtgttgtgc cataatctta aaatt 55

<210> 159
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 159
cgcaagatat aaggcaatcg gaaacggatg gacagttgat gtaatttcac atatttttaa 60

gaatttgaaa aattaatttg gta 83

<210> 160
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 160
ggacatttcg taaatcatat ggagatacgg agttcaagtc aattgaagag cttcctgaat 60

ttagagataa catacttata caactagatt gattg 95

<210> 161
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 161
atcaatacat agatgatgag aaatggagaa aaaaatttgt tcgcccaaca aacactaat 59

<210> 162
<211> 80
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 162
ctggtaatac tgtaaaatct ccgtgtatag ggcaagtaat tgtaactggg gtaattctat 60

ctactattat agttttagaa 80

<210> 163
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 163
cagaagtcgt tcaagttcaa ggtcaaaacg gacaaggaga cggtcgaatt attcag 56

<210> 164
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 164
gggagggtga cattcagaag tcgttcaagt tcaaggtcaa aacggacaag gagacggtcg 60

aattat 66

<210> 165
<211> 102
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 165
aagtgtcttc aacacattga agaaaactct cggtgcaata tatggaaagc tcgatgaaaa 60

cggaaatttt attgagaatg aatgtaataa gtaactggaa ta 102

<210> 166
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 166
ccgtgggagg atttggattt ggttgaagac atcagaaaaa ttttcgaaat ggaatagagg 60

gaaccggaat tttttccggt ttttctttgt cctttcga 98

<210> 167
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 167
cagagtaacc tttcctgata tgttgttaca catttttgta agtgttaaac aactgacgca 60

ttgatattgc cttgtctatt aa 82

<210> 168
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 168
caatcgcgag tttatactga aatgttgtta cactgttttt gtaagtgtta aacaaccttg 60

cacaaatgtc atctaccagt ac 82

<210> 169
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 169
ccgagcgacc cacaaaccta ttgtcgtacg catcatttca catgataata acaacgaata 60

ttcctgcaag catgattt 78

<210> 170
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 170
tatgacatta tgatattgtt gtatgcatca tttcacatgg taataacaac gaagagaaac 60

accgagcgac ccacaaa 77

<210> 171
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 171
acatctttta tgacattatg atattgttgt atgcatcatt tcacatggta ataacaacga 60

agagaaacac cgagcgaccc acaaa 85

<210> 172
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 172
gctaaaatat agtcctgtgg atgttgaata catttctttt aagtgtactt acaaccaacg 60

ctgtacacat tgctaatgga tg 82

<210> 173
<211> 83

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 173
tgctaaaata tagtcctgtg gatgttgaat acatttcttt taagtgtact tacaaccaac 60

gctgtacaca ttgctaatgg atg 83

<210> 174
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 174
caacaccaag gctgaggcaa agaagagggc tgatgatatg aacaaacaga atagggtcat 60

acaccagctg tctgtttatt tgtgtcc 87

<210> 175
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 175
aattagactg ataaacaaag aataatgaga actataatag ggaggtgtac ccccgaattt 60

aagccagtgg agaaccatac aaacctatca tatag 95

<210> 176
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 176
tgggtatgcg ttgtttaata cttaaaaaaa tgtatgtaca acatgtctgt ggaaagtctt 60

tctattgtat at 72

<210> 177
<211> 68
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 177
cgttgtttaa tacttaaaaa aatgtatgta caacatgtct gtggaaagtc tttctattgt 60

atatagga 68

<210> 178
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 178
tgggtatgcg ttgtttaata cttaaaaaaa tgtatgtaca acatgtctgt ggaaagtctt 60

tctattgtat ataggaattt tatataatta tttaattatc aatgaattat attagtat 118

<210> 179
<211> 58
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 179
ggtgggtatg cgttgtttaa tacttaaaaa aatgtatgta caacatgtct gtggaaag 58

