SEQUENCE LISTING

<110> Catalyst Biosciences, Inc;
Torrey Pines Institute for Molecular Studies;
Madison, Edwin

<120> PROTEASE SCREENING METHODS AND PROTEASES IDENTIFIED THEREBY

<130> 19049-002WO1/4902PC

<140> Not yet assigned
<141> Herewith

<150> 60/818,804
<151> 2006-07-05

<150> 60/818,910
<151> 2006-07-05

<160> 636

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<223> Alpha-1-antitrypsin precursor SERPINA1

<400> 1

```
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
 1               5                  10                  15
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
            20                  25                  30
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
        35                  40                  45
Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
    50                  55                  60
Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65                  70                  75                  80
Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
                85                  90                  95
His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
            100                 105                 110
Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
        115                 120                 125
Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
    130                 135                 140
Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145                 150                 155                 160
Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
                165                 170                 175
Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
            180                 185                 190
```

```
Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
        195                 200                 205
Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
    210                 215                 220
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225                 230                 235                 240
Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
                245                 250                 255
Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
            260                 265                 270
Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
        275                 280                 285
Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
    290                 295                 300
Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
305                 310                 315                 320
Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
                325                 330                 335
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
            340                 345                 350
Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
        355                 360                 365
Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
    370                 375                 380
Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
385                 390                 395                 400
Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
                405                 410                 415
Gln Lys
```

<210> 2
<211> 420
<212> PRT
<213> Homo sapiens

<220>
<223> Alpha-1-antitrypsin-related precursor SERPINA2

```
<400> 2
Met Pro Phe Ser Val Ser Trp Gly Val Leu Leu Leu Ala Gly Leu Cys
 1                5                  10                  15
Cys Leu Val Pro Ser Ser Leu Val Glu Asp Pro Gln Gly Asp Ala Ala
            20                  25                  30
Gln Lys Thr Asp Thr Ser His His Asp Gln Gly Asp Trp Glu Asp Leu
        35                  40                  45
Ala Cys Gln Lys Ile Ser Tyr Asn Val Thr Asp Leu Ala Phe Asp Leu
    50                  55                  60
Tyr Lys Ser Trp Leu Ile Tyr His Asn Gln His Val Leu Val Thr Pro
65                  70                  75                  80
Thr Ser Val Ala Met Ala Phe Arg Met Leu Ser Leu Gly Thr Lys Ala
                85                  90                  95
Asp Thr Arg Thr Glu Ile Leu Glu Gly Leu Asn Val Asn Leu Thr Glu
            100                 105                 110
Thr Pro Glu Ala Lys Ile His Glu Cys Phe Gln Gln Val Leu Gln Ala
        115                 120                 125
```

```
Leu Ser Arg Pro Asp Thr Arg Leu Gln Leu Thr Thr Gly Ser Ser Leu
    130                 135                 140
Phe Val Asn Lys Ser Met Lys Leu Val Asp Thr Phe Leu Glu Asp Thr
145                 150                 155                 160
Lys Lys Leu Tyr His Ser Glu Ala Ser Ser Ile Asn Phe Arg Asp Thr
                165                 170                 175
Glu Glu Ala Lys Glu Gln Ile Asn Asn Tyr Val Glu Lys Arg Thr Gly
            180                 185                 190
Arg Lys Val Val Asp Leu Val Lys His Leu Lys Lys Asp Thr Ser Leu
        195                 200                 205
Ala Leu Val Asp Tyr Ile Ser Phe His Gly Lys Trp Lys Asp Lys Phe
    210                 215                 220
Lys Ala Glu Arg Ile Met Val Glu Gly Phe His Val Asp Asp Lys Thr
225                 230                 235                 240
Ile Ile Arg Val Pro Met Ile Asn His Leu Gly Arg Phe Asp Ile His
                245                 250                 255
Arg Asp Arg Glu Leu Ser Ser Trp Val Leu Ala Gln His Tyr Val Gly
            260                 265                 270
Asn Ala Thr Ala Phe Phe Ile Leu Pro Asp Pro Lys Lys Met Trp Gln
        275                 280                 285
Leu Glu Glu Lys Leu Thr Tyr Ser His Leu Glu Asn Ile Gln Arg Ala
    290                 295                 300
Phe Asp Ile Arg Ser Ile Asn Leu His Phe Pro Lys Leu Ser Ile Ser
305                 310                 315                 320
Gly Thr Tyr Lys Leu Lys Arg Val Pro Arg Asn Leu Gly Ile Thr Lys
                325                 330                 335
Ile Phe Ser Asn Glu Ala Asp Leu Ser Gly Val Ser Gln Glu Ala Pro
            340                 345                 350
Leu Lys Leu Ser Lys Ala Val His Val Ala Val Leu Thr Ile Asp Glu
        355                 360                 365
Lys Gly Thr Glu Ala Thr Gly Ala Pro His Leu Glu Glu Lys Ala Trp
    370                 375                 380
Ser Lys Tyr Gln Thr Val Met Phe Asn Arg Pro Phe Leu Val Ile Ile
385                 390                 395                 400
Lys Glu Tyr Ile Thr Asn Phe Pro Leu Phe Ile Gly Lys Val Val Asn
                405                 410                 415
Pro Thr Gln Lys
            420
```

<210> 3
<211> 490
<212> PRT
<213> Homo sapiens

<220>
<223> Alpha-2-antiplasmin SERPINF2

```
<400> 3
Met Ala Leu Leu Trp Gly Leu Leu Val Leu Ser Trp Ser Cys Leu Gln
 1                5                  10                  15
Gly Pro Cys Ser Val Phe Ser Pro Val Ser Ala Met Glu Pro Leu Gly
            20                  25                  30
Arg Gln Leu Thr Ser Gly Pro Asn Gln Glu Gln Val Ser Pro Leu Thr
        35                  40                  45
Leu Leu Lys Leu Gly Asn Gln Glu Pro Gly Gly Gln Thr Ala Leu Lys
    50                  55                  60
```

```
Ser Pro Pro Gly Val Cys Ser Arg Asp Pro Thr Pro Glu Gln Thr His
65                  70                  75                  80
Arg Leu Ala Arg Ala Met Met Ala Phe Thr Ala Asp Leu Phe Ser Leu
                85                  90                  95
Val Ala Gln Thr Ser Thr Cys Pro Asn Leu Ile Leu Ser Pro Leu Ser
            100                 105                 110
Val Ala Leu Ala Leu Ser His Leu Ala Leu Gly Ala Gln Asn His Thr
        115                 120                 125
Leu Gln Arg Leu Gln Gln Val Leu His Ala Gly Ser Gly Pro Cys Leu
    130                 135                 140
Pro His Leu Leu Ser Arg Leu Cys Gln Asp Leu Gly Pro Gly Ala Phe
145                 150                 155                 160
Arg Leu Ala Ala Arg Met Tyr Leu Gln Lys Gly Phe Pro Ile Lys Glu
                165                 170                 175
Asp Phe Leu Glu Gln Ser Glu Gln Leu Phe Gly Ala Lys Pro Val Ser
            180                 185                 190
Leu Thr Gly Lys Gln Glu Asp Asp Leu Ala Asn Ile Asn Gln Trp Val
        195                 200                 205
Lys Glu Ala Thr Glu Gly Lys Ile Gln Glu Phe Leu Ser Gly Leu Pro
    210                 215                 220
Glu Asp Thr Val Leu Leu Leu Leu Asn Ala Ile His Phe Gln Gly Phe
225                 230                 235                 240
Trp Arg Asn Lys Phe Asp Pro Ser Leu Thr Gln Arg Asp Ser Phe His
                245                 250                 255
Leu Asp Glu Gln Phe Thr Val Pro Val Glu Met Met Gln Ala Arg Thr
            260                 265                 270
Tyr Pro Leu Arg Trp Phe Leu Leu Glu Gln Pro Glu Ile Gln Val Ala
        275                 280                 285
His Phe Pro Phe Lys Asn Asn Met Ser Phe Val Val Leu Val Pro Thr
    290                 295                 300
His Phe Glu Trp Asn Val Ser Gln Val Leu Ala Asn Leu Ser Trp Asp
305                 310                 315                 320
Thr Leu His Pro Pro Leu Val Trp Glu Arg Pro Thr Lys Val Arg Leu
                325                 330                 335
Pro Lys Leu Tyr Leu Lys His Gln Met Asp Leu Val Ala Thr Leu Ser
            340                 345                 350
Gln Leu Gly Leu Gln Glu Leu Phe Gln Ala Pro Asp Leu Arg Gly Ile
        355                 360                 365
Ser Glu Gln Ser Leu Val Val Ser Gly Val Gln His Gln Ser Thr Leu
    370                 375                 380
Glu Leu Ser Glu Val Gly Val Glu Ala Ala Ala Ala Thr Ser Ile Ala
385                 390                 395                 400
Met Ser Arg Met Ser Leu Ser Ser Phe Ser Val Asn Arg Pro Phe Leu
                405                 410                 415
Phe Phe Ile Phe Glu Asp Thr Thr Gly Leu Pro Leu Phe Val Gly Ser
            420                 425                 430
Val Arg Asn Pro Asn Pro Ser Ala Pro Arg Glu Leu Lys Glu Gln Gln
        435                 440                 445
Asp Ser Pro Gly Asn Lys Asp Phe Leu Gln Ser Leu Lys Gly Phe Pro
    450                 455                 460
Arg Gly Asp Lys Leu Phe Gly Pro Asp Leu Lys Leu Val Pro Pro Met
465                 470                 475                 480
Glu Glu Asp Tyr Pro Gln Phe Gly Ser Pro
                485                 490
```

<210> 4

<211> 423
<212> PRT
<213> Homo sapiens

<220>
<223> Alpha-1-antichymotrypsin precursor SERPINA3

<400> 4
Met Glu Arg Met Leu Pro Leu Leu Ala Leu Gly Leu Leu Ala Ala Gly
 1   5   10   15
Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu
            20   25   30
Asn Leu Thr Gln Glu Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly
        35   40   45
Leu Ala Ser Ala Asn Val Asp Phe Ala Phe Ser Leu Tyr Lys Gln Leu
    50   55   60
Val Leu Lys Ala Pro Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile
65   70   75   80
Ser Thr Ala Leu Ala Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu
                85   90   95
Thr Glu Ile Leu Lys Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu
            100   105   110
Ala Glu Ile His Gln Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln
        115   120   125
Ser Ser Asp Glu Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys
    130   135   140
Glu Gln Leu Ser Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu
145   150   155   160
Tyr Gly Ser Glu Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala
                165   170   175
Lys Lys Leu Ile Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Lys Ile
            180   185   190
Thr Asp Leu Ile Lys Asp Leu Asp Ser Gln Thr Met Met Val Leu Val
        195   200   205
Asn Tyr Ile Phe Phe Lys Ala Lys Trp Glu Met Pro Phe Asp Pro Gln
    210   215   220
Asp Thr His Gln Ser Arg Phe Tyr Leu Ser Lys Lys Lys Trp Val Met
225   230   235   240
Val Pro Met Met Ser Leu His His Leu Thr Ile Pro Tyr Phe Arg Asp
                245   250   255
Glu Glu Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala
            260   265   270
Ser Ala Leu Phe Ile Leu Pro Asp Gln Asp Lys Met Glu Glu Val Glu
        275   280   285
Ala Met Leu Leu Pro Glu Thr Leu Lys Arg Trp Arg Asp Ser Leu Glu
    290   295   300
Phe Arg Glu Ile Gly Glu Leu Tyr Leu Pro Lys Phe Ser Ile Ser Arg
305   310   315   320
Asp Tyr Asn Leu Asn Asp Ile Leu Leu Gln Leu Gly Ile Glu Glu Ala
                325   330   335
Phe Thr Ser Lys Ala Asp Leu Ser Gly Ile Thr Gly Ala Arg Asn Leu
            340   345   350
Ala Val Ser Gln Val Val His Lys Ala Val Leu Asp Val Phe Glu Glu
        355   360   365
Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu Ser
    370   375   380

```
Ala Leu Val Glu Thr Arg Thr Ile Val Arg Phe Asn Arg Pro Phe Leu
385                 390                 395                 400
Met Ile Ile Val Pro Thr Asp Thr Gln Asn Ile Phe Phe Met Ser Lys
                405                 410                 415
Val Thr Asn Pro Lys Gln Ala
            420
```

<210> 5
<211> 464
<212> PRT
<213> Homo sapiens

<220>
<223> Antithrombin-III precursor SERPINC1

<400> 5

```
Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
 1               5                  10                  15
Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
            20                  25                  30
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
        35                  40                  45
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
    50                  55                  60
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
65                  70                  75                  80
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
                85                  90                  95
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
            100                 105                 110
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
        115                 120                 125
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
    130                 135                 140
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
145                 150                 155                 160
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
                165                 170                 175
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
            180                 185                 190
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
        195                 200                 205
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
    210                 215                 220
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
225                 230                 235                 240
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
                245                 250                 255
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
            260                 265                 270
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
        275                 280                 285
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
    290                 295                 300
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
305                 310                 315                 320
```

```
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
                325                 330                 335
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
            340                 345                 350
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
        355                 360                 365
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
    370                 375                 380
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
385                 390                 395                 400
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
                405                 410                 415
Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val
            420                 425                 430
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
        435                 440                 445
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
    450                 455                 460


<210> 6
<211> 499
<212> PRT
<213> Homo sapiens

<220>
<223> Heparin cofactor 2 precursor   SERPIND1

<400> 6
Met Lys His Ser Leu Asn Ala Leu Leu Ile Phe Leu Ile Ile Thr Ser
 1               5                  10                  15
Ala Trp Gly Gly Ser Lys Gly Pro Leu Asp Gln Leu Glu Lys Gly Gly
            20                  25                  30
Glu Thr Ala Gln Ser Ala Asp Pro Gln Trp Glu Gln Leu Asn Asn Lys
        35                  40                  45
Asn Leu Ser Met Pro Leu Leu Pro Ala Asp Phe His Lys Glu Asn Thr
    50                  55                  60
Val Thr Asn Asp Trp Ile Pro Glu Gly Glu Glu Asp Asp Asp Tyr Leu
65                  70                  75                  80
Asp Leu Glu Lys Ile Phe Ser Glu Asp Asp Asp Tyr Ile Asp Ile Val
                85                  90                  95
Asp Ser Leu Ser Val Ser Pro Thr Asp Ser Asp Val Ser Ala Gly Asn
            100                 105                 110
Ile Leu Gln Leu Phe His Gly Lys Ser Arg Ile Gln Arg Leu Asn Ile
        115                 120                 125
Leu Asn Ala Lys Phe Ala Phe Asn Leu Tyr Arg Val Leu Lys Asp Gln
    130                 135                 140
Val Asn Thr Phe Asp Asn Ile Phe Ile Ala Pro Val Gly Ile Ser Thr
145                 150                 155                 160
Ala Met Gly Met Ile Ser Leu Gly Leu Lys Gly Glu Thr His Glu Gln
                165                 170                 175
Val His Ser Ile Leu His Phe Lys Asp Phe Val Asn Ala Ser Ser Lys
            180                 185                 190
Tyr Glu Ile Thr Thr Ile His Asn Leu Phe Arg Lys Leu Thr His Arg
        195                 200                 205
Leu Phe Arg Arg Asn Phe Gly Tyr Thr Leu Arg Ser Val Asn Asp Leu
    210                 215                 220
```

```
Tyr Ile Gln Lys Gln Phe Pro Ile Leu Leu Asp Phe Lys Thr Lys Val
225                 230                 235                 240
Arg Glu Tyr Tyr Phe Ala Glu Ala Gln Ile Ala Asp Phe Ser Asp Pro
                245                 250                 255
Ala Phe Ile Ser Lys Thr Asn Asn His Ile Met Lys Leu Thr Lys Gly
            260                 265                 270
Leu Ile Lys Asp Ala Leu Glu Asn Ile Asp Pro Ala Thr Gln Met Met
        275                 280                 285
Ile Leu Asn Cys Ile Tyr Phe Lys Gly Ser Trp Val Asn Lys Phe Pro
    290                 295                 300
Val Glu Met Thr His Asn His Asn Phe Arg Leu Asn Glu Arg Glu Val
305                 310                 315                 320
Val Lys Val Ser Met Met Gln Thr Lys Gly Asn Phe Leu Ala Ala Asn
                325                 330                 335
Asp Gln Glu Leu Asp Cys Asp Ile Leu Gln Leu Glu Tyr Val Gly Gly
            340                 345                 350
Ile Ser Met Leu Ile Val Val Pro His Lys Met Ser Gly Met Lys Thr
        355                 360                 365
Leu Glu Ala Gln Leu Thr Pro Arg Val Val Glu Arg Trp Gln Lys Ser
    370                 375                 380
Met Thr Asn Arg Thr Arg Glu Val Leu Leu Pro Lys Phe Lys Leu Glu
385                 390                 395                 400
Lys Asn Tyr Asn Leu Val Glu Ser Leu Lys Leu Met Gly Ile Arg Met
                405                 410                 415
Leu Phe Asp Lys Asn Gly Asn Met Ala Gly Ile Ser Asp Gln Arg Ile
            420                 425                 430
Ala Ile Asp Leu Phe Lys His Gln Gly Thr Ile Thr Val Asn Glu Glu
        435                 440                 445
Gly Thr Gln Ala Thr Thr Val Thr Thr Val Gly Phe Met Pro Leu Ser
    450                 455                 460
Thr Gln Val Arg Phe Thr Val Asp Arg Pro Phe Leu Phe Leu Ile Tyr
465                 470                 475                 480
Glu His Arg Thr Ser Cys Leu Leu Phe Met Gly Arg Val Ala Asn Pro
                485                 490                 495
Ser Arg Ser
```

<210> 7
<211> 500
<212> PRT
<213> Homo sapiens

<220>
<223> Plasma protease C1 inhibitor precursor SERPING1

<400> 7

```
Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu Leu Leu Leu Ala
 1               5                  10                  15
Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser Ser Ser Ser Gln
            20                  25                  30
Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys Val Ala Thr Thr
        35                  40                  45
Val Ile Ser Lys Met Leu Phe Val Glu Pro Ile Leu Glu Val Ser Ser
    50                  55                  60
Leu Pro Thr Thr Asn Ser Thr Thr Asn Ser Ala Thr Lys Ile Thr Ala
65                  70                  75                  80
```

```
Asn Thr Thr Asp Glu Pro Thr Thr Gln Pro Thr Thr Glu Pro Thr Thr
                85                  90                  95
Gln Pro Thr Ile Gln Pro Thr Gln Pro Thr Thr Gln Leu Pro Thr Asp
            100                 105                 110
Ser Pro Thr Gln Pro Thr Thr Gly Ser Phe Cys Pro Gly Pro Val Thr
        115                 120                 125
Leu Cys Ser Asp Leu Glu Ser His Ser Thr Glu Ala Val Leu Gly Asp
    130                 135                 140
Ala Leu Val Asp Phe Ser Leu Lys Leu Tyr His Ala Phe Ser Ala Met
145                 150                 155                 160
Lys Lys Val Glu Thr Asn Met Ala Phe Ser Pro Phe Ser Ile Ala Ser
                165                 170                 175
Leu Leu Thr Gln Val Leu Leu Gly Ala Gly Glu Asn Thr Lys Thr Asn
            180                 185                 190
Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys Val His Gln
        195                 200                 205
Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val Ser Gln Ile
    210                 215                 220
Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val Asn Ala Ser
225                 230                 235                 240
Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn Asn Ser Asp
                245                 250                 255
Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn Asn
            260                 265                 270
Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu Val
        275                 280                 285
Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe Asp
    290                 295                 300
Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val Ile
305                 310                 315                 320
Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe Ile
                325                 330                 335
Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu Ser His Asn
            340                 345                 350
Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His Arg Leu Glu
        355                 360                 365
Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala Ile Met Glu
    370                 375                 380
Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr Leu Pro Arg
385                 390                 395                 400
Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met Glu Lys Leu
                405                 410                 415
Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly Leu Thr Glu
            420                 425                 430
Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr Val Leu Glu
        435                 440                 445
Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala Ile Ser Val
    450                 455                 460
Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe Leu Phe Val
465                 470                 475                 480
Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly Arg Val Tyr
                485                 490                 495
Asp Pro Arg Ala
            500
```

<210> 8

<211> 406
<212> PRT
<213> Homo sapiens

<220>
<223> Plasma serine protease inhibitor precursor
SERPINA5

<400> 8

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

Ala Ser Leu His Arg His His Pro Arg Glu Met Lys Lys Arg Val Glu
            20                  25                  30
Asp Leu His Val Gly Ala Thr Val Ala Pro Ser Ser Arg Arg Asp Phe
        35                  40                  45
Thr Phe Asp Leu Tyr Arg Ala Leu Ala Ser Ala Ala Pro Ser Gln Asn
    50                  55                  60
Ile Phe Phe Ser Pro Val Ser Ile Ser Met Ser Leu Ala Met Leu Ser
65                  70                  75                  80
Leu Gly Ala Gly Ser Ser Thr Lys Met Gln Ile Leu Glu Gly Leu Gly
                85                  90                  95
Leu Asn Leu Gln Lys Ser Ser Glu Lys Glu Leu His Arg Gly Phe Gln
            100                 105                 110
Gln Leu Leu Gln Glu Leu Asn Gln Pro Arg Asp Gly Phe Gln Leu Ser
        115                 120                 125
Leu Gly Asn Ala Leu Phe Thr Asp Leu Val Val Asp Leu Gln Asp Thr
    130                 135                 140
Phe Val Ser Ala Met Lys Thr Leu Tyr Leu Ala Asp Thr Phe Pro Thr
145                 150                 155                 160
Asn Phe Arg Asp Ser Ala Gly Ala Met Lys Gln Ile Asn Asp Tyr Val
                165                 170                 175
Ala Lys Gln Thr Lys Gly Lys Ile Val Asp Leu Leu Lys Asn Leu Asp
            180                 185                 190
Ser Asn Ala Val Val Ile Met Val Asn Tyr Ile Phe Phe Lys Ala Lys
        195                 200                 205
Trp Glu Thr Ser Phe Asn His Lys Gly Thr Gln Glu Gln Asp Phe Tyr
    210                 215                 220
Val Thr Ser Glu Thr Val Val Arg Val Pro Met Met Ser Arg Glu Asp
225                 230                 235                 240
Gln Tyr His Tyr Leu Leu Asp Arg Asn Leu Ser Cys Arg Val Val Gly
                245                 250                 255
Val Pro Tyr Gln Gly Asn Ala Thr Ala Leu Phe Ile Leu Pro Ser Glu
            260                 265                 270
Gly Lys Met Gln Gln Val Glu Asn Gly Leu Ser Glu Lys Thr Leu Arg
        275                 280                 285
Lys Trp Leu Lys Met Phe Lys Lys Arg Gln Leu Glu Leu Tyr Leu Pro
    290                 295                 300
Lys Phe Ser Ile Glu Gly Ser Tyr Gln Leu Glu Lys Val Leu Pro Ser
305                 310                 315                 320
Leu Gly Ile Ser Asn Val Phe Thr Ser His Ala Asp Leu Ser Gly Ile
                325                 330                 335
Ser Asn His Ser Asn Ile Gln Val Ser Glu Met Val His Lys Ala Val
            340                 345                 350
Val Glu Val Asp Glu Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr

        355                 360                 365
```

```
Ile Phe Thr Phe Arg Ser Ala Arg Leu Asn Ser Gln Arg Leu Val Phe
    370                 375                 380
Asn Arg Pro Phe Leu Met Phe Ile Val Asp Asn Asn Ile Leu Phe Leu
385                 390                 395                 400
Gly Lys Val Asn Arg Pro
                405
```

<210> 9
<211> 427
<212> PRT
<213> Homo sapiens

<220>
<223> Kallistatin precursor SERPINA4

<400> 9

```
Met His Leu Ile Asp Tyr Leu Leu Leu Leu Leu Val Gly Leu Leu Ala
 1               5                  10                  15
Leu Ser His Gly Gln Leu His Val Glu His Asp Gly Glu Ser Cys Ser
            20                  25                  30
Asn Ser Ser His Gln Gln Ile Leu Glu Thr Gly Glu Gly Ser Pro Ser
        35                  40                  45
Leu Lys Ile Ala Pro Ala Asn Ala Asp Phe Ala Phe Arg Phe Tyr Tyr
    50                  55                  60
Leu Ile Ala Ser Glu Thr Pro Gly Lys Asn Ile Phe Phe Ser Pro Leu
65                  70                  75                  80
Ser Ile Ser Ala Ala Tyr Ala Met Leu Ser Leu Gly Ala Cys Ser His
                85                  90                  95
Ser Arg Ser Gln Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Leu
            100                 105                 110
Ser Glu Ser Asp Val His Arg Gly Phe Gln His Leu Leu His Thr Leu
        115                 120                 125
Asn Leu Pro Gly His Gly Leu Glu Thr Arg Val Gly Ser Ala Leu Phe
    130                 135                 140
Leu Ser His Asn Leu Lys Phe Leu Ala Lys Phe Leu Asn Asp Thr Met
145                 150                 155                 160
Ala Val Tyr Glu Ala Lys Leu Phe His Thr Asn Phe Tyr Asp Thr Val
                165                 170                 175
Gly Thr Ile Gln Leu Ile Asn Asp His Val Lys Lys Glu Thr Arg Gly
            180                 185                 190
Lys Ile Val Asp Leu Val Ser Glu Leu Lys Lys Asp Val Leu Met Val
        195                 200                 205
Leu Val Asn Tyr Ile Tyr Phe Lys Ala Leu Trp Glu Lys Pro Phe Ile
    210                 215                 220
Ser Ser Arg Thr Thr Pro Lys Asp Phe Tyr Val Asp Glu Asn Thr Thr
225                 230                 235                 240
Val Arg Val Pro Met Met Leu Gln Asp Gln Glu His His Trp Tyr Leu
                245                 250                 255
His Asp Arg Tyr Leu Pro Cys Ser Val Leu Arg Met Asp Tyr Lys Gly
            260                 265                 270
Asp Ala Thr Val Phe Phe Ile Leu Pro Asn Gln Gly Lys Met Arg Glu
        275                 280                 285
Ile Glu Glu Val Leu Thr Pro Glu Met Leu Met Arg Trp Asn Asn Leu
    290                 295                 300
Leu Arg Lys Arg Asn Phe Tyr Lys Lys Leu Glu Leu His Leu Pro Lys
305                 310                 315                 320
```

```
Phe Ser Ile Ser Gly Ser Tyr Val Leu Asp Gln Ile Leu Pro Arg Leu
                325                 330                 335
Gly Phe Thr Asp Leu Phe Ser Lys Trp Ala Asp Leu Ser Gly Ile Thr
            340                 345                 350
Lys Gln Gln Lys Leu Glu Ala Ser Lys Ser Phe His Lys Ala Thr Leu
        355                 360                 365
Asp Val Asp Glu Ala Gly Thr Glu Ala Ala Ala Ala Thr Ser Phe Ala
    370                 375                 380
Ile Lys Phe Phe Ser Ala Gln Thr Asn Arg His Ile Leu Arg Phe Asn
385                 390                 395                 400
Arg Pro Phe Leu Val Val Ile Phe Ser Thr Ser Thr Gln Ser Val Leu
                405                 410                 415
Phe Leu Gly Lys Val Val Asp Pro Thr Lys Pro
            420                 425
```

<210> 10
<211> 410
<212> PRT
<213> Homo sapiens

<220>
<223> Neuroserpin precursor SERPINII

<400> 10

```
Met Ala Phe Leu Gly Leu Phe Ser Leu Leu Val Leu Gln Ser Met Ala
 1               5                  10                  15
Thr Gly Ala Thr Phe Pro Glu Glu Ala Ile Ala Asp Leu Ser Val Asn
            20                  25                  30
Met Tyr Asn Arg Leu Arg Ala Thr Gly Glu Asp Glu Asn Ile Leu Phe
        35                  40                  45
Ser Pro Leu Ser Ile Ala Leu Ala Met Gly Met Met Glu Leu Gly Ala
    50                  55                  60
Gln Gly Ser Thr Gln Lys Glu Ile Arg His Ser Met Gly Tyr Asp Ser
65                  70                  75                  80
Leu Lys Asn Gly Glu Glu Phe Ser Phe Leu Lys Glu Phe Ser Asn Met
                85                  90                  95
Val Thr Ala Lys Glu Ser Gln Tyr Val Met Lys Ile Ala Asn Ser Leu
            100                 105                 110
Phe Val Gln Asn Gly Phe His Val Asn Glu Glu Phe Leu Gln Met Met
        115                 120                 125
Lys Lys Tyr Phe Asn Ala Ala Val Asn His Val Asp Phe Ser Gln Asn
    130                 135                 140
Val Ala Val Ala Asn Tyr Ile Asn Lys Trp Val Glu Asn Asn Thr Asn
145                 150                 155                 160
Asn Leu Val Lys Asp Leu Val Ser Pro Arg Asp Phe Asp Ala Ala Thr
                165                 170                 175
Tyr Leu Ala Leu Ile Asn Ala Val Tyr Phe Lys Gly Asn Trp Lys Ser
            180                 185                 190
Gln Phe Arg Pro Glu Asn Thr Arg Thr Phe Ser Phe Thr Lys Asp Asp
        195                 200                 205
Glu Ser Glu Val Gln Ile Pro Met Met Tyr Gln Gln Gly Glu Phe Tyr
    210                 215                 220
Tyr Gly Glu Phe Ser Asp Gly Ser Asn Glu Ala Gly Gly Ile Tyr Gln
225                 230                 235                 240
Val Leu Glu Ile Pro Tyr Glu Gly Asp Glu Ile Ser Met Met Leu Val
                245                 250                 255
```

```
Leu Ser Arg Gln Glu Val Pro Leu Ala Thr Leu Glu Pro Leu Val Lys
            260                 265                 270
Ala Gln Leu Val Glu Glu Trp Ala Asn Ser Val Lys Lys Gln Lys Val
        275                 280                 285
Glu Val Tyr Leu Pro Arg Phe Thr Val Glu Gln Glu Ile Asp Leu Lys
    290                 295                 300
Asp Val Leu Lys Ala Leu Gly Ile Thr Glu Ile Phe Ile Lys Asp Ala
305                 310                 315                 320
Asn Leu Thr Gly Leu Ser Asp Asn Lys Glu Ile Phe Leu Ser Lys Ala
                325                 330                 335
Ile His Lys Ser Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
            340                 345                 350
Ala Val Ser Gly Met Ile Ala Ile Ser Arg Met Ala Val Leu Tyr Pro
        355                 360                 365
Gln Val Ile Val Asp His Pro Phe Phe Phe Leu Ile Arg Asn Arg Arg
    370                 375                 380
Thr Gly Thr Ile Leu Phe Met Gly Arg Val Met His Pro Glu Thr Met
385                 390                 395                 400
Asn Thr Ser Gly His Asp Phe Glu Glu Leu
                405                 410
```

<210> 11
<211> 402
<212> PRT
<213> Homo sapiens

<220>
<223> Plasminogen activator inhibitor 1 precursor
SERPINE1

<400> 11

```
Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
 1               5                  10                  15
Val Phe Gly Glu Gly Ser Ala Val His His Pro Pro Ser Tyr Val Ala
            20                  25                  30
His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln
        35                  40                  45
Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser
    50                  55                  60
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln
65                  70                  75                  80
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro
                85                  90                  95
Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp
            100                 105                 110
Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg Asp Leu Lys Leu
        115                 120                 125
Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe Arg Ser Thr Val
    130                 135                 140
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn
145                 150                 155                 160
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly
                165                 170                 175
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu
            180                 185                 190
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His
```

```
        195                 200                 205
Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met
    210                 215                 220
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp
225                 230                 235                 240
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu
                245                 250                 255
Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala
            260                 265                 270
Leu Thr Asn Ile Leu Ser Ala Gln Leu Ile Ser His Trp Lys Gly Asn
        275                 280                 285
Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys Phe Ser Leu Glu
    290                 295                 300
Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu Gly Met Thr Asp
305                 310                 315                 320
Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu
                325                 330                 335
Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn
            340                 345                 350
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala
        355                 360                 365
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val
    370                 375                 380
Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met Gly Gln Val Met
385                 390                 395                 400
Glu Pro
```

<210> 12
<211> 405
<212> PRT
<213> Homo sapiens

<220>
<223> Myoepithelium-derived serine protease inhibitor
SERPIN12

<400> 12

```
Met Asp Thr Ile Phe Leu Trp Ser Leu Leu Leu Leu Phe Phe Gly Ser
 1               5                  10                  15
Gln Ala Ser Arg Cys Ser Ala Gln Lys Asn Thr Glu Phe Ala Val Asp
            20                  25                  30
Leu Tyr Gln Glu Val Ser Leu Ser His Lys Asp Asn Ile Ile Phe Ser
        35                  40                  45
Pro Leu Gly Ile Thr Leu Val Leu Glu Met Val Gln Leu Gly Ala Lys
    50                  55                  60
Gly Lys Ala Gln Gln Gln Ile Arg Gln Thr Leu Lys Gln Gln Glu Thr
65                  70                  75                  80
Ser Ala Gly Glu Glu Phe Phe Val Leu Lys Ser Phe Phe Ser Ala Ile
                85                  90                  95
Ser Glu Lys Lys Gln Glu Phe Thr Phe Asn Leu Ala Asn Ala Leu Tyr
            100                 105                 110
Leu Gln Glu Gly Phe Thr Val Lys Glu Gln Tyr Leu His Gly Asn Lys
        115                 120                 125
Glu Phe Phe Gln Ser Ala Ile Lys Leu Val Asp Phe Gln Asp Ala Lys
```

```
    130                 135                 140
Ala Cys Ala Glu Met Ile Ser Thr Trp Val Glu Arg Lys Thr Asp Gly
145                 150                 155                 160
Lys Ile Lys Asp Met Phe Ser Gly Glu Glu Phe Gly Pro Leu Thr Arg
                165                 170                 175
Leu Val Leu Val Asn Ala Ile Tyr Phe Lys Gly Asp Trp Lys Gln Lys
            180                 185                 190
Phe Arg Lys Glu Asp Thr Gln Leu Ile Asn Phe Thr Lys Lys Asn Gly
        195                 200                 205
Ser Thr Val Lys Ile Pro Met Met Lys Ala Leu Leu Arg Thr Lys Tyr
    210                 215                 220
Gly Tyr Phe Ser Glu Ser Ser Leu Asn Tyr Gln Val Leu Glu Leu Ser
225                 230                 235                 240
Tyr Lys Gly Asp Glu Phe Ser Leu Ile Ile Ile Leu Pro Ala Glu Gly
                245                 250                 255
Met Asp Ile Glu Glu Val Glu Lys Leu Ile Thr Ala Gln Gln Ile Leu
            260                 265                 270
Lys Trp Leu Ser Glu Met Gln Glu Glu Glu Val Glu Ile Ser Leu Pro
        275                 280                 285
Arg Phe Lys Val Glu Gln Lys Val Asp Phe Lys Asp Val Leu Tyr Ser
    290                 295                 300
Leu Asn Ile Thr Glu Ile Phe Ser Gly Gly Cys Asp Leu Ser Gly Ile
305                 310                 315                 320
Thr Asp Ser Ser Glu Val Tyr Val Ser Gln Val Thr Gln Lys Val Phe
                325                 330                 335
Phe Glu Ile Asn Glu Asp Gly Ser Glu Ala Ala Thr Ser Thr Gly Ile
            340                 345                 350
His Ile Pro Val Ile Met Ser Leu Ala Gln Ser Gln Phe Ile Ala Asn
        355                 360                 365
His Pro Phe Leu Phe Ile Met Lys His Asn Pro Thr Glu Ser Ile Leu
    370                 375                 380
Phe Met Gly Arg Val Thr Asn Pro Asp Thr Gln Glu Ile Lys Gly Arg
385                 390                 395                 400

Asp Leu Asp Ser Leu
                405
```

<210> 13
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<223> Protein Z-dependent protease inhibitor precursor
SERPINA10

<400> 13

```
Met Lys Val Val Pro Ser Leu Leu Leu Ser Val Leu Leu Ala Gln Val
 1               5                  10                  15
Trp Leu Val Pro Gly Leu Ala Pro Ser Pro Gln Ser Pro Glu Thr Pro
            20                  25                  30
Ala Pro Gln Asn Gln Thr Ser Arg Val Val Gln Ala Pro Lys Glu Glu
        35                  40                  45
Glu Glu Asp Glu Gln Glu Ala Ser Glu Glu Lys Ala Ser Glu Glu Glu
    50                  55                  60
Lys Ala Trp Leu Met Ala Ser Arg Gln Gln Leu Ala Lys Glu Thr Ser
```

```
65                  70                  75                  80
Asn Phe Gly Phe Ser Leu Leu Arg Lys Ile Ser Met Arg His Asp Gly
                85                  90                  95
Asn Met Val Phe Ser Pro Phe Gly Met Ser Leu Ala Met Thr Gly Leu
            100                 105                 110
Met Leu Gly Ala Thr Gly Pro Thr Glu Thr Gln Ile Lys Arg Gly Leu
        115                 120                 125
His Leu Gln Ala Leu Lys Pro Thr Lys Pro Gly Leu Leu Pro Ser Leu
    130                 135                 140
Phe Lys Gly Leu Arg Glu Thr Leu Ser Arg Asn Leu Glu Leu Gly Leu
145                 150                 155                 160
Thr Gln Gly Ser Phe Ala Phe Ile His Lys Asp Phe Asp Val Lys Glu
                165                 170                 175
Thr Phe Phe Asn Leu Ser Lys Arg Tyr Phe Asp Thr Glu Cys Val Pro
            180                 185                 190
Met Asn Phe Arg Asn Ala Ser Gln Ala Lys Arg Leu Met Asn His Tyr
        195                 200                 205
Ile Asn Lys Glu Thr Arg Gly Lys Ile Pro Lys Leu Phe Asp Glu Ile
    210                 215                 220
Asn Pro Glu Thr Lys Leu Ile Leu Val Asp Tyr Ile Leu Phe Lys Gly
225                 230                 235                 240
Lys Trp Leu Thr Pro Phe Asp Pro Val Phe Thr Glu Val Asp Thr Phe
                245                 250                 255
His Leu Asp Lys Tyr Lys Thr Ile Lys Val Pro Met Met Tyr Gly Ala
            260                 265                 270
Gly Lys Phe Ala Ser Thr Phe Asp Lys Asn Phe Arg Cys His Val Leu
        275                 280                 285
Lys Leu Pro Tyr Gln Gly Asn Ala Thr Met Leu Val Val Leu Met Glu
    290                 295                 300
Lys Met Gly Asp His Leu Ala Leu Glu Asp Tyr Leu Thr Thr Asp Leu
305                 310                 315                 320
Val Glu Thr Trp Leu Arg Asn Met Lys Thr Arg Asn Met Glu Val Phe
                325                 330                 335
Phe Pro Lys Phe Lys Leu Asp Gln Lys Tyr Glu Met His Glu Leu Leu
            340                 345                 350
Arg Gln Met Gly Ile Arg Arg Ile Phe Ser Pro Phe Ala Asp Leu Ser
        355                 360                 365
Glu Leu Ser Ala Thr Gly Arg Asn Leu Gln Val Ser Arg Val Leu Gln
    370                 375                 380
Arg Thr Val Ile Glu Val Asp Glu Arg Gly Thr Glu Ala Val Ala Gly
385                 390                 395                 400
Ile Leu Ser Glu Ile Thr Ala Tyr Ser Met Pro Pro Val Ile Lys Val
                405                 410                 415
Asp Arg Pro Phe His Phe Met Ile Tyr Glu Glu Thr Ser Gly Met Leu
            420                 425                 430
Leu Phe Leu Gly Arg Val Val Asn Pro Thr Leu Leu
        435                 440
```

<210> 14
<211> 398
<212> PRT
<213> Homo sapiens

<220>
<223> Glia-derived nexin precursor SERPINE2

<400> 14