<210> 180
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 180
aatgaacgag attgttggga tatacctttt ataggatttt cacaacatct gagttgtttg 60

atgttaaaaa ctt 73

<210> 181
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 181
gataaaaatg aacgagattg ttgggatata ccttttatag gattttcaca acatctgagt 60

tgtttgatgt taaaaacttt 80

<210> 182
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 182
gctaatataa agattgtact gtgttgagat acacttttag aggtatttac aacaaaatgc 60

gtgatatgga aatga 75

<210> 183
<211> 90
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 183
ataccaacat aaatacaggt cttgctgttt ctggtcggtc gtaaacacct ctaaaaggat 60

tgtttcgaca taggttactg acgcttcaag 90

<210> 184

<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 184
aatgaagaaa taactgtgtt gagatacact tttagaggta tttacaacac catataaacc 60

tgaccatctc ct 72

<210> 185
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 185
aggaagatgt cagacgtttt tattgttgga atactcgttt tttacggtat ttacaactgc 60

cccgtagcgg aatcaaaata ccac 84

<210> 186
<211> 76
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 186
atgtcagacg tttttattgt tggaatactc gtttttttacg gtatttacaa ctgccccgta 60

gcggaatcaa aatacc 76

<210> 187
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 187

aaataacaaa aattctggac gggaaaggaa gatgtcagac gtttttattg ttggaatact 60

cgtttttac ggtatttaca actgccccgt agcggaatc 99

<210> 188
<211> 96
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 188
ataacaaaaa ttctggacgg gaaaggaaga tgtcagacgt ttttattgtt ggaatactcg 60

ttttttacgg tatttacaac tgccccgtag cggaat 96

<210> 189
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 189
tattgcaact attacaacaa acttagcgaa tggattggca aagatatgta taacacgccg 60

<210> 190
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 190
attgcaacta ttacaacaaa cttagcgaat ggattggcaa agatatgtat aacacgccg 59

<210> 191
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 191
gtatgatgac agaagaaaca cggaagacaa tagagagcgt catagtggtt ctcggcatag 60

caatcatgct g 71

<210> 192
<211> 118
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 192
atgatgacag aagaaacacg gaagacaata gagagcgtca tagtggttct cggcatagca 60

atcatgctgg cagccgccgt ccgaataatg acgcagaaca aagcaattgt gaaatatg 118

<210> 193
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 193
agaaggtact gccgccttat gaccgacgag aacggagtgt ggctcctgag gaaaaac 57

<210> 194
<211> 163
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 194
gacgagaacg gagtgtggct cctgaggaaa aacgacaaac atccaacata ttttatctac 60

cagaacggaa cactctatca atatgaggaa gattgattag ttgatgtttt cataataatt 120

ttatctggaa tttgaaaaga ttccagattt ttttttatt tcg 163

<210> 195
<211> 92

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 195
tttttgttat atatttgtcc tgttaggtta aatcaccgcg cctgatgacg aagtcggtgg 60

tagaattaga ctaatattaa atatgtctca tg 92

<210> 196
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 196
cctattagat attccgtatt tctttaagac tgttataata caaatatact acaaatcatg 60

caatttttga tttttaacaa aa 82

<210> 197
<211> 103
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 197
tcgttgaata cgatatcgcc gaaacaattg attggagaag tacgctttgt ttcaagacat 60

ggaatacgta tggttctcct caatgggact cgaagatcaa gaa 103

<210> 198
<211> 108
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 198
atcgttgaat acgatatcgc cgaaacaatt gattggagaa gtacgctttg tttcaagaca 60

tggaatacgt atggttctcc tcaatgggac tcgaagatca agaaccag 108

<210> 199
<211> 73
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 199
gagcttttct ggcaatgtag acattaaagc tggtatcgtt gaatacgata tcgccgaaac 60

aattgattgg aga 73

<210> 200
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 200
tttttcattg ttctcaaatt gttggataat gttttgtgtg tttcattttt gtcattgtgt 60

caccttaact gacaaggtgg cacatttttt atgtcaat 98

<210> 201
<211> 98
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 201
ttttcattgt tctcaaattg ttggataatg ttttgtgtgt ttcatttttg tcattgtgtc 60

accttaactg acaaggtggc acatttttta tgtcaata 98

<210> 202
<211> 122
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 202
aatatatctg ctaaggtcat atttttcatt gttctcaaat tgttggataa tgttttgtgt 60

gtttcatttt tgtcattgtg tcaccttaac tgacaaggtg gcacattttt tatgtcaata 120

tg 122

<210> 203
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 203
acaaattttt gattatggca cacaaaaaga acataggagc agagatagta aaaacttact 60

cttttaaggt gaaga 75

<210> 204
<211> 136
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 204
ttattttata ggataataga gctaacaagc attaacaatt attaaaacga tttatattga 60

aaataaattt tgtgggaata tttatttta ctacctttgc atcgtaatac aattaaacaa 120

attttgatt atggca 136

<210> 205
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 205

cctgttgtga atactctttt ataggtatca aacaacggaa gtggttggtc agcatggatt 60

a 61

<210> 206
<211> 25
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
target sequence