```
Met Asn Trp His Leu Pro Leu Phe Leu Leu Ala Ser Val Thr Leu Pro
 1               5                  10                  15
Ser Ile Cys Ser His Phe Asn Pro Leu Ser Leu Glu Glu Leu Gly Ser
            20                  25                  30
Asn Thr Gly Ile Gln Val Phe Asn Gln Ile Val Lys Ser Arg Pro His
        35                  40                  45
Asp Asn Ile Val Ile Ser Pro His Gly Ile Ala Ser Val Leu Gly Met
    50                  55                  60
Leu Gln Leu Gly Ala Asp Gly Arg Thr Lys Lys Gln Leu Ala Met Val
65                  70                  75                  80

Met Arg Tyr Gly Val Asn Gly Val Gly Lys Ile Leu Lys Lys Ile Asn
                85                  90                  95
Lys Ala Ile Val Ser Lys Lys Asn Lys Asp Ile Val Thr Val Ala Asn
            100                 105                 110
Ala Val Phe Val Lys Asn Ala Ser Glu Ile Glu Val Pro Phe Val Thr
        115                 120                 125
Arg Asn Lys Asp Val Phe Gln Cys Glu Val Arg Asn Val Asn Phe Glu
    130                 135                 140
Asp Pro Ala Ser Ala Cys Asp Ser Ile Asn Ala Trp Val Lys Asn Glu
145                 150                 155                 160
Thr Arg Asp Met Ile Asp Asn Leu Leu Ser Pro Asp Leu Ile Asp Gly
                165                 170                 175
Val Leu Thr Arg Leu Val Leu Val Asn Ala Val Tyr Phe Lys Gly Leu
            180                 185                 190
Trp Lys Ser Arg Phe Gln Pro Glu Asn Thr Lys Lys Arg Thr Phe Val
        195                 200                 205
Ala Ala Asp Gly Lys Ser Tyr Gln Val Pro Met Leu Ala Gln Leu Ser
    210                 215                 220
Val Phe Arg Cys Gly Ser Thr Ser Ala Pro Asn Asp Leu Trp Tyr Asn
225                 230                 235                 240
Phe Ile Glu Leu Pro Tyr His Gly Glu Ser Ile Ser Met Leu Ile Ala
                245                 250                 255
Leu Pro Thr Glu Ser Ser Thr Pro Leu Ser Ala Ile Ile Pro His Ile
            260                 265                 270
Ser Thr Lys Thr Ile Asp Ser Trp Met Ser Ile Met Val Pro Lys Arg
        275                 280                 285
Val Gln Val Ile Leu Pro Lys Phe Thr Ala Val Ala Gln Thr Asp Leu
    290                 295                 300
Lys Glu Pro Leu Lys Val Leu Gly Ile Thr Asp Met Phe Asp Ser Ser
305                 310                 315                 320
Lys Ala Asn Phe Ala Lys Ile Thr Thr Gly Ser Glu Asn Leu His Val
                325                 330                 335
Ser His Ile Leu Gln Lys Ala Lys Ile Glu Val Ser Glu Asp Gly Thr
            340                 345                 350
Lys Ala Ser Ala Ala Thr Thr Ala Ile Leu Ile Ala Arg Ser Ser Pro
        355                 360                 365
Pro Trp Phe Ile Val Asp Arg Pro Phe Leu Phe Phe Ile Arg His Asn
    370                 375                 380
Pro Thr Gly Ala Val Leu Phe Met Gly Gln Ile Asn Lys Pro
385                 390                 395
```

<210> 15
<211> 379
<212> PRT

<213> Homo sapiens

<220>
<223> Leukocyte elastase inhibitor SERPINB1

<400> 15

```
Met Glu Gln Leu Ser Ser Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe
 1               5                  10                  15
Leu Ala Leu Ser Glu Asn Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro
            20                  25                  30
Phe Ser Ile Ser Ser Ala Met Ala Met Val Phe Leu Gly Thr Arg Gly
        35                  40                  45
Asn Thr Ala Ala Gln Leu Ser Lys Thr Phe His Phe Asn Thr Val Glu
    50                  55                  60
Glu Val His Ser Arg Phe Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg
65                  70                  75                  80
Gly Ala Ser Tyr Ile Leu Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys
                85                  90                  95
Thr Tyr Asn Phe Leu Pro Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr
            100                 105                 110
Gly Ala Asp Leu Ala Ser Val Asp Phe Gln His Ala Ser Glu Asp Ala
        115                 120                 125
Arg Lys Thr Ile Asn Gln Trp Val Lys Gly Gln Thr Glu Gly Lys Ile
    130                 135                 140
Pro Glu Leu Leu Ala Ser Gly Met Val Asp Asn Met Thr Lys Leu Val
145                 150                 155                 160
Leu Val Asn Ala Ile Tyr Phe Lys Gly Asn Trp Lys Asp Lys Phe Met
                165                 170                 175
Lys Glu Ala Thr Thr Asn Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg
            180                 185                 190
Lys Thr Val Lys Met Met Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr
        195                 200                 205
Ile Glu Asp Leu Lys Cys Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu
    210                 215                 220
Glu Leu Ser Met Val Ile Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser
225                 230                 235                 240
Thr Gly Leu Lys Lys Ile Glu Glu Gln Leu Thr Leu Glu Lys Leu His
                245                 250                 255
Glu Trp Thr Lys Pro Glu Asn Leu Asp Phe Ile Glu Val Asn Val Ser
            260                 265                 270
Leu Pro Arg Phe Lys Leu Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu
        275                 280                 285
Ala Arg Leu Gly Val Gln Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu
    290                 295                 300
Ser Gly Met Ser Gly Ala Arg Asp Ile Phe Ile Ser Lys Ile Val His
305                 310                 315                 320
Lys Ser Phe Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala
                325                 330                 335
Thr Ala Gly Ile Ala Thr Phe Cys Met Leu Met Pro Glu Glu Asn Phe
            340                 345                 350
Thr Ala Asp His Pro Phe Leu Phe Phe Ile Arg His Asn Ser Ser Gly
        355                 360                 365
Ser Ile Leu Phe Leu Gly Arg Phe Ser Ser Pro
    370                 375
```

<210> 16

<211> 415
<212> PRT
<213> Homo sapiens

<220>
<223> Plasminogen activator inhibitor 2 precursor
SERPINB2

<400> 16
Met Glu Asp Leu Cys Val Ala Asn Thr Leu Phe Ala Leu Asn Leu Phe
1 5 10 15
Lys His Leu Ala Lys Ala Ser Pro Thr Gln Asn Leu Phe Leu Ser Pro
20 25 30
Trp Ser Ile Ser Ser Thr Met Ala Met Val Tyr Met Gly Ser Arg Gly
35 40 45
Ser Thr Glu Asp Gln Met Ala Lys Val Leu Gln Phe Asn Glu Val Gly
50 55 60
Ala Asn Ala Val Thr Pro Met Thr Pro Glu Asn Phe Thr Ser Cys Gly
65 70 75 80
Phe Met Gln Gln Ile Gln Lys Gly Ser Tyr Pro Asp Ala Ile Leu Gln
85 90 95
Ala Gln Ala Ala Asp Lys Ile His Ser Ser Phe Arg Ser Leu Ser Ser
100 105 110
Ala Ile Asn Ala Ser Thr Gly Asn Tyr Leu Leu Glu Ser Val Asn Lys
115 120 125
Leu Phe Gly Glu Lys Ser Ala Ser Phe Arg Glu Glu Tyr Ile Arg Leu
130 135 140
Cys Gln Lys Tyr Tyr Ser Ser Glu Pro Gln Ala Val Asp Phe Leu Glu
145 150 155 160
Cys Ala Glu Glu Ala Arg Lys Lys Ile Asn Ser Trp Val Lys Thr Gln
165 170 175
Thr Lys Gly Lys Ile Pro Asn Leu Leu Pro Glu Gly Ser Val Asp Gly
180 185 190
Asp Thr Arg Met Val Leu Val Asn Ala Val Tyr Phe Lys Gly Lys Trp
195 200 205

Lys Thr Pro Phe Glu Lys Lys Leu Asn Gly Leu Tyr Pro Phe Arg Val
210 215 220
Asn Ser Ala Gln Arg Thr Pro Val Gln Met Met Tyr Leu Arg Glu Lys
225 230 235 240
Leu Asn Ile Gly Tyr Ile Glu Asp Leu Lys Ala Gln Ile Leu Glu Leu
245 250 255
Pro Tyr Ala Gly Asp Val Ser Met Phe Leu Leu Leu Pro Asp Glu Ile
260 265 270
Ala Asp Val Ser Thr Gly Leu Glu Leu Leu Glu Ser Glu Ile Thr Tyr
275 280 285
Asp Lys Leu Asn Lys Trp Thr Ser Lys Asp Lys Met Ala Glu Asp Glu
290 295 300
Val Glu Val Tyr Ile Pro Gln Phe Lys Leu Glu Glu His Tyr Glu Leu
305 310 315 320
Arg Ser Ile Leu Arg Ser Met Gly Met Glu Asp Ala Phe Asn Lys Gly
325 330 335
Arg Ala Asn Phe Ser Gly Met Ser Glu Arg Asn Asp Leu Phe Leu Ser
340 345 350
Glu Val Phe His Gln Ala Met Val Asp Val Asn Glu Glu Gly Thr Glu
355 360 365
Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly Arg Thr Gly His Gly

```
    370                 375                 380
Gly Pro Gln Phe Val Ala Asp His Pro Phe Leu Phe Leu Ile Met His
385                 390                 395                 400
Lys Ile Thr Asn Cys Ile Leu Phe Phe Gly Arg Phe Ser Ser Pro
                405                 410                 415
```

<210> 17
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<223> Placental thrombin inhibitor SERPINB6

<400> 17

```
Met Asp Val Leu Ala Glu Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu
 1               5                  10                  15
Lys Thr Leu Gly Lys Asp Asn Ser Lys Asn Val Phe Phe Ser Pro Met
            20                  25                  30
Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
        35                  40                  45
Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
    50                  55                  60
Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
65                  70                  75                  80
Lys Thr Gly Thr Gln Tyr Leu Leu Arg Val Ala Asn Arg Leu Phe Gly
                85                  90                  95
Glu Lys Ser Cys Asp Phe Leu Ser Ser Phe Arg Asp Ser Cys Gln Lys
            100                 105                 110
Phe Tyr Gln Ala Glu Met Glu Glu Leu Asp Phe Ile Ser Ala Val Glu
        115                 120                 125
Lys Ser Arg Lys His Ile Asn Thr Trp Val Ala Glu Lys Thr Glu Gly
    130                 135                 140
Lys Ile Ala Glu Leu Leu Ser Pro Gly Ser Val Asp Pro Leu Thr Arg
145                 150                 155                 160
Leu Val Leu Val Asn Ala Val Tyr Phe Arg Gly Asn Trp Asp Glu Gln
                165                 170                 175
Phe Asp Lys Glu Asn Thr Glu Glu Arg Leu Phe Lys Val Ser Lys Asn
            180                 185                 190
Glu Glu Lys Pro Val Gln Met Met Phe Lys Gln Ser Thr Phe Lys Lys
        195                 200                 205
Thr Tyr Ile Gly Glu Ile Phe Thr Gln Ile Leu Val Leu Pro Tyr Val
    210                 215                 220
Gly Lys Glu Leu Asn Met Ile Ile Met Leu Pro Asp Glu Thr Thr Asp
225                 230                 235                 240
Leu Arg Thr Val Glu Lys Glu Leu Thr Tyr Glu Lys Phe Val Glu Trp
                245                 250                 255
Thr Arg Leu Asp Met Met Asp Glu Glu Glu Val Glu Val Ser Leu Pro
            260                 265                 270
Arg Phe Lys Leu Glu Glu Ser Tyr Asp Met Glu Ser Val Leu Arg Asn
        275                 280                 285
Leu Gly Met Thr Asp Ala Phe Glu Leu Gly Lys Ala Asp Phe Ser Gly
    290                 295                 300
Met Ser Gln Thr Asp Leu Ser Leu Ser Lys Val Val His Lys Ser Phe
305                 310                 315                 320
```

```
Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Ala
                325                 330                 335
Ile Met Met Met Arg Cys Ala Arg Phe Val Pro Arg Phe Cys Ala Asp
            340                 345                 350
His Pro Phe Leu Phe Phe Ile Gln His Ser Lys Thr Asn Gly Ile Leu
        355                 360                 365
Phe Cys Gly Arg Phe Ser Ser Pro
    370                 375
```

<210> 18
<211> 397
<212> PRT
<213> Homo sapiens

<220>
<223> Bomapin SERPINB10

<400> 18

```
Met Asp Ser Leu Ala Thr Ser Ile Asn Gln Phe Ala Leu Glu Leu Ser
 1               5                  10                  15
Lys Lys Leu Ala Glu Ser Ala Gln Gly Lys Asn Ile Phe Phe Ser Ser
            20                  25                  30
Trp Ser Ile Ser Thr Ser Leu Thr Ile Val Tyr Leu Gly Ala Lys Gly
        35                  40                  45
Thr Thr Ala Ala Gln Met Ala Gln Val Leu Gln Phe Asn Arg Asp Gln
    50                  55                  60
Gly Val Lys Cys Asp Pro Glu Ser Glu Lys Lys Arg Lys Met Glu Phe
65                  70                  75                  80
Asn Leu Ser Asn Ser Glu Glu Ile His Ser Asp Phe Gln Thr Leu Ile
                85                  90                  95
Ser Glu Ile Leu Lys Pro Asn Asp Asp Tyr Leu Leu Lys Thr Ala Asn
            100                 105                 110
Ala Ile Tyr Gly Glu Lys Thr Tyr Ala Phe His Asn Lys Tyr Leu Glu
        115                 120                 125
Asp Met Lys Thr Tyr Phe Gly Ala Glu Pro Gln Pro Val Asn Phe Val
    130                 135                 140
Glu Ala Ser Asp Gln Ile Arg Lys Asp Ile Asn Ser Trp Val Glu Arg
145                 150                 155                 160
Gln Thr Glu Gly Lys Ile Gln Asn Leu Leu Pro Asp Asp Ser Val Asp
                165                 170                 175
Ser Thr Thr Arg Met Ile Leu Val Asn Ala Leu Tyr Phe Lys Gly Ile
            180                 185                 190
Trp Glu His Gln Phe Leu Val Gln Asn Thr Thr Glu Lys Pro Phe Arg
        195                 200                 205
Ile Asn Glu Thr Thr Ser Lys Pro Val Gln Met Met Phe Met Lys Lys
    210                 215                 220
Lys Leu His Ile Phe His Ile Glu Lys Pro Lys Ala Val Gly Leu Gln
225                 230                 235                 240
Leu Tyr Tyr Lys Ser Arg Asp Leu Ser Leu Leu Ile Leu Leu Pro Glu
                245                 250                 255
Asp Ile Asn Gly Leu Glu Gln Leu Glu Lys Ala Ile Thr Tyr Glu Lys
            260                 265                 270
Leu Asn Glu Trp Thr Ser Ala Asp Met Met Glu Leu Tyr Glu Val Gln
        275                 280                 285
Leu His Leu Pro Lys Phe Lys Leu Glu Asp Ser Tyr Asp Leu Lys Ser
    290                 295                 300
```

```
Thr Leu Ser Ser Met Gly Met Ser Asp Ala Phe Ser Gln Ser Lys Ala
305                 310                 315                 320
Asp Phe Ser Gly Met Ser Ser Ala Arg Asn Leu Phe Leu Ser Asn Val
                325                 330                 335
Phe His Lys Ala Phe Val Glu Ile Asn Glu Gln Gly Thr Glu Ala Ala
            340                 345                 350
Ala Gly Ser Gly Ser Glu Ile Asp Ile Arg Ile Arg Val Pro Ser Ile
        355                 360                 365
Glu Phe Asn Ala Asn His Pro Phe Leu Phe Phe Ile Arg His Asn Lys
    370                 375                 380
Thr Asn Thr Ile Leu Phe Tyr Gly Arg Leu Cys Ser Pro
385                 390                 395
```

<210> 19
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<223> Epipen SERPINB11

<400> 19

```
Met Gly Ser Leu Ser Thr Ala Asn Val Glu Phe Cys Leu Asp Val Phe
 1               5                  10                  15
Lys Glu Leu Asn Ser Asn Asn Ile Gly Asp Asn Ile Phe Phe Ser Ser
            20                  25                  30
Leu Ser Leu Leu Tyr Ala Leu Ser Met Val Leu Leu Gly Ala Arg Gly
        35                  40                  45
Glu Thr Ala Glu Gln Leu Glu Lys Val Leu His Phe Ser His Thr Val
    50                  55                  60
Asp Ser Leu Lys Pro Gly Phe Lys Asp Ser Pro Lys Cys Ser Gln Ala
65                  70                  75                  80
Gly Arg Ile His Ser Glu Phe Gly Val Glu Phe Ser Gln Ile Asn Gln
                85                  90                  95
Pro Asp Ser Asn Cys Thr Leu Ser Ile Ala Asn Arg Leu Tyr Gly Thr
            100                 105                 110
Lys Thr Met Ala Phe His Gln Gln Tyr Leu Ser Cys Ser Glu Lys Trp
        115                 120                 125
Tyr Gln Ala Arg Leu Gln Thr Val Asp Phe Glu Gln Ser Thr Glu Glu
    130                 135                 140
Thr Arg Lys Met Ile Asn Ala Trp Val Glu Asn Lys Thr Asn Gly Lys
145                 150                 155                 160
Val Ala Asn Leu Phe Gly Lys Ser Thr Ile Asp Pro Ser Ser Val Met
                165                 170                 175
Val Leu Val Asn Ile Ile Tyr Phe Lys Gly Gln Arg Gln Asn Lys Phe
            180                 185                 190
Gln Val Arg Glu Thr Val Lys Ser Pro Phe Gln Leu Ser Glu Gly Lys
        195                 200                 205
Asn Val Thr Val Glu Met Met Tyr Gln Ile Gly Thr Phe Lys Leu Ala
    210                 215                 220
Phe Val Lys Glu Pro Gln Met Gln Val Leu Glu Leu Pro Tyr Val Asn
225                 230                 235                 240
Asn Lys Leu Ser Met Ile Ile Leu Leu Pro Val Gly Ile Ala Asn Leu
                245                 250                 255
Lys Gln Ile Glu Lys Gln Leu Asn Ser Gly Thr Phe His Glu Trp Thr
```

```
            260                 265                 270
Ser Ser Ser Asn Met Met Glu Arg Glu Val Glu Val His Leu Pro Arg
        275                 280                 285
Phe Lys Leu Glu Ile Lys Tyr Glu Leu Asn Ser Leu Leu Lys Pro Leu
    290                 295                 300
Gly Val Thr Asp Leu Phe Asn Gln Val Lys Ala Asp Leu Ser Gly Met
305                 310                 315                 320
Ser Pro Thr Lys Gly Leu Tyr Leu Ser Lys Ala Ile His Lys Ser Tyr
                325                 330                 335
Leu Asp Val Ser Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Asp
            340                 345                 350
Ser Ile Ala Val Lys Ser Leu Pro Met Arg Ala Gln Phe Lys Ala Asn
        355                 360                 365
His Pro Phe Leu Phe Phe Ile Arg His Thr His Thr Asn Thr Ile Leu
    370                 375                 380
Phe Cys Gly Lys Leu Ala Ser Pro
385                 390
```

<210> 20
<211> 405
<212> PRT
<213> Homo sapiens

<220>
<223> Yukopin SERPINB12

<400> 20

```
Met Asp Ser Leu Val Thr Ala Asn Thr Lys Phe Cys Phe Asp Leu Phe
 1               5                  10                  15
Gln Glu Ile Gly Lys Asp Asp Arg His Lys Asn Ile Phe Phe Ser Pro
            20                  25                  30
Leu Ser Leu Ser Ala Ala Leu Gly Met Val Arg Leu Gly Ala Arg Ser
        35                  40                  45
Asp Ser Ala His Gln Ile Asp Glu Val Leu His Phe Asn Glu Phe Ser
    50                  55                  60
Gln Asn Glu Ser Lys Glu Pro Asp Pro Cys Leu Lys Ser Asn Lys Gln
65                  70                  75                  80
Lys Ala Gly Ser Leu Asn Asn Glu Ser Gly Leu Val Ser Cys Tyr Phe
                85                  90                  95
Gly Gln Leu Leu Ser Lys Leu Asp Arg Ile Lys Thr Asp Tyr Thr Leu
            100                 105                 110
Ser Ile Ala Asn Arg Leu Tyr Gly Glu Gln Glu Phe Pro Ile Cys Gln
        115                 120                 125
Glu Tyr Leu Asp Gly Val Ile Gln Phe Tyr His Thr Thr Ile Glu Ser
    130                 135                 140
Val Asp Phe Gln Lys Asn Pro Glu Lys Ser Arg Gln Glu Ile Asn Phe
145                 150                 155                 160
Trp Val Glu Cys Gln Ser Gln Gly Lys Ile Lys Glu Leu Phe Ser Lys
                165                 170                 175
Asp Ala Ile Asn Ala Glu Thr Val Leu Val Leu Val Asn Ala Val Tyr
            180                 185                 190
Phe Lys Ala Lys Trp Glu Thr Tyr Phe Asp His Glu Asn Thr Val Asp
        195                 200                 205
Ala Pro Phe Cys Leu Asn Ala Asn Glu Asn Lys Ser Val Lys Met Met
    210                 215                 220
Thr Gln Lys Gly Leu Tyr Arg Ile Gly Phe Ile Glu Glu Val Lys Ala
```

225 230 235 240
Gln Ile Leu Glu Met Arg Tyr Thr Lys Gly Lys Leu Ser Met Phe Val
245 250 255
Leu Leu Pro Ser His Ser Lys Asp Asn Leu Lys Gly Leu Glu Glu Leu
260 265 270
Glu Arg Lys Ile Thr Tyr Glu Lys Met Val Ala Trp Ser Ser Ser Glu
275 280 285
Asn Met Ser Glu Glu Ser Val Val Leu Ser Phe Pro Arg Phe Thr Leu
290 295 300
Glu Asp Ser Tyr Asp Leu Asn Ser Ile Leu Gln Asp Met Gly Ile Thr
305 310 315 320
Asp Ile Phe Asp Glu Thr Arg Ala Asp Leu Thr Gly Ile Ser Pro Ser
325 330 335
Pro Asn Leu Tyr Leu Ser Lys Ile Ile His Lys Thr Phe Val Glu Val
340 345 350
Asp Glu Asn Gly Thr Gln Ala Ala Ala Ala Thr Gly Ala Val Val Ser
355 360 365
Glu Arg Ser Leu Arg Ser Trp Val Glu Phe Asn Ala Asn His Pro Phe
370 375 380
Leu Phe Phe Ile Arg His Asn Lys Thr Gln Thr Ile Leu Phe Tyr Gly
385 390 395 400
Arg Val Cys Ser Pro
405

<210> 21
<211> 391
<212> PRT
<213> Homo sapiens

<220>
<223> Headpin SERPINB13

<400> 21
Met Asp Ser Leu Gly Ala Val Ser Thr Arg Leu Gly Phe Asp Leu Phe
1 5 10 15
Lys Glu Leu Lys Lys Thr Asn Asp Gly Asn Ile Phe Phe Ser Pro Val
20 25 30
Gly Ile Leu Thr Ala Ile Gly Met Val Leu Leu Gly Thr Arg Gly Ala
35 40 45
Thr Ala Ser Gln Leu Glu Glu Val Phe His Ser Glu Lys Glu Thr Lys
50 55 60
Ser Ser Arg Ile Lys Ala Glu Glu Lys Glu Val Ile Glu Asn Thr Glu
65 70 75 80
Ala Val His Gln Gln Phe Gln Lys Phe Leu Thr Glu Ile Ser Lys Leu
85 90 95
Thr Asn Asp Tyr Glu Leu Asn Ile Thr Asn Arg Leu Phe Gly Glu Lys
100 105 110
Thr Tyr Leu Phe Leu Gln Lys Tyr Leu Asp Tyr Val Glu Lys Tyr Tyr
115 120 125
His Ala Ser Leu Glu Pro Val Asp Phe Val Asn Ala Ala Asp Glu Ser
130 135 140
Arg Lys Lys Ile Asn Ser Trp Val Glu Ser Lys Thr Asn Glu Lys Ile
145 150 155 160
Lys Asp Leu Phe Pro Asp Gly Ser Ile Ser Ser Ser Thr Lys Leu Val
165 170 175
Leu Val Asn Met Val Tyr Phe Lys Gly Gln Trp Asp Arg Glu Phe Lys

```
                180                 185                 190
Lys Glu Asn Thr Lys Glu Glu Lys Phe Trp Met Asn Lys Ser Thr Ser
        195                 200                 205
Lys Ser Val Gln Met Met Thr Gln Ser His Ser Phe Ser Phe Thr Phe
    210                 215                 220
Leu Glu Asp Leu Gln Ala Lys Ile Leu Gly Ile Pro Tyr Lys Asn Asn
225                 230                 235                 240
Asp Leu Ser Met Phe Val Leu Leu Pro Asn Asp Ile Asp Gly Leu Glu
                245                 250                 255
Lys Ile Ile Asp Lys Ile Ser Pro Glu Lys Leu Val Glu Trp Thr Ser
            260                 265                 270
Pro Gly His Met Glu Glu Arg Lys Val Asn Leu His Leu Pro Arg Phe
        275                 280                 285
Glu Val Glu Asp Gly Tyr Asp Leu Glu Ala Val Leu Ala Ala Met Gly
    290                 295                 300
Met Gly Asp Ala Phe Ser Glu His Lys Ala Asp Tyr Ser Gly Met Ser
305                 310                 315                 320
Ser Gly Ser Gly Leu Tyr Ala Gln Lys Phe Leu His Ser Ser Phe Val
                325                 330                 335
Ala Val Thr Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Gly Ile Gly
            340                 345                 350
Phe Thr Val Thr Ser Ala Pro Gly His Glu Asn Val His Cys Asn His
        355                 360                 365
Pro Phe Leu Phe Phe Ile Arg His Asn Glu Ser Asn Ser Ile Leu Phe
    370                 375                 380
Phe Gly Arg Phe Ser Ser Pro
385                 390
```

<210> 22
<211> 390
<212> PRT
<213> Homo sapiens

<220>
<223> Squamous cell carcinoma antigen 1 SERPINB3

<400> 22

```
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1               5                  10                  15
Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
            20                  25                  30
Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
        35                  40                  45
Thr Ala Gln Gln Ile Lys Lys Val Leu His Phe Asp Gln Val Thr Glu
    50                  55                  60
Asn Thr Thr Gly Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65                  70                  75                  80
Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
                85                  90                  95
Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
            100                 105                 110
Tyr Leu Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
        115                 120                 125
Thr Ser Val Glu Ser Val Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
    130                 135                 140
Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
```

```
145                 150                 155                 160
Asn Leu Ile Pro Glu Gly Asn Ile Gly Ser Asn Thr Thr Leu Val Leu
                165                 170                 175
Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Lys Lys Phe Asn Lys
            180                 185                 190
Glu Asp Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
        195                 200                 205
Ser Ile Gln Met Met Arg Gln Tyr Thr Ser Phe His Phe Ala Ser Leu
    210                 215                 220
Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225                 230                 235                 240
Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
                245                 250                 255
Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
            260                 265                 270
Gln Asn Met Arg Glu Thr Arg Val Asp Leu His Leu Pro Arg Phe Lys
        275                 280                 285
Val Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290                 295                 300
Val Asp Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Gly Ser
305                 310                 315                 320
Arg Gly Leu Val Leu Ser Gly Val Leu His Lys Ala Phe Val Glu Val
                325                 330                 335
Thr Glu Glu Gly Ala Glu Ala Ala Ala Ala Thr Ala Val Val Gly Phe
            340                 345                 350
Gly Ser Ser Pro Thr Ser Thr Asn Glu Glu Phe His Cys Asn His Pro
        355                 360                 365
Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
    370                 375                 380
Gly Arg Phe Ser Ser Pro
385                 390
```

<210> 23
<211> 390
<212> PRT
<213> Homo sapiens

<220>
<223> Squamous cell carcinoma antigen 2 SERPINB4

<400> 23

```
Met Asn Ser Leu Ser Glu Ala Asn Thr Lys Phe Met Phe Asp Leu Phe
 1               5                  10                  15
Gln Gln Phe Arg Lys Ser Lys Glu Asn Asn Ile Phe Tyr Ser Pro Ile
            20                  25                  30
Ser Ile Thr Ser Ala Leu Gly Met Val Leu Leu Gly Ala Lys Asp Asn
        35                  40                  45
Thr Ala Gln Gln Ile Ser Lys Val Leu His Phe Asp Gln Val Thr Glu
    50                  55                  60
Asn Thr Thr Glu Lys Ala Ala Thr Tyr His Val Asp Arg Ser Gly Asn
65                  70                  75                  80
Val His His Gln Phe Gln Lys Leu Leu Thr Glu Phe Asn Lys Ser Thr
                85                  90                  95
Asp Ala Tyr Glu Leu Lys Ile Ala Asn Lys Leu Phe Gly Glu Lys Thr
            100                 105                 110
Tyr Gln Phe Leu Gln Glu Tyr Leu Asp Ala Ile Lys Lys Phe Tyr Gln
```

```
        115                 120                 125
Thr Ser Val Glu Ser Thr Asp Phe Ala Asn Ala Pro Glu Glu Ser Arg
    130                 135                 140
Lys Lys Ile Asn Ser Trp Val Glu Ser Gln Thr Asn Glu Lys Ile Lys
145                 150                 155                 160
Asn Leu Phe Pro Asp Gly Thr Ile Gly Asn Asp Thr Thr Leu Val Leu
                165                 170                 175
Val Asn Ala Ile Tyr Phe Lys Gly Gln Trp Glu Asn Lys Phe Lys Lys
            180                 185                 190
Glu Asn Thr Lys Glu Glu Lys Phe Trp Pro Asn Lys Asn Thr Tyr Lys
        195                 200                 205
Ser Val Gln Met Met Arg Gln Tyr Asn Ser Phe Asn Phe Ala Leu Leu
    210                 215                 220
Glu Asp Val Gln Ala Lys Val Leu Glu Ile Pro Tyr Lys Gly Lys Asp
225                 230                 235                 240
Leu Ser Met Ile Val Leu Leu Pro Asn Glu Ile Asp Gly Leu Gln Lys
                245                 250                 255
Leu Glu Glu Lys Leu Thr Ala Glu Lys Leu Met Glu Trp Thr Ser Leu
            260                 265                 270
Gln Asn Met Arg Glu Thr Cys Val Asp Leu His Leu Pro Arg Phe Lys
        275                 280                 285
Met Glu Glu Ser Tyr Asp Leu Lys Asp Thr Leu Arg Thr Met Gly Met
    290                 295                 300
Val Asn Ile Phe Asn Gly Asp Ala Asp Leu Ser Gly Met Thr Trp Ser
305                 310                 315                 320
His Gly Leu Ser Val Ser Lys Val Leu His Lys Ala Phe Val Glu Val
                325                 330                 335
Thr Glu Glu Gly Val Glu Ala Ala Ala Ala Thr Ala Val Val Val Val
            340                 345                 350
Glu Leu Ser Ser Pro Ser Thr Asn Glu Glu Phe Cys Cys Asn His Pro
        355                 360                 365
Phe Leu Phe Phe Ile Arg Gln Asn Lys Thr Asn Ser Ile Leu Phe Tyr
    370                 375                 380
Gly Arg Phe Ser Ser Pro
385                 390
```

<210> 24
<211> 380
<212> PRT
<213> Homo sapiens

<220>
<223> Megsin SERPINB7

<400> 24

```
Met Ala Ser Leu Ala Ala Ala Asn Ala Glu Phe Cys Phe Asn Leu Phe
 1               5                  10                  15
Arg Glu Met Asp Asp Asn Gln Gly Asn Gly Asn Val Phe Phe Ser Ser
            20                  25                  30
Leu Ser Leu Phe Ala Ala Leu Ala Leu Val Arg Leu Gly Ala Gln Asp
        35                  40                  45
Asp Ser Leu Ser Gln Ile Asp Lys Leu Leu His Val Asn Thr Ala Ser
    50                  55                  60
Gly Tyr Gly Asn Ser Ser Asn Ser Gln Ser Gly Leu Gln Ser Gln Leu
65                  70                  75                  80
Lys Arg Val Phe Ser Asp Ile Asn Ala Ser His Lys Asp Tyr Asp Leu
```

```
                85                  90                  95
Ser Ile Val Asn Gly Leu Phe Ala Glu Lys Val Tyr Gly Phe His Lys
            100                 105                 110
Asp Tyr Ile Glu Cys Ala Glu Lys Leu Tyr Asp Ala Lys Val Glu Arg
        115                 120                 125
Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn Ile Asn Lys
    130                 135                 140
Trp Val Glu Asn Glu Thr His Gly Lys Ile Lys Asn Val Ile Gly Glu
145                 150                 155                 160
Gly Gly Ile Ser Ser Ser Ala Val Met Val Leu Val Asn Ala Val Tyr
                165                 170                 175
Phe Lys Gly Lys Trp Gln Ser Ala Phe Thr Lys Ser Glu Thr Ile Asn
            180                 185                 190
Cys His Phe Lys Ser Pro Lys Cys Ser Gly Lys Ala Val Ala Met Met
        195                 200                 205
His Gln Glu Arg Lys Phe Asn Leu Ser Val Ile Glu Asp Pro Ser Met
    210                 215                 220
Lys Ile Leu Glu Leu Arg Tyr Asn Gly Gly Ile Asn Met Tyr Val Leu
225                 230                 235                 240
Leu Pro Glu Asn Asp Leu Ser Glu Ile Glu Asn Lys Leu Thr Phe Gln
                245                 250                 255
Asn Leu Met Glu Trp Thr Asn Pro Arg Arg Met Thr Ser Lys Tyr Val
            260                 265                 270
Glu Val Phe Phe Pro Gln Phe Lys Ile Glu Lys Asn Tyr Glu Met Lys
        275                 280                 285
Gln Tyr Leu Arg Ala Leu Gly Leu Lys Asp Ile Phe Asp Glu Ser Lys
    290                 295                 300
Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
305                 310                 315                 320
Met Met His Lys Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala
                325                 330                 335
Thr Ala Ala Thr Gly Ser Asn Ile Val Glu Lys Gln Leu Pro Gln Ser
            340                 345                 350
Thr Leu Phe Arg Ala Asp His Pro Phe Leu Phe Val Ile Arg Lys Asp
        355                 360                 365
Asp Ile Ile Leu Phe Ser Gly Lys Val Ser Cys Pro
    370                 375                 380
```

<210> 25
<211> 374
<212> PRT
<213> Homo sapiens

<220>
<223> Cytoplasmic antiproteinase 2 SERPINB8

<400> 25

```
Met Asp Asp Leu Cys Glu Ala Asn Gly Thr Phe Ala Ile Ser Leu Phe
 1                5                  10                  15
Lys Ile Leu Gly Glu Glu Asp Asn Ser Arg Asn Val Phe Phe Ser Pro
            20                  25                  30
Met Ser Ile Ser Ser Ala Leu Ala Met Val Phe Met Gly Ala Lys Gly
        35                  40                  45
Ser Thr Ala Ala Gln Met Ser Gln Ala Leu Cys Leu Tyr Lys Asp Gly
    50                  55                  60
```

```
Asp Ile His Arg Gly Phe Gln Ser Leu Leu Ser Glu Val Asn Arg Thr
65                  70                  75                  80
Gly Thr Gln Tyr Leu Leu Arg Thr Ala Asn Arg Leu Phe Gly Glu Lys
                85                  90                  95
Thr Cys Asp Phe Leu Pro Asp Phe Lys Glu Tyr Cys Gln Lys Phe Tyr
            100                 105                 110
Gln Ala Glu Leu Glu Glu Leu Ser Phe Ala Glu Asp Thr Glu Glu Cys
        115                 120                 125
Arg Lys His Ile Asn Asp Trp Val Ala Glu Lys Thr Glu Gly Lys Ile
    130                 135                 140
Ser Glu Val Leu Asp Ala Gly Thr Val Asp Pro Leu Thr Lys Leu Val
145                 150                 155                 160
Leu Val Asn Ala Ile Tyr Phe Lys Gly Lys Trp Asn Glu Gln Phe Asp
                165                 170                 175
Arg Lys Tyr Thr Arg Gly Met Leu Phe Lys Thr Asn Glu Glu Lys Lys
            180                 185                 190
Thr Val Gln Met Met Phe Lys Glu Ala Lys Phe Lys Met Gly Tyr Ala
        195                 200                 205
Asp Glu Val His Thr Gln Val Leu Glu Leu Pro Tyr Val Glu Glu Glu
    210                 215                 220
Leu Ser Met Val Ile Leu Leu Pro Asp Asp Asn Thr Asp Leu Ala Val
225                 230                 235                 240
Val Glu Lys Ala Leu Thr Tyr Glu Lys Phe Lys Ala Trp Thr Asn Ser
                245                 250                 255
Glu Lys Leu Thr Lys Ser Lys Val Gln Val Phe Leu Pro Arg Leu Lys
            260                 265                 270
Leu Glu Glu Ser Tyr Asp Leu Glu Pro Phe Leu Arg Arg Leu Gly Met
        275                 280                 285
Ile Asp Ala Phe Asp Glu Ala Lys Ala Asp Phe Ser Gly Met Ser Thr

    290                 295                 300
Glu Lys Asn Val Pro Leu Ser Lys Val Ala His Lys Cys Phe Val Glu
305                 310                 315                 320
Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Val Val Arg
                325                 330                 335
Asn Ser Arg Cys Ser Arg Met Glu Pro Arg Phe Cys Ala Asp His Pro
            340                 345                 350
Phe Leu Phe Phe Ile Arg Arg His Lys Thr Asn Cys Ile Leu Phe Cys
        355                 360                 365
Gly Arg Phe Ser Ser Pro
    370
```

<210> 26
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<223> Cytoplasmic antiproteinase 3 SERPINB9

<400> 26

```
Met Glu Thr Leu Ser Asn Ala Ser Gly Thr Phe Ala Ile Arg Leu Leu
 1               5                  10                  15
Lys Ile Leu Cys Gln Asp Asn Pro Ser His Asn Val Phe Cys Ser Pro
            20                  25                  30
Val Ser Ile Ser Ser Ala Leu Ala Met Val Leu Leu Gly Ala Lys Gly
```