<400> 206
ggaagtggtt ggtcagcatg gatta 25

<210> 207
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 207
cctgttgtga atactctttt ataggtatca aacaactgtg aagtgacctg ggagctaact 60

g 61

<210> 208
<211> 25
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
target sequence

<400> 208
tgtgaagtga cctgggagct aactg 25

<210> 209
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 209
attgttgtag acacctttt ataaggattg aacaacaacc cccgtctacc tgcccacagg 60

g 61

<210> 210
<211> 25
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
target sequence

<400> 210
aacccccgtc tacctgccca caggg 25

<210> 211
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 211
cttgttgtat atgtcctttt ataggtatta aacaacgtag agggagaaat ggaatccata 60

t 61

<210> 212
<211> 25
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
target sequence

<400> 212
gtagagggag aaatggaatc catat 25

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

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 213
cttgttgtat atgtcctttt ataggtatta aacaac 36

<210> 214
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 214
attgttgtag acacctttt ataaggattg aacaacgcac caacgggtag atttggtggt 60

g 61

<210> 215
<211> 25
<212> DNA
<213> Unknown

<220>
<223> Description of Unknown:
target sequence

<400> 215
gcaccaacgg gtagatttgg tggtg 25

<210> 216
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> L, M, I, C, or F

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Y, W, or F

<220>
<221> MOD_RES
<222> (4)..(4)
<223> K, T, C, R, W, Y, H, or V

<220>
<221> MOD_RES
<222> (5)..(5)
<223> I, L, or M

<400> 216
Pro Xaa Xaa Xaa Xaa Phe
1   5

<210> 217
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> I, L, M, Y, T, or F

<220>
<221> MOD_RES
<222> (3)..(3)
<223> R, Q, K, E, S, or T

<220>
<221> MOD_RES
<222> (4)..(4)
<223> L, I, T, C, M, or K

<400> 217
Arg Xaa Xaa Xaa Leu
1   5

<210> 218
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> I, L, or F

<220>
<221> MOD_RES
<222> (4)..(4)
<223> K, R, V, or E

<400> 218
Asn Xaa Tyr Xaa
1

<210> 219
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> T, I, N, A, S, F, or V

<220>
<221> MOD_RES
<222> (3)..(3)
<223> I, V, L, or S

<220>
<221> MOD_RES
<222> (4)..(4)
<223> H, S, G, or R

<220>
<221> MOD_RES
<222> (7)..(7)
<223> D, S, or E

<220>
<221> MOD_RES
<222> (8)..(8)
<223> I, V, M, T, or N

<400> 219
Lys Xaa Xaa Xaa Phe Ala Xaa Xaa Lys Asp

1 5 10

<210> 220
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> G, S, C, or T

<220>
<221> MOD_RES
<222> (4)..(4)
<223> N, Y, K, or S

<400> 220
Leu Xaa Asn Xaa
1

<210> 221
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> S, P, or A

<220>
<221> MOD_RES
<222> (3)..(3)
<223> Y, S, A, P, E, Y, Q, or N

<220>
<221> MOD_RES
<222> (4)..(4)
<223> F, Y, or H

<220>

<221> MOD_RES
<222> (5)..(5)
<223> T or S

<220>
<221> MOD_RES
<222> (8)..(8)
<223> M, T, or I

<400> 221
Pro Xaa Xaa Xaa Xaa Ser Gln Xaa Asp Ser
1   5   10

<210> 222
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> N, K, W, R, E, T, or Y

<220>
<221> MOD_RES
<222> (3)..(3)
<223> M, R, L, S, K, V, E, T, I, or D

<220>
<221> MOD_RES
<222> (6)..(6)
<223> L, R, H, P, T, K, Q, P, S, or A

<220>
<221> MOD_RES
<222> (7)..(7)
<223> G, Q, N, R, K, E, I, T, S, or C

<220>
<221> MOD_RES
<222> (10)..(10)
<223> R, W, Y, K, T, F, S, or Q

<400> 222
Lys Xaa Xaa Val Arg Xaa Xaa Gln Glu Xaa His
1   5   10

<210> 223
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<220>
<221> MOD_RES
<222> (1)..(1)
<223> I, K, V, or L

<220>
<221> MOD_RES
<222> (4)..(4)
<223> L or M

<220>
<221> MOD_RES
<222> (5)..(5)
<223> N, H, or P

<220>
<221> MOD_RES
<222> (6)..(6)
<223> A, S, or C

<220>
<221> MOD_RES
<222> (8)..(8)
<223> V, Y, I, F, T, N, or Y

<220>
<221> MOD_RES
<222> (10)..(10)
<223> A or S

<220>
<221> MOD_RES
<222> (11)..(11)
<223> S, A, or P

<220>
<221> MOD_RES
<222> (12)..(12)
<223> M, C, L, R, N, S, K, or L

<400> 223
Xaa Asn Gly Xaa Xaa Xaa Asp Xaa Asn Xaa Xaa Xaa Asn
1 5 10

<210> 224
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 224
vhtdkdddd 9

<210> 225
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 225
attgttgda 9

<210> 226
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (8)..(8)
<223> a, c, t, g, unknown or other

<400> 226
hdhwdwwnv 9

<210> 227
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 227
ttttwtarg 9

<210> 228
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 228
vmmac 5

<210> 229
<211> 5
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 229
acaac 5

<210> 230
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (18)..(18)
<223> a, c, t, g, unknown or other

<400> 230
atattgttgd akrwwyyntt ttwtargkww wwwacaacwr b 41

<210> 231
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 231
Asn Leu Thr Ser Ile Thr Ile Gly
1 5

<210> 232
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 232
Asn Tyr Arg Thr Lys Ile Arg Thr Leu Asn
1 5 10

<210> 233
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 233
Ile Ser Tyr Ile Glu Asn Val Glu Asn
1 5

<210> 234
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 234
Glu Leu Leu Ser Val Glu Gln Leu Lys
1 5

<210> 235
<211> 15

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 235
His Ile Asn Ser Met Thr Ile Asn Ile Gln Asp Phe Lys Ile Glu
1 5 10 15

<210> 236
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 236
Lys Glu Asn Ser Leu Gly Phe Ile Leu
1 5

<210> 237
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 237
Gly Asn Arg Gln Ile Lys Lys Gly
1 5

<210> 238
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 238
Asp Val Asn Phe Lys His Ala
1 5

<210> 239
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 239
Gly Tyr Ile Asn Leu Tyr Lys Tyr Leu Leu Glu His
1 5 10

<210> 240
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 240
Lys Glu Gln Val Leu Ser Lys Leu Leu Tyr
1 5 10

<210> 241
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 241
Glu Tyr Ile Tyr Val Ser Cys Val Asn Lys Leu Arg Ala Lys Tyr Val
1 5 10 15

Ser Tyr Phe Ile Leu Lys Glu Lys Tyr Tyr Glu Lys Gln Lys Glu Tyr
20 25 30

Asp Ile Glu Met Gly Phe
35

<210> 242
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 242
Asp Asp Ser Thr Glu Ser Lys Glu Ser Met Asp Lys Arg Arg
1 5 10

<210> 243
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 243
Asn Val Gln Gln Asp Ile Asn Gly Cys Leu Lys Asn Ile Ile Asn Tyr
1 5 10 15

<210> 244
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 244
Ala Leu Glu Asn Leu Glu Asn Ser Asn Phe Glu Lys
1 5 10

<210> 245
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 245
Gln Val Leu Pro Thr Ile Lys Ser Leu Leu
1 5 10

<210> 246
<211> 8

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 246
Tyr His Lys Leu Glu Asn Gln Asn
1 5

<210> 247
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 247
Ala Ser Asp Lys Val Lys Glu Tyr Ile Glu
1 5 10

<210> 248
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 248
Thr Asn Glu Asn Asn Glu Ile Val Asp Ala Lys Tyr Thr
1 5 10

<210> 249
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 249
Ala Asn Phe Phe Asn Leu Met Met Lys Ser Leu His Phe Ala Ser
1 5 10 15

<210> 250
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 250
Leu Leu Ser Asn Asn Gly Lys Thr Gln Ile Ala Leu Val Pro Ser Glu
1 5 10 15

<210> 251
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 251
His Ile Asn Gly Leu Asn Ala Asp Phe Asn Ala Ala Asn Asn Ile Lys
1 5 10 15