```
        35                  40                  45
Asn Thr Ala Thr Gln Met Ala Gln Ala Leu Ser Leu Asn Thr Glu Glu
    50                  55                  60
Asp Ile His Arg Ala Phe Gln Ser Leu Leu Thr Glu Val Asn Lys Ala
65                  70                  75                  80
Gly Thr Gln Tyr Leu Leu Arg Thr Ala Asn Arg Leu Phe Gly Glu Lys
                85                  90                  95
Thr Cys Gln Phe Leu Ser Thr Phe Lys Glu Ser Cys Leu Gln Phe Tyr
            100                 105                 110
His Ala Glu Leu Lys Glu Leu Ser Phe Ile Arg Ala Ala Glu Glu Ser
        115                 120                 125
Arg Lys His Ile Asn Thr Trp Val Ser Lys Lys Thr Glu Gly Lys Ile
    130                 135                 140
Glu Glu Leu Leu Pro Gly Ser Ser Ile Asp Ala Glu Thr Arg Leu Val
145                 150                 155                 160
Leu Val Asn Ala Ile Tyr Phe Lys Gly Lys Trp Asn Glu Pro Phe Asp
                165                 170                 175
Glu Thr Tyr Thr Arg Glu Met Pro Phe Lys Ile Asn Gln Glu Glu Gln
            180                 185                 190
Arg Pro Val Gln Met Met Tyr Gln Glu Ala Thr Phe Lys Leu Ala His
        195                 200                 205
Val Gly Glu Val Arg Ala Gln Leu Leu Glu Leu Pro Tyr Ala Arg Lys
    210                 215                 220
Glu Leu Ser Leu Leu Val Leu Leu Pro Asp Asp Gly Val Glu Leu Ser
225                 230                 235                 240
Thr Val Glu Lys Ser Leu Thr Phe Glu Lys Leu Thr Ala Trp Thr Lys
                245                 250                 255
Pro Asp Cys Met Lys Ser Thr Glu Val Glu Val Leu Leu Pro Lys Phe
            260                 265                 270
Lys Leu Gln Glu Asp Tyr Asp Met Glu Ser Val Leu Arg His Leu Gly
        275                 280                 285
Ile Val Asp Ala Phe Gln Gln Gly Lys Ala Asp Leu Ser Ala Met Ser
    290                 295                 300
Ala Glu Arg Asp Leu Cys Leu Ser Lys Phe Val His Lys Ser Phe Val
305                 310                 315                 320
Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Ser Ser Cys Phe
                325                 330                 335
Val Val Ala Glu Cys Cys Met Glu Ser Gly Pro Arg Phe Cys Ala Asp
            340                 345                 350
His Pro Phe Leu Phe Phe Ile Arg His Asn Arg Ala Asn Ser Ile Leu
        355                 360                 365
Phe Cys Gly Arg Phe Ser Ser Pro
    370                 375
```

<210> 27
<211> 376
<212> PRT
<213> Homo sapiens

<220>
<223> Placental thrombin inhibitor SERPINB6

<400> 27

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

```
            20                  25                  30
Ser Met Ser Cys Ala Leu Ala Met Val Tyr Met Gly Ala Lys Gly Asn
        35                  40                  45
Thr Ala Ala Gln Met Ala Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly
    50                  55                  60
Gly Gly Asp Ile His Gln Gly Phe Gln Ser Leu Leu Thr Glu Val Asn
65                  70                  75                  80
Lys Thr Gly Thr Gln Tyr Leu Leu Arg Val Ala Asn Arg Leu Phe Gly
                85                  90                  95
Glu Lys Ser Cys Asp Phe Leu Ser Ser Phe Arg Asp Ser Cys Gln Lys
            100                 105                 110
Phe Tyr Gln Ala Glu Met Glu Glu Leu Asp Phe Ile Ser Ala Val Glu
        115                 120                 125
Lys Ser Arg Lys His Ile Asn Thr Trp Val Ala Glu Lys Thr Glu Gly
    130                 135                 140
Lys Ile Ala Glu Leu Leu Ser Pro Gly Ser Val Asp Pro Leu Thr Arg
145                 150                 155                 160
Leu Val Leu Val Asn Ala Val Tyr Phe Arg Gly Asn Trp Asp Glu Gln
                165                 170                 175
Phe Asp Lys Glu Asn Thr Glu Glu Arg Leu Phe Lys Val Ser Lys Asn
            180                 185                 190
Glu Glu Lys Pro Val Gln Met Met Phe Lys Gln Ser Thr Phe Lys Lys
        195                 200                 205
Thr Tyr Ile Gly Glu Ile Phe Thr Gln Ile Leu Val Leu Pro Tyr Val
    210                 215                 220
Gly Lys Glu Leu Asn Met Ile Ile Met Leu Pro Asp Glu Thr Thr Asp
225                 230                 235                 240
Leu Arg Thr Val Glu Lys Glu Leu Thr Tyr Glu Lys Phe Val Glu Trp
                245                 250                 255
Thr Arg Leu Asp Met Met Asp Glu Glu Glu Val Glu Val Ser Leu Pro
            260                 265                 270
Arg Phe Lys Leu Glu Glu Ser Tyr Asp Met Glu Ser Val Leu Arg Asn
        275                 280                 285
Leu Gly Met Thr Asp Ala Phe Glu Leu Gly Lys Ala Asp Phe Ser Gly
    290                 295                 300
Met Ser Gln Thr Asp Leu Ser Leu Ser Lys Val Val His Lys Ser Phe
305                 310                 315                 320
Val Glu Val Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Ala
                325                 330                 335
Ile Met Met Met Arg Cys Ala Arg Phe Val Pro Arg Phe Cys Ala Asp
            340                 345                 350
His Pro Phe Leu Phe Phe Ile Gln His Ser Lys Thr Asn Gly Ile Leu
        355                 360                 365
Phe Cys Gly Arg Phe Ser Ser Pro
    370                 375
```

<210> 28
<211> 485
<212> PRT
<213> Homo sapiens

<220>
<223> Angiotensinogen precursor SERPINA8

<400> 28
Met Arg Lys Arg Ala Pro Gln Ser Glu Met Ala Pro Ala Gly Val Ser

```
 1               5                  10                  15
Leu Arg Ala Thr Ile Leu Cys Leu Leu Ala Trp Ala Gly Leu Ala Ala
            20                  25                  30
Gly Asp Arg Val Tyr Ile His Pro Phe His Leu Val Ile His Asn Glu
        35                  40                  45
Ser Thr Cys Glu Gln Leu Ala Lys Ala Asn Ala Gly Lys Pro Lys Asp
    50                  55                  60
Pro Thr Phe Ile Pro Ala Pro Ile Gln Ala Lys Thr Ser Pro Val Asp
65                  70                  75                  80
Glu Lys Ala Leu Gln Asp Gln Leu Val Leu Val Ala Ala Lys Leu Asp
                85                  90                  95
Thr Glu Asp Lys Leu Arg Ala Ala Met Val Gly Met Leu Ala Asn Phe
            100                 105                 110
Leu Gly Phe Arg Ile Tyr Gly Met His Ser Glu Leu Trp Gly Val Val
        115                 120                 125
His Gly Ala Thr Val Leu Ser Pro Thr Ala Val Phe Gly Thr Leu Ala
    130                 135                 140
Ser Leu Tyr Leu Gly Ala Leu Asp His Thr Ala Asp Arg Leu Gln Ala
145                 150                 155                 160
Ile Leu Gly Val Pro Trp Lys Asp Lys Asn Cys Thr Ser Arg Leu Asp
                165                 170                 175
Ala His Lys Val Leu Ser Ala Leu Gln Ala Val Gln Gly Leu Leu Val
            180                 185                 190
Ala Gln Gly Arg Ala Asp Ser Gln Ala Gln Leu Leu Leu Ser Thr Val
        195                 200                 205
Val Gly Val Phe Thr Ala Pro Gly Leu His Leu Lys Gln Pro Phe Val
    210                 215                 220
Gln Gly Leu Ala Leu Tyr Thr Pro Val Val Leu Pro Arg Ser Leu Asp
225                 230                 235                 240
Phe Thr Glu Leu Asp Val Ala Ala Glu Lys Ile Asp Arg Phe Met Gln
                245                 250                 255
Ala Val Thr Gly Trp Lys Thr Gly Cys Ser Leu Met Gly Ala Ser Val
            260                 265                 270
Asp Ser Thr Leu Ala Phe Asn Thr Tyr Val His Phe Gln Gly Lys Met
        275                 280                 285
Lys Gly Phe Ser Leu Leu Ala Glu Pro Gln Glu Phe Trp Val Asp Asn
    290                 295                 300
Ser Thr Ser Val Ser Val Pro Met Leu Ser Gly Met Gly Thr Phe Gln
305                 310                 315                 320
His Trp Ser Asp Ile Gln Asp Asn Phe Ser Val Thr Gln Val Pro Phe
                325                 330                 335
Thr Glu Ser Ala Cys Leu Leu Leu Ile Gln Pro His Tyr Ala Ser Asp
            340                 345                 350
Leu Asp Lys Val Glu Gly Leu Thr Phe Gln Gln Asn Ser Leu Asn Trp
        355                 360                 365
Met Lys Lys Leu Ser Pro Arg Thr Ile His Leu Thr Met Pro Gln Leu
    370                 375                 380
Val Leu Gln Gly Ser Tyr Asp Leu Gln Asp Leu Leu Ala Gln Ala Glu
385                 390                 395                 400
Leu Pro Ala Ile Leu His Thr Glu Leu Asn Leu Gln Lys Leu Ser Asn
                405                 410                 415
Asp Arg Ile Arg Val Gly Glu Val Leu Asn Ser Ile Phe Phe Glu Leu
            420                 425                 430
Glu Ala Asp Glu Arg Glu Pro Thr Glu Ser Thr Gln Gln Leu Asn Lys
        435                 440                 445
Pro Glu Val Leu Glu Val Thr Leu Asn Arg Pro Phe Leu Phe Ala Val
    450                 455                 460
```

```
Tyr Asp Gln Ser Ala Thr Ala Leu His Phe Leu Gly Arg Val Ala Asn
465                 470                 475                 480
Pro Leu Ser Thr Ala
                485
```

<210> 29
<211> 405
<212> PRT
<213> Homo sapiens

<220>
<223> Corticosteroid-binding globulin precursor SERPINA6

<400> 29

```
Met Pro Leu Leu Leu Tyr Thr Cys Leu Leu Trp Leu Pro Thr Ser Gly
 1               5                  10                  15
Leu Trp Thr Val Gln Ala Met Asp Pro Asn Ala Ala Tyr Val Asn Met
            20                  25                  30
Ser Asn His His Arg Gly Leu Ala Ser Ala Asn Val Asp Phe Ala Phe
        35                  40                  45
Ser Leu Tyr Lys His Leu Val Ala Leu Ser Pro Lys Lys Asn Ile Phe
    50                  55                  60
Ile Ser Pro Val Ser Ile Ser Met Ala Leu Ala Met Leu Ser Leu Gly
65                  70                  75                  80
Thr Cys Gly His Thr Arg Ala Gln Leu Leu Gln Gly Leu Gly Phe Asn
                85                  90                  95
Leu Thr Glu Arg Ser Glu Thr Glu Ile His Gln Gly Phe Gln His Leu
            100                 105                 110
His Gln Leu Phe Ala Lys Ser Asp Thr Ser Leu Glu Met Thr Met Gly
        115                 120                 125
Asn Ala Leu Phe Leu Asp Gly Ser Leu Glu Leu Leu Glu Ser Phe Ser
    130                 135                 140
Ala Asp Ile Lys His Tyr Tyr Glu Ser Glu Val Leu Ala Met Asn Phe
145                 150                 155                 160
Gln Asp Trp Ala Thr Ala Ser Arg Gln Ile Asn Ser Tyr Val Lys Asn
                165                 170                 175
Lys Thr Gln Gly Lys Ile Val Asp Leu Phe Ser Gly Leu Asp Ser Pro
            180                 185                 190
Ala Ile Leu Val Leu Val Asn Tyr Ile Phe Phe Lys Gly Thr Trp Thr
        195                 200                 205
Gln Pro Phe Asp Leu Ala Ser Thr Arg Glu Glu Asn Phe Tyr Val Asp
    210                 215                 220
Glu Thr Thr Val Val Lys Val Pro Met Met Leu Gln Ser Ser Thr Ile
225                 230                 235                 240
Ser Tyr Leu His Asp Ser Glu Leu Pro Cys Gln Leu Val Gln Met Asn
                245                 250                 255
Tyr Val Gly Asn Gly Thr Val Phe Phe Ile Leu Pro Asp Lys Gly Lys
            260                 265                 270
Met Asn Thr Val Ile Ala Ala Leu Ser Arg Asp Thr Ile Asn Arg Trp
        275                 280                 285
Ser Ala Gly Leu Thr Ser Ser Gln Val Asp Leu Tyr Ile Pro Lys Val
    290                 295                 300
Thr Ile Ser Gly Val Tyr Asp Leu Gly Asp Val Leu Glu Glu Met Gly
305                 310                 315                 320
Ile Ala Asp Leu Phe Thr Asn Gln Ala Asn Phe Ser Arg Ile Thr Gln
                325                 330                 335
```

```
Asp Ala Gln Leu Lys Ser Ser Lys Val Val His Lys Ala Val Leu Gln
            340                 345                 350
Leu Asn Glu Glu Gly Val Asp Thr Ala Gly Ser Thr Gly Val Thr Leu
        355                 360                 365
Asn Leu Thr Ser Lys Pro Ile Ile Leu Arg Phe Asn Gln Pro Phe Ile
    370                 375                 380
Ile Met Ile Phe Asp His Phe Thr Trp Ser Ser Leu Phe Leu Ala Arg
385                 390                 395                 400
Val Met Asn Pro Val
                405
```

<210> 30
<211> 417
<212> PRT
<213> Homo sapiens

<220>
<223> 47 kDa heat shock protein precursor SERPINH1

<400> 30

```
Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
 1               5                  10                  15
Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
            20                  25                  30
Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
        35                  40                  45
Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
    50                  55                  60
Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
65                  70                  75                  80
Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
                85                  90                  95
Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
            100                 105                 110
Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
        115                 120                 125
Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
    130                 135                 140
Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
145                 150                 155                 160
Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
                165                 170                 175
Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
            180                 185                 190
Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
        195                 200                 205
Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
    210                 215                 220
Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly
225                 230                 235                 240
Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
                245                 250                 255
Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
            260                 265                 270
His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
        275                 280                 285
```

```
Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
    290                 295                 300
Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
305                 310                 315                 320
Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
                325                 330                 335
Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
            340                 345                 350
Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
        355                 360                 365
Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
    370                 375                 380
His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
385                 390                 395                 400
Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
                405                 410                 415
Leu
```

<210> 31
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<223> Pigment epithelium-derived factor precursor
SERPINF1

<400> 31

```
Met Gln Ala Leu Val Leu Leu Leu Cys Ile Gly Ala Leu Leu Gly His
 1               5                  10                  15
Ser Ser Cys Gln Asn Pro Ala Ser Pro Pro Glu Glu Gly Ser Pro Asp
            20                  25                  30
Pro Asp Ser Thr Gly Ala Leu Val Glu Glu Glu Asp Pro Phe Phe Lys
        35                  40                  45
Val Pro Val Asn Lys Leu Ala Ala Ala Val Ser Asn Phe Gly Tyr Asp
    50                  55                  60
Leu Tyr Arg Val Arg Ser Ser Met Ser Pro Thr Thr Asn Val Leu Leu
65                  70                  75                  80
Ser Pro Leu Ser Val Ala Thr Ala Leu Ser Ala Leu Ser Leu Gly Ala
                85                  90                  95
Glu Gln Arg Thr Glu Ser Ile Ile His Arg Ala Leu Tyr Tyr Asp Leu
            100                 105                 110
Ile Ser Ser Pro Asp Ile His Gly Thr Tyr Lys Glu Leu Leu Asp Thr
        115                 120                 125
Val Thr Ala Pro Gln Lys Asn Leu Lys Ser Ala Ser Arg Ile Val Phe
    130                 135                 140
Glu Lys Lys Leu Arg Ile Lys Ser Ser Phe Val Ala Pro Leu Glu Lys
145                 150                 155                 160
Ser Tyr Gly Thr Arg Pro Arg Val Leu Thr Gly Asn Pro Arg Leu Asp
                165                 170                 175
Leu Gln Glu Ile Asn Asn Trp Val Gln Ala Gln Met Lys Gly Lys Leu
            180                 185                 190
Ala Arg Ser Thr Lys Glu Ile Pro Asp Glu Ile Ser Ile Leu Leu Leu
        195                 200                 205
Gly Val Ala His Phe Lys Gly Gln Trp Val Thr Lys Phe Asp Ser Arg
```

```
    210                 215                 220
Lys Thr Ser Leu Glu Asp Phe Tyr Leu Asp Glu Glu Arg Thr Val Arg
225                 230                 235                 240
Val Pro Met Met Ser Asp Pro Lys Ala Val Leu Arg Tyr Gly Leu Asp
                245                 250                 255
Ser Asp Leu Ser Cys Lys Ile Ala Gln Leu Pro Leu Thr Gly Ser Met
            260                 265                 270
Ser Ile Ile Phe Phe Leu Pro Leu Lys Val Thr Gln Asn Leu Thr Leu
        275                 280                 285
Ile Glu Glu Ser Leu Thr Ser Glu Phe Ile His Asp Ile Asp Arg Glu
    290                 295                 300
Leu Lys Thr Val Gln Ala Val Leu Thr Val Pro Lys Leu Lys Leu Ser
305                 310                 315                 320
Tyr Glu Gly Glu Val Thr Lys Ser Leu Gln Glu Met Lys Leu Gln Ser
                325                 330                 335
Leu Phe Asp Ser Pro Asp Phe Ser Lys Ile Thr Gly Lys Pro Ile Lys
            340                 345                 350
Leu Thr Gln Val Glu His Arg Ala Gly Phe Glu Trp Asn Glu Asp Gly
        355                 360                 365
Ala Gly Thr Thr Pro Ser Pro Gly Leu Gln Pro Ala His Leu Thr Phe
    370                 375                 380
Pro Leu Asp Tyr His Leu Asn Gln Pro Phe Ile Phe Val Leu Arg Asp
385                 390                 395                 400
Thr Asp Thr Gly Ala Leu Leu Phe Ile Gly Lys Ile Leu Asp Pro Arg
                405                 410                 415
Gly Pro
```

<210> 32
<211> 375
<212> PRT
<213> Homo sapiens

<220>
<223> Maspin SERPINB5

```
<400> 32
Met Asp Ala Leu Gln Leu Ala Asn Ser Ala Phe Ala Val Asp Leu Phe
 1                5                  10                  15
Lys Gln Leu Cys Glu Lys Glu Pro Leu Gly Asn Val Leu Phe Ser Pro
            20                  25                  30
Ile Cys Leu Ser Thr Ser Leu Ser Leu Ala Gln Val Gly Ala Lys Gly
        35                  40                  45
Asp Thr Ala Asn Glu Ile Gly Gln Val Leu His Phe Glu Asn Val Lys

    50                  55                  60
Asp Ile Pro Phe Gly Phe Gln Thr Val Thr Ser Asp Val Asn Lys Leu
65                  70                  75                  80
Ser Ser Phe Tyr Ser Leu Lys Leu Ile Lys Arg Leu Tyr Val Asp Lys
                85                  90                  95
Ser Leu Asn Leu Ser Thr Glu Phe Ile Ser Ser Thr Lys Arg Pro Tyr
            100                 105                 110
Ala Lys Glu Leu Glu Thr Val Asp Phe Lys Asp Lys Leu Glu Glu Thr
        115                 120                 125
Lys Gly Gln Ile Asn Asn Ser Ile Lys Asp Leu Thr Asp Gly His Phe
    130                 135                 140
```