Tyr Ile

<210> 252
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 252
cctgttgtga atactctttt ataggtatca aacaacgaga ggtgagggac ttgggggta 60

a 61

<210> 253
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 253
gagaggtgag ggacttgggg ggtaa 25

<210> 254
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 254
cctgttgtga atactctttt ataggtatca aacaactgag aatggtgcgt cctaggtgtt 60

c 61

<210> 255
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 255
tgagaatggt gcgtcctagg tgttc 25

<210> 256
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 256
cctgttgtga atactctttt ataggtatca aacaacgcag cctgtgctga cccatgcagt 60

c 61

<210> 257
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 257
gcagcctgtg ctgacccatg cagtc 25

<210> 258
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 258
cctgttgtga atactctttt ataggtatca aacaacggaa gtggttggtc agcatggatt 60

a 61

<210> 259
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 259
ggaagtggtt ggtcagcatg gatta 25

<210> 260
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 260
cctgttgtga atactctttt ataggtatca aacaacagcc agtgttgcta gtcaagggca 60

g 61

<210> 261
<211> 25
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 261
agccagtgtt gctagtcaag ggcag 25

<210> 262
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 262
cctgttgtga atactctttt ataggtatca aacaacttga cattgtccac acctggaatc 60

g 61

<210> 263
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 263
ttgacattgt ccacacctgg aatcg 25

<210> 264
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 264
cctgttgtga atactctttt ataggtatca aacaacgaaa tctattgagg ctctggagag 60

a 61

<210> 265

<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 265
gaaatctatt gaggctctgg agaga 25

<210> 266
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 266
cctgttgtga atactctttt ataggtatca aacaacggaa gctggatgag cctggtccat 60

g 61

<210> 267
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 267
ggaagctgga tgagcctggt ccatg 25

<210> 268
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 268
cctgttgtga atactctttt ataggtatca aacaacccca tactggggac caaggaagtg 60

t 61

<210> 269
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 269
cccatactgg ggaccaagga agtgt 25

<210> 270
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 270
cctgttgtga atactctttt ataggtatca aacaacatga tgctttgccg taacccttcg 60

t 61

<210> 271
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 271
atgatgcttt gccgtaaccc ttcgt 25

<210> 272
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 272
cctgttgtga atactctttt ataggtatca aacaacaaga gtcattgccc cactttaccc 60

t 61

<210> 273
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 273
aagagtcatt gccccacttt accct 25

<210> 274
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 274
cctgttgtga atactctttt ataggtatca aacaacgaga ggtgagggac ttgggggta 60

a 61

<210> 275
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 275
gagaggtgag ggacttgggg ggtaa 25

<210> 276
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 276

cctgttgtga atactctttt ataggtatca aacaacgtga agttctaaac ttcatattac 60

c 61

<210> 277
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 277
gtgaagttct aaacttcata ttacc 25

<210> 278
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 278
cttgttgtat atgtcctttt ataggtatta aacaacgtag agggagaaat ggaatccata 60

t 61

<210> 279
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 279
gtagagggag aaatggaatc catat 25

<210> 280
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 280
cttgttgtat atgtcctttt ataggtatta aacaacgagt cgctttaact ggccctggct 60

t 61

<210> 281
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 281
gagtcgcttt aactggccct ggctt 25

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 282
cttgttgtat atgtcctttt ataggtatta aacaactcca cacctggaat cggctttcag 60

c 61

<210> 283
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 283
tccacacctg gaatcggctt tcagc 25

<210> 284
<211> 61
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 284
cttgttgtat atgtcctttt ataggtatta aacaacaacc cccgtctacc tgcccacagg 60

g 61

<210> 285
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 285
aacccccgtc tacctgccca caggg 25

<210> 286
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 286
cttgttgtat atgtcctttt ataggtatta aacaacgtag agggagaaat ggaatccata 60

t 61

<210> 287
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 287
gtagagggag aaatggaatc catat 25

<210> 288
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 288
cttgttgtat atgtcctttt ataggtatta aacaacgacc catgggagca gctggtcaga 60

g 61

<210> 289
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 289
gacccatggg agcagctggt cagag 25

<210> 290
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 290
Glu Cys Pro Ile Thr Lys Asp Val Ile Asn Glu Tyr Lys
1 5 10