```
Glu Asn Ile Leu Ala Asp Asn Ser Val Asn Asp Gln Thr Lys Ile Leu
145                 150                 155                 160
Val Val Asn Ala Ala Tyr Phe Val Gly Lys Trp Met Lys Lys Phe Pro
                165                 170                 175
Glu Ser Glu Thr Lys Glu Cys Pro Phe Arg Leu Asn Lys Thr Asp Thr
            180                 185                 190
Lys Pro Val Gln Met Met Asn Met Glu Ala Thr Phe Cys Met Gly Asn
        195                 200                 205
Ile Asp Ser Ile Asn Cys Lys Ile Ile Glu Leu Pro Phe Gln Asn Lys
    210                 215                 220
His Leu Ser Met Phe Ile Leu Leu Pro Lys Asp Val Glu Asp Glu Ser
225                 230                 235                 240
Thr Gly Leu Glu Lys Ile Glu Lys Gln Leu Asn Ser Glu Ser Leu Ser
                245                 250                 255
Gln Trp Thr Asn Pro Ser Thr Met Ala Asn Ala Lys Val Lys Leu Ser
            260                 265                 270
Ile Pro Lys Phe Lys Val Glu Lys Met Ile Asp Pro Lys Ala Cys Leu
        275                 280                 285
Glu Asn Leu Gly Leu Lys His Ile Phe Ser Glu Asp Thr Ser Asp Phe
    290                 295                 300
Ser Gly Met Ser Glu Thr Lys Gly Val Ala Leu Ser Asn Val Ile His
305                 310                 315                 320
Lys Val Cys Leu Glu Ile Thr Glu Asp Gly Gly Asp Ser Ile Glu Val
                325                 330                 335
Pro Gly Ala Arg Ile Leu Gln His Lys Asp Glu Leu Asn Ala Asp His
            340                 345                 350
Pro Phe Ile Tyr Ile Ile Arg His Asn Lys Thr Arg Asn Ile Ile Phe
        355                 360                 365
Phe Gly Lys Phe Cys Ser Pro
    370                 375
```

<210> 33
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<223> Collagen-binding protein 2 precursor SERPINH2

<400> 33

```
Met Arg Ser Leu Leu Leu Leu Ser Ala Phe Cys Leu Leu Glu Ala Ala
 1               5                  10                  15
Leu Ala Ala Glu Val Lys Lys Pro Ala Ala Ala Ala Ala Pro Gly Thr
            20                  25                  30
Ala Glu Lys Leu Ser Pro Lys Ala Ala Thr Leu Ala Glu Arg Ser Ala
        35                  40                  45
Gly Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val
    50                  55                  60
Glu Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu
65                  70                  75                  80
Val Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val
                85                  90                  95
Leu Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly
            100                 105                 110
Glu Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp
        115                 120                 125
```

```
Lys Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp
    130                 135                 140
Asp Phe Val Arg Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys
145                 150                 155                 160
Ile Asn Phe Arg Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp
                165                 170                 175
Ala Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val
            180                 185                 190
Glu Arg Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro
        195                 200                 205
His Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe
    210                 215                 220
Met Val Thr Arg Ser Tyr Thr Val Gly Val Met Met Met His Arg Thr
225                 230                 235                 240
Gly Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Ile Val
                245                 250                 255
Glu Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro
            260                 265                 270
His His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu
        275                 280                 285
Gln Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile
    290                 295                 300
Ser Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His
305                 310                 315                 320
Leu Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp
                325                 330                 335
Leu Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe
            340                 345                 350
His Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln
        355                 360                 365
Asp Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala
    370                 375                 380
Asp His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu
385                 390                 395                 400
Leu Phe Ile Gly Arg Leu Val Arg Pro Lys Gly Asp Lys Met Arg Asp
                405                 410                 415
Glu Leu
```

<210> 34
<211> 415
<212> PRT
<213> Homo sapiens

<220>
<223> Thyroxine-binding globulin precursor SERPINA7

<400> 34

```
Met Ser Pro Phe Leu Tyr Leu Val Leu Leu Val Leu Gly Leu His Ala
 1               5                  10                  15
Thr Ile His Cys Ala Ser Pro Glu Gly Lys Val Thr Ala Cys His Ser
            20                  25                  30
Ser Gln Pro Asn Ala Thr Leu Tyr Lys Met Ser Ser Ile Asn Ala Asp
        35                  40                  45
Phe Ala Phe Asn Leu Tyr Arg Arg Phe Thr Val Glu Thr Pro Asp Lys
    50                  55                  60
```

```
Asn Ile Phe Phe Ser Pro Val Ser Ile Ser Ala Ala Leu Val Met Leu
65                  70                  75                  80
Ser Phe Gly Ala Cys Cys Ser Thr Gln Thr Glu Ile Val Glu Thr Leu
                85                  90                  95
Gly Phe Asn Leu Thr Asp Thr Pro Met Val Glu Ile Gln His Gly Phe
            100                 105                 110
Gln His Leu Ile Cys Ser Leu Asn Phe Pro Lys Lys Glu Leu Glu Leu
        115                 120                 125
Gln Ile Gly Asn Ala Leu Phe Ile Gly Lys His Leu Lys Pro Leu Ala
    130                 135                 140
Lys Phe Leu Asn Asp Val Lys Thr Leu Tyr Glu Thr Glu Val Phe Ser
145                 150                 155                 160
Thr Asp Phe Ser Asn Ile Ser Ala Ala Lys Gln Glu Ile Asn Ser His
                165                 170                 175
Val Glu Met Gln Thr Lys Gly Lys Val Val Gly Leu Ile Gln Asp Leu
            180                 185                 190
Lys Pro Asn Thr Ile Met Val Leu Val Asn Tyr Ile His Phe Lys Ala
        195                 200                 205
Gln Trp Ala Asn Pro Phe Asp Pro Ser Lys Thr Glu Asp Ser Ser Ser
    210                 215                 220
Phe Leu Ile Asp Lys Thr Thr Thr Val Gln Val Pro Met Met His Gln
225                 230                 235                 240
Met Glu Gln Tyr Tyr His Leu Val Asp Met Glu Leu Asn Cys Thr Val
                245                 250                 255
Leu Gln Met Asp Tyr Ser Lys Asn Ala Leu Ala Leu Phe Val Leu Pro
            260                 265                 270
Lys Glu Gly Gln Met Glu Ser Val Glu Ala Ala Met Ser Ser Lys Thr
        275                 280                 285
Leu Lys Lys Trp Asn Arg Leu Leu Gln Lys Gly Trp Val Asp Leu Phe
    290                 295                 300
Val Pro Lys Phe Ser Ile Ser Ala Thr Tyr Asp Leu Gly Ala Thr Leu
305                 310                 315                 320
Leu Lys Met Gly Ile Gln His Ala Tyr Ser Glu Asn Ala Asp Phe Ser
                325                 330                 335
Gly Leu Thr Glu Asp Asn Gly Leu Lys Leu Ser Asn Ala Ala His Lys
            340                 345                 350
Ala Val Leu His Ile Gly Glu Lys Gly Thr Glu Ala Ala Ala Val Pro
        355                 360                 365
Glu Val Glu Leu Ser Asp Gln Pro Glu Asn Thr Phe Leu His Pro Ile
    370                 375                 380
Ile Gln Ile Asp Arg Ser Phe Met Leu Leu Ile Leu Glu Arg Ser Thr
385                 390                 395                 400
Arg Ser Ile Leu Phe Leu Gly Lys Val Val Asn Pro Thr Glu Ala
                405                 410                 415
```

<210> 35
<211> 417
<212> PRT
<213> Homo sapiens

<220>
<223> Germinal center B-cell expressed transcript 1 protein
SERPINA9

<400> 35

```
Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys Ala
 1               5                  10                  15
Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr Pro Arg
            20                  25                  30
Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr Ser Leu Asn
        35                  40                  45
Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val Leu Glu Thr Pro
    50                  55                  60
Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val Ser Thr Ser Leu Ala
65                  70                  75                  80
Met Leu Ser Leu Gly Ala His Ser Val Thr Lys Thr Gln Ile Leu Gln
                85                  90                  95
Gly Leu Gly Phe Asn Leu Thr His Thr Pro Glu Ser Ala Ile His Gln
            100                 105                 110
Gly Phe Gln His Leu Val His Ser Leu Thr Val Pro Ser Lys Asp Leu
        115                 120                 125
Thr Leu Lys Met Gly Ser Ala Leu Phe Val Lys Lys Glu Leu Gln Leu
    130                 135                 140
Gln Ala Asn Phe Leu Gly Asn Val Lys Arg Leu Tyr Glu Ala Glu Val
145                 150                 155                 160
Phe Ser Thr Asp Phe Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn
                165                 170                 175
Ser His Val Lys Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln
            180                 185                 190
Gly Leu Asp Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe
        195                 200                 205
Lys Ala Lys Trp Glu Lys Pro Phe His Pro Glu Tyr Thr Arg Lys Asn
    210                 215                 220
Phe Pro Phe Leu Val Gly Glu Gln Val Thr Val His Val Pro Met Met
225                 230                 235                 240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn Cys
                245                 250                 255
Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe Phe Val
            260                 265                 270
Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala Leu Ser Ala
        275                 280                 285
Arg Thr Leu Arg Lys Trp Ser His Ser Leu Gln Lys Arg Trp Ile Glu
    290                 295                 300
Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser Tyr Asn Leu Glu Thr
305                 310                 315                 320
Ile Leu Pro Lys Met Gly Ile Gln Asn Ala Phe Asp Lys Asn Ala Asp
                325                 330                 335
Phe Ser Gly Ile Ala Lys Arg Asp Ser Leu Gln Val Ser Lys Ala Thr
            340                 345                 350
His Lys Ala Val Leu Asp Val Ser Glu Glu Gly Thr Glu Ala Thr Ala
        355                 360                 365
Ala Thr Thr Thr Lys Phe Ile Val Arg Ser Lys Asp Gly Pro Ser Tyr
    370                 375                 380
Phe Thr Val Ser Phe Asn Arg Thr Phe Leu Met Met Ile Thr Asn Lys
385                 390                 395                 400
Ala Thr Asp Gly Ile Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys
                405                 410                 415
Ser
```

<210> 36

<211> 414
<212> PRT
<213> Homo sapiens

<220>
<223> Vaspin SERPINA12

<400> 36
Met Asn Pro Thr Leu Gly Leu Ala Ile Phe Leu Ala Val Leu Leu Thr
1 5 10 15
Val Lys Gly Leu Leu Lys Pro Ser Phe Ser Pro Arg Asn Tyr Lys Ala
20 25 30
Leu Ser Glu Val Gln Gly Trp Lys Gln Arg Met Ala Ala Lys Glu Leu
35 40 45
Ala Arg Gln Asn Met Asp Leu Gly Phe Lys Leu Leu Lys Lys Leu Ala
50 55 60
Phe Tyr Asn Pro Gly Arg Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser
65 70 75 80
Thr Ala Phe Ser Met Leu Cys Leu Gly Ala Gln Asp Ser Thr Leu Asp
85 90 95
Glu Ile Lys Gln Gly Phe Asn Phe Arg Lys Met Pro Glu Lys Asp Leu
100 105 110
His Glu Gly Phe His Tyr Ile Ile His Glu Leu Thr Gln Lys Thr Gln
115 120 125
Asp Leu Lys Leu Ser Ile Gly Asn Thr Leu Phe Ile Asp Gln Arg Leu
130 135 140
Gln Pro Gln Arg Lys Phe Leu Glu Asp Ala Lys Asn Phe Tyr Ser Ala
145 150 155 160
Glu Thr Ile Leu Thr Asn Phe Gln Asn Leu Glu Met Ala Gln Lys Gln
165 170 175
Ile Asn Asp Phe Ile Ser Gln Lys Thr His Gly Lys Ile Asn Asn Leu
180 185 190
Ile Glu Asn Ile Asp Pro Gly Thr Val Met Leu Leu Ala Asn Tyr Ile
195 200 205
Phe Phe Arg Ala Arg Trp Lys His Glu Phe Asp Pro Asn Val Thr Lys
210 215 220
Glu Glu Asp Phe Phe Leu Glu Lys Asn Ser Ser Val Lys Val Pro Met
225 230 235 240
Met Phe Arg Ser Gly Ile Tyr Gln Val Gly Tyr Asp Asp Lys Leu Ser
245 250 255
Cys Thr Ile Leu Glu Ile Pro Tyr Gln Lys Asn Ile Thr Ala Ile Phe
260 265 270
Ile Leu Pro Asp Glu Gly Lys Leu Lys His Leu Glu Lys Gly Leu Gln
275 280 285
Val Asp Thr Phe Ser Arg Trp Lys Thr Leu Leu Ser Arg Arg Val Val
290 295 300
Asp Val Ser Val Pro Arg Leu His Met Thr Gly Thr Phe Asp Leu Lys
305 310 315 320
Lys Thr Leu Ser Tyr Ile Gly Val Ser Lys Ile Phe Glu Glu His Gly
325 330 335
Asp Leu Thr Lys Ile Ala Pro His Arg Ser Leu Lys Val Gly Glu Ala
340 345 350
Val His Lys Ala Glu Leu Lys Met Asp Glu Arg Gly Thr Glu Gly Ala
355 360 365
Ala Gly Thr Gly Ala Gln Thr Leu Pro Met Glu Thr Pro Leu Val Val
370 375 380
Lys Ile Asp Lys Pro Tyr Leu Leu Leu Ile Tyr Ser Glu Lys Ile Pro

385 390 395 400
Ser Val Leu Phe Leu Gly Lys Ile Val Asn Pro Ile Gly Lys
405 410

<210> 37
<211> 422
<212> PRT
<213> Homo sapiens

<220>
<223> Serpin A11 precursor SERPINA11

<400> 37
Met Gly Pro Ala Trp Leu Trp Leu Leu Gly Thr Gly Ile Leu Ala Ser
1 5 10 15
Val His Cys Gln Pro Leu Leu Ala His Gly Asp Lys Ser Leu Gln Gly
20 25 30
Pro Gln Pro Pro Arg His Gln Leu Ser Glu Pro Ala Pro Ala Tyr His
35 40 45
Arg Ile Thr Pro Thr Ile Thr Asn Phe Ala Leu Arg Leu Tyr Lys Glu
50 55 60
Leu Ala Ala Asp Ala Pro Gly Asn Ile Phe Phe Ser Pro Val Ser Ile
65 70 75 80
Ser Thr Thr Leu Ala Leu Leu Ser Leu Gly Ala Gln Ala Asn Thr Ser
85 90 95
Ala Leu Ile Leu Glu Gly Leu Gly Phe Asn Leu Thr Glu Thr Pro Glu
100 105 110
Ala Asp Ile His Gln Gly Phe Arg Ser Leu Leu His Thr Leu Ala Leu
115 120 125
Pro Ser Pro Lys Leu Glu Leu Lys Val Gly Asn Ser Leu Phe Leu Asp
130 135 140
Lys Arg Leu Lys Pro Arg Gln His Tyr Leu Asp Ser Ile Lys Glu Leu
145 150 155 160
Tyr Gly Ala Phe Ala Phe Ser Ala Asn Phe Thr Asp Ser Val Thr Thr
165 170 175
Gly Arg Gln Ile Asn Asp Tyr Leu Arg Arg Gln Thr Tyr Gly Gln Val
180 185 190
Val Asp Cys Leu Pro Glu Phe Ser Gln Asp Thr Phe Met Val Leu Ala
195 200 205
Asn Tyr Ile Phe Phe Lys Ala Lys Trp Lys His Pro Phe Ser Arg Tyr
210 215 220
Gln Thr Gln Lys Gln Glu Ser Phe Phe Val Asp Glu Arg Thr Ser Leu
225 230 235 240
Gln Val Pro Met Met His Gln Lys Glu Met His Arg Phe Leu Tyr Asp
245 250 255
Gln Asp Leu Ala Cys Thr Val Leu Gln Ile Glu Tyr Arg Gly Asn Ala
260 265 270
Leu Ala Leu Leu Val Leu Pro Asp Pro Gly Lys Met Lys Gln Val Glu
275 280 285
Ala Ala Leu Gln Pro Gln Thr Leu Arg Lys Trp Gly Gln Leu Leu Leu
290 295 300
Pro Ser Leu Leu Asp Leu His Leu Pro Arg Phe Ser Ile Ser Gly Thr
305 310 315 320
Tyr Asn Leu Glu Asp Ile Leu Pro Gln Ile Gly Leu Thr Asn Ile Leu
325 330 335
Asn Leu Glu Ala Asp Phe Ser Gly Val Thr Gly Gln Leu Asn Lys Thr

```
            340                 345                 350
Ile Ser Lys Val Ser His Lys Ala Met Val Asp Met Ser Glu Lys Gly
        355                 360                 365
Thr Glu Ala Gly Ala Ala Ser Gly Leu Leu Ser Gln Pro Pro Ser Leu
    370                 375                 380
Asn Thr Met Ser Asp Pro His Ala His Phe Asn Arg Pro Phe Leu Leu
385                 390                 395                 400
Leu Leu Trp Glu Val Thr Thr Gln Ser Leu Leu Phe Leu Gly Lys Val
                405                 410                 415
Val Asn Pro Val Ala Gly
            420
```

<210> 38
<211> 307
<212> PRT
<213> Homo sapiens

<220>
<223> Serpin A13 precursor SERPINA13

<400> 38

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Met Glu Ala Ser Arg Trp Trp Leu Leu Val Thr Val Leu Met Ala Gly
 1               5                  10                  15
Ala His Cys Val Ala Leu Val Asp Gln Glu Ala Ser Asp Leu Ile His
            20                  25                  30
Ser Gly Pro Gln Asp Ser Ser Pro Gly Pro Ala Leu Pro Cys His Lys
        35                  40                  45
Ile Ser Val Ser Asn Ile Asp Phe Ala Phe Lys Leu Tyr Arg Gln Leu
    50                  55                  60
Ala Leu Asn Ala Pro Gly Glu Asn Ile Leu Phe Phe Pro Val Ser Ile
65                  70                  75                  80
Ser Leu Ala Leu Ala Met Leu Ser Trp Gly Ala Pro Val Ala Ser Arg
                85                  90                  95

Thr Gln Leu Leu Glu Gly Leu Gly Phe Thr Leu Thr Val Val Pro Glu
            100                 105                 110
Glu Glu Ile Gln Glu Gly Phe Trp Asp Leu Leu Ile Arg Leu Arg Gly
        115                 120                 125
Gln Gly Pro Arg Leu Leu Leu Thr Met Asp Gln Arg Arg Phe Ser Gly
    130                 135                 140
Leu Gly Ala Arg Ala Asn Gln Ser Leu Glu Glu Ala Gln Lys His Ile
145                 150                 155                 160
Asp Glu Tyr Thr Glu Gln Gln Thr Gln Gly Lys Leu Gly Ala Trp Glu
                165                 170                 175
Lys Asp Leu Gly Ser Glu Thr Thr Ala Val Leu Val Asn His Met Leu
            180                 185                 190
Leu Arg Ala Glu Trp Met Lys Pro Phe Asp Ser His Ala Thr Ser Pro
        195                 200                 205
Lys Glu Phe Phe Val Asp Glu His Ser Ala Val Trp Val Pro Met Met
    210                 215                 220
Lys Glu Lys Ala Ser His Arg Phe Leu His Asp Arg Glu Leu Gln Cys
225                 230                 235                 240
Ser Val Leu Arg Met Asp His Ala Gly Asn Thr Thr Thr Phe Phe Ile
                245                 250                 255
Phe Pro Asn Arg Gly Lys Met Arg His Leu Glu Asp Ala Leu Leu Pro
            260                 265                 270
```

```
Glu Thr Leu Ile Lys Trp Asp Ser Leu Leu Arg Thr Arg Glu Leu Asp
        275                 280                 285
Phe His Phe Pro Lys Phe Ser Ile Ser Arg Thr Cys Arg Leu Glu Met
    290                 295                 300
Leu Leu Pro
305
```

<210> 39
<211> 934
<212> DNA
<213> Homo sapiens

<220>
<223> granzyme B

<400> 39
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tgagaagatg caaccaatcc tgcttctgct ggccttcctc ctgctgccca gggcagatgc 60
aggggagatc atcgggggac atgaggccaa gccccactcc cgcccctaca tggcttatct 120
tatgatctgg gatcagaagt ctctgaagag gtgcggtggc ttcctgatac aagacgactt 180
cgtgctgaca gctgctcact gttggggaag ctccataaat gtcaccttgg gggcccacaa 240
tatcaaagaa caggagccga cccagcagtt tatccctgtg aaaagaccca tcccccatcc 300
agcctataat cctaagaact tctccaacga catcatgcta ctgcagctgg agagaaaggc 360
caagcggacc agagctgtgc agcccctcag gctacctagc aacaaggccc aggtgaagcc 420
agggcagaca tgcagtgtgg ccggctgggg gcagacggcc cccctgggaa aacactcaca 480
cacactacaa gaggtgaaga tgacagtgca ggaagatcga aagtgcgaat ctgacttacg 540
ccattattac gacagtacca ttgagttgtg cgtgggggac ccagagatta aaaagacttc 600
ctttaagggg gactctggag gccctcttgt gtgtaacaag gtggcccagg gcattgtctc 660
ctatggacga aacaatggca tgcctccacg agcctgcacc aaagtctcaa gctttgtaca 720
ctggataaag aaaaccatga aacgctacta actacaggaa gcaaactaag cccccgctgt 780
aatgaaacac cttctctgga gccaagtcca gatttacact gggagaggtg ccagcaactg 840
aataaatacc tctcccagtg taaatctgga gccaagtcca gatttacact gggagaggtg 900
ccagcaactg aataaatacc tcttagctga gtgg                              934
```

<210> 40
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> granzyme B

<400> 40
```
Met Gln Pro Ile Leu Leu Leu Leu Ala Phe Leu Leu Leu Pro Arg Ala
 1               5                  10                  15
Asp Ala Gly Glu Ile Ile Gly Gly His Glu Ala Lys Pro His Ser Arg
            20                  25                  30
Pro Tyr Met Ala Tyr Leu Met Ile Trp Asp Gln Lys Ser Leu Lys Arg
        35                  40                  45
Cys Gly Gly Phe Leu Ile Gln Asp Asp Phe Val Leu Thr Ala Ala His
    50                  55                  60
Cys Trp Gly Ser Ser Ile Asn Val Thr Leu Gly Ala His Asn Ile Lys
65                  70                  75                  80
Glu Gln Glu Pro Thr Gln Gln Phe Ile Pro Val Lys Arg Pro Ile Pro
                85                  90                  95
His Pro Ala Tyr Asn Pro Lys Asn Phe Ser Asn Asp Ile Met Leu Leu
            100                 105                 110
```

```
Gln Leu Glu Arg Lys Ala Lys Arg Thr Arg Ala Val Gln Pro Leu Arg
        115                 120                 125
Leu Pro Ser Asn Lys Ala Gln Val Lys Pro Gly Gln Thr Cys Ser Val
    130                 135                 140
Ala Gly Trp Gly Gln Thr Ala Pro Leu Gly Lys His Ser His Thr Leu
145                 150                 155                 160
Gln Glu Val Lys Met Thr Val Gln Glu Asp Arg Lys Cys Glu Ser Asp
                165                 170                 175
Leu Arg His Tyr Tyr Asp Ser Thr Ile Glu Leu Cys Val Gly Asp Pro
            180                 185                 190
Glu Ile Lys Lys Thr Ser Phe Lys Gly Asp Ser Gly Gly Pro Leu Val
        195                 200                 205
Cys Asn Lys Val Ala Gln Gly Ile Val Ser Tyr Gly Arg Asn Asn Gly
    210                 215                 220
Met Pro Pro Arg Ala Cys Thr Lys Val Ser Ser Phe Val His Trp Ile
225                 230                 235                 240
Lys Lys Thr Met Lys Arg Tyr
                245
```

<210> 41
<211> 1165
<212> DNA
<213> Homo sapiens

<220>
<223> Testisin transcript variant 1

<400> 41
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gctgggagta gagggcagag ctcccacccc gccccgcccc cagggggcgc cccgggcccg 60
gcgcgagagg aggcagaggg ggcgtcaggc cgcggagag gaggccatgg gcgcgcgcgg 120
ggcgctgctg ctggcgctgc tgctggctcg ggctggactc aggaagccgg agtcgcagga 180
ggcggcgccg ttatcaggac catgcggccg acgggtcatc acgtcgcgca tcgtgggtgg 240
agaggacgcc gaactcgggc gttggccgtg gcaggggagc ctgcgcctgt gggattccca 300
cgtatgcgga gtgagcctgc tcagccaccg ctgggcactc acggcggcgc actgctttga 360
aacctatagt gaccttagtg atccctccgg gtggatggtc cagtttggcc agctgacttc 420
catgccatcc ttctggagcc tgcaggccta ctacacccgt tacttcgtat cgaatatcta 480
tctgagccct cgctacctgg ggaattcacc ctatgacatt gccttggtga agctgtctgc 540
acctgtcacc tacactaaac acatccagcc catctgtctc caggcctcca catttgagtt 600
tgagaaccgg acagactgct gggtgactgg ctgggggtac atcaaagagg atgaggcact 660
gccatctccc cacaccctcc aggaagttca ggtcgccatc ataaacaact ctatgtgcaa 720
ccacctcttc ctcaagtaca gtttccgcaa ggacatcttt ggagacatgg tttgtgctgg 780
caatgcccaa ggcgggaagg atgcctgctt cggtgactca ggtggaccct tggcctgtaa 840
caagaatgga ctgtggtatc agattggagt cgtgagctgg ggagtgggct gtggtcggcc 900
caatcggccc ggtgtctaca ccaatatcag ccaccacttt gagtggatcc agaagctgat 960
ggcccagagt ggcatgtccc agccagaccc ctcctggccg ctactctttt tccctcttct 1020
ctgggctctc ccactcctgg ggccggtctg agcctacctg agcccatgca gcctggggcc 1080
actgccaagt caggccctgg ttctcttctg tcttgtttgg taataaacac attccagttg 1140
atgccttgca gggcattctt caaaa                                      1165
```

<210> 42
<211> 314
<212> PRT
<213> Homo sapiens

<220>

<223> Testisin isoform 1

<400> 42
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala
1 5 10 15
Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
20 25 30
Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
35 40 45
Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
50 55 60
His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
65 70 75 80
Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
85 90 95
Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
100 105 110
Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
115 120 125
Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser
130 135 140
Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
145 150 155 160
Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
165 170 175
Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
180 185 190
Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
195 200 205
Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala
210 215 220
Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
225 230 235 240
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val
245 250 255
Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
260 265 270
Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser
275 280 285
Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu
290 295 300
Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
305 310

<210> 43
<211> 1159
<212> DNA
<213> Homo sapiens

<220>
<223> Testisin transcript variant 2

<400> 43
gctgggagta gagggcagag ctcccacccc gccccgcccc caggggcgc cccgggcccg 60
gcgcgagagg aggcagaggg ggcgtcaggc cgcgggagag gaggccatgg gcgcgcgcgg 120
ggcgctgctg ctggcgctgc tgctggctcg ggctggactc aggaagccgg agtcgcagga 180

```
ggcggcgccg ttatcaggac catgcggccg acgggtcatc acgtcgcgca tcgtgggtgg 240
agaggacgcc gaactcgggc gttggccgtg gcaggggagc ctgcgcctgt gggattccca 300
cgtatgcgga gtgagcctgc tcagccaccg ctgggcactc acggcggcgc actgctttga 360
aactgacctt agtgatccct ccgggtggat ggtccagttt ggccagctga cttccatgcc 420
atccttctgg agcctgcagg cctactacac ccgttacttc gtatcgaata tctatctgag 480
ccctcgctac ctggggaatt caccctatga cattgccttg gtgaagctgt ctgcacctgt 540
cacctacact aaacacatcc agcccatctg tctccaggcc tccacatttg agtttgagaa 600
ccggacagac tgctgggtga ctggctgggg gtacatcaaa gaggatgagg cactgccatc 660
tccccacacc ctccaggaag ttcaggtcgc catcataaac aactctatgt gcaaccacct 720
cttcctcaag tacagtttcc gcaaggacat ctttggagac atggtttgtg ctggcaatgc 780
ccaaggcggg aaggatgcct gcttcggtga ctcaggtgga cccttggcct gtaacaagaa 840
tggactgtgg tatcagattg gagtcgtgag ctggggagtg ggctgtggtc ggcccaatcg 900
gcccggtgtc tacaccaata tcagccacca ctttgagtgg atccagaagc tgatggccca 960
gagtggcatg tcccagccag acccctcctg gccgctactc tttttccctc ttctctgggc 1020
tctcccactc ctggggccgg tctgagccta cctgagccca tgcagcctgg ggccactgcc 1080
aagtcaggcc ctggttctct tctgtcttgt ttggtaataa acacattcca gttgatgcct 1140
tgcagggcat tcttcaaaa                                          1159
```

<210> 44
<211> 312
<212> PRT
<213> Homo sapiens

<220>
<223> Testisin isoform 2

<400> 44

```
Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala
 1               5                  10                  15
Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
            20                  25                  30
Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
        35                  40                  45
Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
    50                  55                  60
His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
65                  70                  75                  80
Ala His Cys Phe Glu Thr Asp Leu Ser Asp Pro Ser Gly Trp Met Val
                85                  90                  95
Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala
            100                 105                 110
Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr
        115                 120                 125
Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro
    130                 135                 140
Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr
145                 150                 155                 160
Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr
                165                 170                 175
Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val
            180                 185                 190
Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
        195                 200                 205
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly Asn
    210                 215                 220
Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly Pro Leu
225                 230                 235                 240
```

```
Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val Ser Trp
                245                 250                 255
Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr Asn Ile
            260                 265                 270
Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser Gly Met
        275                 280                 285
Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu Leu Trp
    290                 295                 300
Ala Leu Pro Leu Leu Gly Pro Val
305                 310
```

<210> 45
<211> 1135
<212> DNA
<213> Homo sapiens

<220>
<223> Testisin transcript variant 3

<400> 45
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gctgggagta gagggcagag ctcccacccc gccccgcccc caggggcgc cccgggcccg 60
gcgcgagagg aggcagaggg ggcgtcaggc cgcgggagag gaggccatgg gcgcgcgcgg 120
ggcgctgctg ctggcgctgc tgctggctcg ggctggactc aggaagccgg agtcgcagga 180
ggcggcgccg ttatcaggac catgcggccg acgggtcatc acgtcgcgca tcgtgggtgg 240
agaggacgcc gaactcgggc gttggccgtg gcaggggagc ctgcgcctgt gggattccca 300
cgtatgcgga gtgagcctgc tcagccaccg ctgggcactc acggcggcgc actgctttga 360
aacctatagt gaccttagtg atccctccgg gtggatggtc cagtttggcc agctgacttc 420
catgccatcc ttctggagcc tgcaggccta ctacacccgt tacttcgtat cgaatatcta 480
tctgagccct cgctacctgg ggaattcacc ctatgacatt gccttggtga agctgtctgc 540
acctgtcacc tacactaaac acatccagcc catctgtctc caggcctcca catttgagtt 600
tgagaaccgg acagactgct gggtgactgg ctgggggtac atcaaagagg atgaggcact 660
gccatctccc cacaccctcc aggaagttca ggtcgccatc ataaacaact ctatgtgcaa 720
ccacctcttc ctcaagtaca gtttccgcaa ggacatcttt ggagacatgg gtgactcagg 780
tggacccttg gcctgtaaca agaatggact gtggtatcag attggagtcg tgagctgggg 840
agtgggctgt ggtcggccca atcggcccgg tgtctacacc aatatcagcc accactttga 900
gtggatccag aagctgatgg cccagagtgg catgtcccag ccagacccct cctggccgct 960
actcttttttc cctcttctct gggctctccc actcctgggg ccggtctgag cctacctgag 1020
cccatgcagc ctggggccac tgccaagtca ggccctggtt ctcttctgtc ttgtttggta 1080
ataaacacat tccagttgat gccttgcagg gcattcttca aaaaaaaaaa aaaaa      1135
```

<210> 46
<211> 300
<212> PRT
<213> Homo sapiens

<220>
<223> Testisin isoform 3

<400> 46
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Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala
 1               5                  10                  15
Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
            20                  25                  30
Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
        35                  40                  45
Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
```

```
    50                  55                  60
His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
65                  70                  75                  80
Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
                85                  90                  95
Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
            100                 105                 110
Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
        115                 120                 125
Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser
    130                 135                 140
Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
145                 150                 155                 160
Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
                165                 170                 175
Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
            180                 185                 190
Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
        195                 200                 205
Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Gly Asp Ser
    210                 215                 220
Gly Gly Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly
225                 230                 235                 240
Val Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
                245                 250                 255
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala
            260                 265                 270
Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe
        275                 280                 285
Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
    290                 295                 300
```

<210> 47
<211> 1194
<212> DNA
<213> Homo sapiens

<220>
<223> trypstase beta 1

<400> 47

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ataaatgggg aggggagagc ccactgggta gaaggaacag ggagcggcca ggatgctgaa 60
tctgctgctg ctggcgctgc ccgtcctggc gagccgcgcc tacgcggccc ctgccccagg 120
ccaggccctg cagcgagtgg gcatcgtcgg gggtcaggag gcccccagga gcaagtggcc 180
ctggcaggtg agcctgagag tccacggccc atactggatg cacttctgcg ggggctccct 240
catccacccc cagtgggtgc tgaccgcagc gcactgcgtg ggaccggacg tcaaggatct 300
ggccgccctc agggtgcaac tgcgggagca gcacctctac taccaggacc agctgctgcc 360
ggtcagcagg atcatcgtgc acccacagtt ctacaccgcc cagatcggag cggacatcgc 420
cctgctggag ctggaggagc cggtgaacgt ctccagccac gtccacacgg tcaccctgcc 480
ccctgcctca gagaccttcc ccccggggat gccgtgctgg gtcactggct ggggcgatgt 540
ggacaatgat gagcgcctcc caccgccatt tcctctgaag caggtgaagg tccccataat 600
ggaaaaccac atttgtgacg caaaatacca ccttggcgcc tacacgggag acgacgtccg 660
catcgtccgt gacgacatgc tgtgtgccgg gaacacccgg agggactcat gccagggcga 720
ctccggaggg cccctggtgt gcaaggtgaa tggcacctgg ctgcaggcgg gcgtggtcag 780
ctggggcgag ggctgtgccc agcccaaccg gcctggcatc tacacccgtg tcacctacta 840
cttggactgg atccaccact atgtccccaa aaagccgtga gtcaggcctg ggttggccac 900
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ctgggtcact ggaggaccaa cccctgctgt ccaaaacacc actgcttcct acccaggtgg 960
cgactgcccc ccacaccttc cctgccccgt cctgagtgcc ccttcctgtc ctaagccccc 1020
tgctctcttc tgagcccctt cccctgtcct gaggaccctt ccctatcctg agccccttc 1080
cctgtcctaa gcctgacgcc tgcaccgggc cctccagccc tcccctgccc agatagctgg 1140
tggtgggcgc taatcctcct gagtgctgga cctcattaaa gtgcatggaa atca 1194

<210> 48
<211> 275
<212> PRT
<213> Homo sapiens

<220>
<223> trypstase beta 1

<400> 48
Met Leu Asn Leu Leu Leu Leu Ala Leu Pro Val Leu Ala Ser Arg Ala
1 5 10 15
Tyr Ala Ala Pro Ala Pro Gly Gln Ala Leu Gln Arg Val Gly Ile Val
20 25 30
Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp Pro Trp Gln Val Ser Leu
35 40 45
Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser Leu Ile
50 55 60
His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro Asp Val
65 70 75 80
Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His Leu Tyr
85 90 95
Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His Pro Gln
100 105 110
Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu Leu Glu
115 120 125
Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu Pro Pro
130 135 140
Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr Gly Trp
145 150 155 160
Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro Leu Lys
165 170 175
Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala Lys Tyr
180 185 190
His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg Asp Asp
195 200 205
Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly Asp Ser
210 215 220
Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln Ala Gly
225 230 235 240
Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro Gly Ile
245 250 255
Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr Val Pro
260 265 270
Lys Lys Pro
275

<210> 49
<211> 1528
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hk5

<400> 49
ggaaggcaca ggcctgagaa gtctgcggct gagctgggag caaatccccc acccccctacc 60
tgggggacag ggcaagtgag acctggtgag ggtggctcag caggaaggga aggagaggtg 120
tctgtgcgtc ctgcacccac atctttctct gtcccctcct tgccctgtct ggaggctgct 180
agactcctat cttctgaatt ctatagtgcc tgggtctcag cgcagtgccg atggtggccc 240
gtccttgtgg ttcctctcta cctggggaaa taaggtgcag cggccatggc tacagcaaga 300
ccccccctgga tgtgggtgct ctgtgctctg atcacagcct tgcttctggg ggtcacagag 360
catgttctcg ccaacaatga tgtttcctgt gaccacccct ctaacaccgt gccctctggg 420
agcaaccagg acctgggagc tggggccggg gaagacgccc ggtcggatga cagcagcagc 480
cgcatcatca atggatccga ctgcgatatg cacacccagc cgtggcaggc cgcgctgttg 540
ctaaggccca accagctcta ctgcggggcg gtgttggtgc atccacagtg gctgctcacg 600
gccgcccact gcaggaagaa agttttcaga gtccgtctcg gccactactc cctgtcacca 660
gtttatgaat ctgggcagca gatgttccag ggggtcaaat ccatccccca ccctggctac 720
tcccaccctg gccactctaa cgacctcatg ctcatcaaac tgaacagaag aattcgtccc 780
actaaagatg tcagacccat caacgtctcc tctcattgtc cctctgctgg gacaaagtgc 840
ttggtgtctg gctgggggac aaccaagagc ccccaagtgc acttccctaa ggtcctccag 900
tgcttgaata tcagcgtgct aagtcagaaa aggtgcgagg atgcttaccc gagacagata 960
gatgacacca tgttctgcgc cggtgacaaa gcaggtagag actcctgcca gggtgattct 1020
gggggggcctg tggtctgcaa tggctccctg cagggactcg tgtcctgggg agattaccct 1080
tgtgcccggc ccaacagacc gggtgtctac acgaacctct gcaagttcac caagtggatc 1140
caggaaacca tccaggccaa ctcctgagtc atcccaggac tcagcacacc ggcatcccca 1200
cctgctgcag ggacagccct gacactcctt tcagaccctc attccttccc agagatgttg 1260
agaatgttca tctctccagc ccctgacccc atgtctcctg gactcagggt ctgcttcccc 1320
cacattgggc tgaccgtgtc tctctagttg aaccctggga acaatttcca aaactgtcca 1380
gggcgggggt tgcgtctcaa tctccctggg gcactttcat cctcaagctc agggcccatc 1440
ccttctctgc agctctgacc caaatttagt cccagaaata aactgagaag tggaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1528

<210> 50
<211> 293
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hk5

<400> 50
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Val Ser Cys Asp His Pro Ser Asn Thr Val Pro Ser Gly Ser Asn Gln
        35   40   45
Asp Leu Gly Ala Gly Ala Gly Glu Asp Ala Arg Ser Asp Asp Ser Ser
    50   55   60
Ser Arg Ile Ile Asn Gly Ser Asp Cys Asp Met His Thr Gln Pro Trp
65   70   75   80
Gln Ala Ala Leu Leu Leu Arg Pro Asn Gln Leu Tyr Cys Gly Ala Val
                85   90   95
Leu Val His Pro Gln Trp Leu Leu Thr Ala Ala His Cys Arg Lys Lys
            100   105   110
Val Phe Arg Val Arg Leu Gly His Tyr Ser Leu Ser Pro Val Tyr Glu
        115   120   125

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Ser Gly Gln Gln Met Phe Gln Gly Val Lys Ser Ile Pro His Pro Gly
    130                 135                 140
Tyr Ser His Pro Gly His Ser Asn Asp Leu Met Leu Ile Lys Leu Asn
145                 150                 155                 160
Arg Arg Ile Arg Pro Thr Lys Asp Val Arg Pro Ile Asn Val Ser Ser
                165                 170                 175
His Cys Pro Ser Ala Gly Thr Lys Cys Leu Val Ser Gly Trp Gly Thr
            180                 185                 190
Thr Lys Ser Pro Gln Val His Phe Pro Lys Val Leu Gln Cys Leu Asn
        195                 200                 205
Ile Ser Val Leu Ser Gln Lys Arg Cys Glu Asp Ala Tyr Pro Arg Gln
    210                 215                 220
Ile Asp Asp Thr Met Phe Cys Ala Gly Asp Lys Ala Gly Arg Asp Ser
225                 230                 235                 240
Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly Ser Leu Gln
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Gly Leu Val Ser Trp Gly Asp Tyr Pro Cys Ala Arg Pro Asn Arg Pro
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Ile Gln Ala Asn Ser
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<210> 51
<211> 4942
<212> DNA
<213> Homo sapiens

<220>
<223> Corin

<400> 51
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<212> PRT
<213> Homo sapiens

<220>
<223> Corin

<400> 52
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35 40 45
Leu Val Leu Ile Pro Cys Ile Cys Ala Leu Val Leu Leu Leu Val Ile
50 55 60
Leu Leu Ser Tyr Val Gly Thr Leu Gln Lys Val Tyr Phe Lys Ser Asn
65 70 75 80
Gly Ser Glu Pro Leu Val Thr Asp Gly Glu Ile Gln Gly Ser Asp Val
85 90 95
Ile Leu Thr Asn Thr Ile Tyr Asn Gln Ser Thr Val Val Ser Thr Ala
100 105 110
His Pro Asp Gln His Val Pro Ala Trp Thr Thr Asp Ala Ser Leu Pro
115 120 125
Gly Asp Gln Ser His Arg Asn Thr Ser Ala Cys Met Asn Ile Thr His
130 135 140
Ser Gln Cys Gln Met Leu Pro Tyr His Ala Thr Leu Thr Pro Leu Leu
145 150 155 160
Ser Val Val Arg Asn Met Glu Met Glu Lys Phe Leu Lys Phe Phe Thr
165 170 175
Tyr Leu His Arg Leu Ser Cys Tyr Gln His Ile Met Leu Phe Gly Cys
180 185 190
Thr Leu Ala Phe Pro Glu Cys Ile Ile Asp Gly Asp Asp Ser His Gly
195 200 205
Leu Leu Pro Cys Arg Ser Phe Cys Glu Ala Ala Lys Glu Gly Cys Glu
210 215 220
Ser Val Leu Gly Met Val Asn Tyr Ser Trp Pro Asp Phe Leu Arg Cys
225 230 235 240
Ser Gln Phe Arg Asn Gln Thr Glu Ser Ser Asn Val Ser Arg Ile Cys
245 250 255
Phe Ser Pro Gln Gln Glu Asn Gly Lys Gln Leu Leu Cys Gly Arg Gly
260 265 270
Glu Asn Phe Leu Cys Ala Ser Gly Ile Cys Ile Pro Gly Lys Leu Gln
275 280 285
Cys Asn Gly Tyr Asn Asp Cys Asp Asp Trp Ser Asp Glu Ala His Cys
290 295 300
Asn Cys Ser Glu Asn Leu Phe His Cys His Thr Gly Lys Cys Leu Asn
305 310 315 320
Tyr Ser Leu Val Cys Asp Gly Tyr Asp Asp Cys Gly Asp Leu Ser Asp
325 330 335
Glu Gln Asn Cys Asp Cys Asn Pro Thr Thr Glu His Arg Cys Gly Asp
340 345 350
Gly Arg Cys Ile Ala Met Glu Trp Val Cys Asp Gly Asp His Asp Cys

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Val Asp Lys Ser Asp Glu Val Asn Cys Ser Cys His Ser Gln Gly Leu
    370                 375                 380
Val Glu Cys Arg Asn Gly Gln Cys Ile Pro Ser Thr Phe Gln Cys Asp
385                 390                 395                 400
Gly Asp Glu Asp Cys Lys Asp Gly Ser Asp Glu Glu Asn Cys Ser Val
                405                 410                 415
Ile Gln Thr Ser Cys Gln Glu Gly Asp Gln Arg Cys Leu Tyr Asn Pro
            420                 425                 430
Cys Leu Asp Ser Cys Gly Gly Ser Ser Leu Cys Asp Pro Asn Asn Ser
        435                 440                 445
Leu Asn Asn Cys Ser Gln Cys Glu Pro Ile Thr Leu Glu Leu Cys Met
    450                 455                 460
Asn Leu Pro Tyr Asn Ser Thr Ser Tyr Pro Asn Tyr Phe Gly His Arg
465                 470                 475                 480
Thr Gln Lys Glu Ala Ser Ile Ser Trp Glu Ser Ser Leu Phe Pro Ala
                485                 490                 495
Leu Val Gln Thr Asn Cys Tyr Lys Tyr Leu Met Phe Phe Ser Cys Thr
            500                 505                 510
Ile Leu Val Pro Lys Cys Asp Val Asn Thr Gly Glu His Ile Pro Pro
        515                 520                 525
Cys Arg Ala Leu Cys Glu His Ser Lys Glu Arg Cys Glu Ser Val Leu
    530                 535                 540
Gly Ile Val Gly Leu Gln Trp Pro Glu Asp Thr Asp Cys Ser Gln Phe
545                 550                 555                 560
Pro Glu Glu Asn Ser Asp Asn Gln Thr Cys Leu Met Pro Asp Glu Tyr
                565                 570                 575
Val Glu Glu Cys Ser Pro Ser His Phe Lys Cys Arg Ser Gly Gln Cys
            580                 585                 590
Val Leu Ala Ser Arg Arg Cys Asp Gly Gln Ala Asp Cys Asp Asp Asp
        595                 600                 605
Ser Asp Glu Glu Asn Cys Gly Cys Lys Glu Arg Asp Leu Trp Glu Cys
    610                 615                 620
Pro Ser Asn Lys Gln Cys Leu Lys His Thr Val Ile Cys Asp Gly Phe
625                 630                 635                 640
Pro Asp Cys Pro Asp Tyr Met Asp Glu Lys Asn Cys Ser Phe Cys Gln
                645                 650                 655
Asp Asp Glu Leu Glu Cys Ala Asn His Ala Cys Val Ser Arg Asp Leu
            660                 665                 670
Trp Cys Asp Gly Glu Ala Asp Cys Ser Asp Ser Ser Asp Glu Trp Asp
        675                 680                 685
Cys Val Thr Leu Ser Ile Asn Val Asn Ser Ser Ser Phe Leu Met Val
    690                 695                 700
His Arg Ala Ala Thr Glu His His Val Cys Ala Asp Gly Trp Gln Glu
705                 710                 715                 720
Ile Leu Ser Gln Leu Ala Cys Lys Gln Met Gly Leu Gly Glu Pro Ser
                725                 730                 735
Val Thr Lys Leu Ile Gln Glu Gln Glu Lys Glu Pro Arg Trp Leu Thr
            740                 745                 750
Leu His Ser Asn Trp Glu Ser Leu Asn Gly Thr Thr Leu His Glu Leu
        755                 760                 765
Leu Val Asn Gly Gln Ser Cys Glu Ser Arg Ser Lys Ile Ser Leu Leu
    770                 775                 780
Cys Thr Lys Gln Asp Cys Gly Arg Arg Pro Ala Ala Arg Met Asn Lys
785                 790                 795                 800
Arg Ile Leu Gly Gly Arg Thr Ser Arg Pro Gly Arg Trp Pro Trp Gln
                805                 810                 815
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Cys Ser Leu Gln Ser Glu Pro Ser Gly His Ile Cys Gly Cys Val Leu
            820                 825                 830
Ile Ala Lys Lys Trp Val Leu Thr Val Ala His Cys Phe Glu Gly Arg
        835                 840                 845
Glu Asn Ala Ala Val Trp Lys Val Val Leu Gly Ile Asn Asn Leu Asp
    850                 855                 860
His Pro Ser Val Phe Met Gln Thr Arg Phe Val Lys Thr Ile Ile Leu
865                 870                 875                 880
His Pro Arg Tyr Ser Arg Ala Val Val Asp Tyr Asp Ile Ser Ile Val
                885                 890                 895
Glu Leu Ser Glu Asp Ile Ser Glu Thr Gly Tyr Val Arg Pro Val Cys
            900                 905                 910
Leu Pro Asn Pro Glu Gln Trp Leu Glu Pro Asp Thr Tyr Cys Tyr Ile
        915                 920                 925
Thr Gly Trp Gly His Met Gly Asn Lys Met Pro Phe Lys Leu Gln Glu
    930                 935                 940
Gly Glu Val Arg Ile Ile Ser Leu Glu His Cys Gln Ser Tyr Phe Asp
945                 950                 955                 960
Met Lys Thr Ile Thr Thr Arg Met Ile Cys Ala Gly Tyr Glu Ser Gly
                965                 970                 975
Thr Val Asp Ser Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Glu
            980                 985                 990
Lys Pro Gly Gly Arg Trp Thr Leu Phe Gly Leu Thr Ser Trp Gly Ser
        995                 1000                1005
Val Cys Phe Ser Lys Val Leu Gly Pro Gly Val Tyr Ser Asn Val Ser
    1010                1015                1020
Tyr Phe Val Glu Trp Ile Lys Arg Gln Ile Tyr Ile Gln Thr Phe Leu
1025                1030                1035                1040
Leu Asn
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<210> 53
<211> 945
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 12 transcript variant 1

<400> 53

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gggctcagca tctttttgct cctgtgtgtt cttgggctca gccaggcagc cacaccgaag 180
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ctgggaactt cttggaactt taactcctgc cagcccttct aagacccacg agcggggtga 900
gagaagtgtg caatagtctg gaataaatat aaatgaagga ggggc                 945
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<210> 54
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 12 isoform 1

<400> 54
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Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg Asn Ser
            20   25   30
Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly
        35   40   45
Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser
    50   55   60
Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His Ser Leu Ser Gln Leu
65   70   75   80
Asp Trp Thr Glu Gln Ile Arg His Ser Gly Phe Ser Val Thr His Pro
                85   90   95
Gly Tyr Leu Gly Ala Ser Thr Ser His Glu His Asp Leu Arg Leu Leu
            100   105   110
Arg Leu Arg Leu Pro Val Arg Val Thr Ser Ser Val Gln Pro Leu Pro
        115   120   125
Leu Pro Asn Asp Cys Ala Thr Ala Gly Thr Glu Cys His Val Ser Gly
    130   135   140
Trp Gly Ile Thr Asn His Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln
145   150   155   160
Cys Leu Asn Leu Ser Ile Val Ser His Ala Thr Cys His Gly Val Tyr
                165   170   175
Pro Gly Arg Ile Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly
            180   185   190
Gln Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
        195   200   205
Val Leu Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln
    210   215   220
Asp Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Asn Ser Thr Leu Val
225   230   235   240
Gly Leu Gly Thr Ser Trp Asn Phe Asn Ser Cys Gln Pro Phe
                245   250

<210> 55
<211> 1074
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 12 transcript variant 2

<400> 55
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gggctcagca tctttttgct cctgtgtgtt cttgggctca gccaggcagc cacaccgaag 180
attttcaatg gcactgagtg tgggcgtaac tcacagccgt ggcaggtggg gctgtttgag 240

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tggaccgagc agatccggca cagcggcttc tctgtgaccc atcccggcta cctgggagcc 420
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cttgttggcc tgggaacttc ttggaacttt aactcctgcc agcccttcta agacccacga 1020
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<210> 56
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 12 isoform 2

<400> 56
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            20                  25                  30
Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly
        35                  40                  45
Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser
    50                  55                  60
Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His Ser Leu Ser Gln Leu
65                  70                  75                  80
Asp Trp Thr Glu Gln Ile Arg His Ser Gly Phe Ser Val Thr His Pro
                85                  90                  95
Gly Tyr Leu Gly Ala Ser Thr Ser His Glu His Asp Leu Arg Leu Leu
            100                 105                 110
Arg Leu Arg Leu Pro Val Arg Val Thr Ser Ser Val Gln Pro Leu Pro
        115                 120                 125
Leu Pro Asn Asp Cys Ala Thr Ala Gly Thr Glu Cys His Val Ser Gly
    130                 135                 140
Trp Gly Ile Thr Asn His Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln
145                 150                 155                 160
Cys Leu Asn Leu Ser Ile Val Ser His Ala Thr Cys His Gly Val Tyr
                165                 170                 175
Pro Gly Arg Ile Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly
            180                 185                 190
Gln Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
        195                 200                 205
Val Leu Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln
    210                 215                 220
Asp Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
225                 230                 235                 240
Ile Arg Met Ile Met Arg Asn Asn
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<210> 57
<211> 814
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 12 transcript variant 3

<400> 57
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agaggatctg gcagacaaag agacaaggtg agaaggagac tttggaagtg acccaccatg 120
gggctcagca tctttttgct cctgtgtgtt cttgggctca gccaggcagc cacaccgaag 180
attttcaatg gcactgagtg tgggcgtaac tcacagccgt ggcaggtggg gctgtttgag 240
ggcaccagcc tgcgctgcgg gggtgtcctt attgaccaca ggtgggtcct cacagcggct 300
cactgcagcg gcagacccat tcccggatct gctccagtgc ctcaacctct ccatcgtctc 360
ccatgccacc tgccatggtg tgtatcccgg gagaatcacg agcaacatgg tgtgtgcagg 420
cggcgtcccg gggcaggatg cctgccaggg tgattctggg ggccccctgg tgtgtggggg 480
agtccttcaa ggtctggtgt cctgggggtc tgtggggccc tgtggacaag atggcatccc 540
tggagtctac acctatattt gcaagtatgt ggactggatc cggatgatca tgaggaacaa 600
ctgacctgtt tcctccacct ccacccccac cccttaactt gggtaccccc ctggccctca 660
gagcaccaat atctcctcca tcacttcccc tagctccact cttgttggcc tgggaacttc 720
ttggaacttt aactcctgcc agcccttcta agacccacga gcggggtgag agaagtgtgc 780
aatagtctgg aataaatata aatgaaggag gggc 814

<210> 58
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 12 isoform 3

<400> 58
Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser Gln
 1   5   10   15
Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg Asn Ser
            20   25   30
Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu Arg Cys Gly
        35   40   45
Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala Ala His Cys Ser
    50   55   60
Gly Arg Pro Ile Pro Gly Ser Ala Pro Val Pro Gln Pro Leu His Arg
65   70   75   80
Leu Pro Cys His Leu Pro Trp Cys Val Ser Arg Glu Asn His Glu Gln
                85   90   95
His Gly Val Cys Arg Arg Arg Pro Gly Ala Gly Cys Leu Pro Gly
            100   105   110

<210> 59
<211> 1471
<212> DNA
<213> Homo sapiens

<220>
<223> DESC1 oritease

<400> 59
tgacttggat gtagacctcg accttcacag gactcttcat tgctggttgg caatgatgta 60
tcggccagat gtggtgaggg ctaggaaaag agtttgttgg gaaccctggg ttatcggcct 120
cgtcatcttc atatccctga ttgtcctggc agtgtgcatt ggactcactg ttcattatgt 180
gagatataat caaaagaaga cctacaatta ctatagcaca ttgtcattta caactgacaa 240
actatatgct gagtttggca gagaggcttc taacaatttt acagaaatga gccagagact 300
tgaatcaatg gtgaaaaatg cattttataa atctccatta agggaagaat ttgtcaagtc 360
tcaggttatc aagttcagtc aacagaagca tggagtgttg gctcatatgc tgttgatttg 420
tagatttcac tctactgagg atcctgaaac tgtagataaa attgttcaac ttgttttaca 480
tgaaaagctg caagatgctg taggaccccc taaagtagat cctcactcag ttaaaattaa 540
aaaaatcaac aagacagaaa cagacagcta tctaaaccat tgctgcggaa cacgaagaag 600
taaaactcta ggtcagagtc tcaggatcgt tggtgggaca gaagtagaag agggtgaatg 660
gccctggcag gctagcctgc agtgggatgg gagtcatcgc tgtggagcaa ccttaattaa 720
tgccacatgg cttgtgagtg ctgctcactg ttttacaaca tataagaacc ctgccagatg 780
gactgcttcc tttggagtaa caataaaacc ttcgaaaatg aaacggggtc tccggagaat 840
aattgtccat gaaaaataca aacacccatc acatgactat gatatttctc ttgcagagct 900
ttctagccct gttccctaca caaatgcagt acatagagtt tgtctccctg atgcatccta 960
tgagtttcaa ccaggtgatg tgatgtttgt gacaggattt ggagcactga aaaatgatgg 1020
ttacagtcaa aatcatcttc gacaagcaca ggtgactctc atagacgcta caacttgcaa 1080
tgaacctcaa gcttacaatg acgccataac tcctagaatg ttatgtgctg gctccttaga 1140
aggaaaaaca gatgcatgcc agggtgactc tggaggacca ctggttagtt cagatgctag 1200
agatatctgg taccttgctg gaatagtgag ctggggagat gaatgtgcga aacccaacaa 1260
gcctggtgtt tatactagag ttacggcctt gcgggactgg attacttcaa aaactggtat 1320
ctaagagaga aaagcctcat ggaacagata acatttttt ttgtttttg ggtgtggagg 1380
ccatttttag agatacagaa ttggagaaga cttgcaaaac agctagattt gactgatctc 1440
aataaactgt ttgcttgatg caaaaaaaaa a 1471

<210> 60
<211> 422
<212> PRT
<213> Homo sapiens

<220>
<223> DESC1 oritease

<400> 60
Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys Trp Glu
 1   5   10   15
Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile Val Leu Ala
            20   25   30
Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr Asn Gln Lys Lys
        35   40   45
Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr Thr Asp Lys Leu Tyr
    50   55   60
Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn Phe Thr Glu Met Ser Gln
65   70   75   80
Arg Leu Glu Ser Met Val Lys Asn Ala Phe Tyr Lys Ser Pro Leu Arg
                85   90   95
Glu Glu Phe Val Lys Ser Gln Val Ile Lys Phe Ser Gln Gln Lys His
            100   105   110
Gly Val Leu Ala His Met Leu Leu Ile Cys Arg Phe His Ser Thr Glu
        115   120   125
Asp Pro Glu Thr Val Asp Lys Ile Val Gln Leu Val Leu His Glu Lys
    130   135   140
Leu Gln Asp Ala Val Gly Pro Pro Lys Val Asp Pro His Ser Val Lys
145   150   155   160

```
Ile Lys Lys Ile Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys
                165                 170                 175
Cys Gly Thr Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val
            180                 185                 190
Gly Gly Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
        195                 200                 205
Gln Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
    210                 215                 220
Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro Ala
225                 230                 235                 240
Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys Met Lys
                245                 250                 255
Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys His Pro Ser
            260                 265                 270
His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser Pro Val Pro Tyr
        275                 280                 285
Thr Asn Ala Val His Arg Val Cys Leu Pro Asp Ala Ser Tyr Glu Phe
    290                 295                 300
Gln Pro Gly Asp Val Met Phe Val Thr Gly Phe Gly Ala Leu Lys Asn
305                 310                 315                 320
Asp Gly Tyr Ser Gln Asn His Leu Arg Gln Ala Gln Val Thr Leu Ile
                325                 330                 335
Asp Ala Thr Thr Cys Asn Glu Pro Gln Ala Tyr Asn Asp Ala Ile Thr
            340                 345                 350
Pro Arg Met Leu Cys Ala Gly Ser Leu Glu Gly Lys Thr Asp Ala Cys
        355                 360                 365
Gln Gly Asp Ser Gly Gly Pro Leu Val Ser Ser Asp Ala Arg Asp Ile
    370                 375                 380
Trp Tyr Leu Ala Gly Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro
385                 390                 395                 400
Asn Lys Pro Gly Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile
                405                 410                 415
Thr Ser Lys Thr Gly Ile
            420
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<210> 61
<211> 1124
<212> DNA
<213> Homo sapiens

<220>
<223> tryptase gamma 1

<400> 61
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ggactttgca gccagggtgt ggccggccgc aggtttcgga tgcaggcggc cggatcgtgg 120
ggggtcacgc tgccccggcc ggcgcatggc catggcaggc cagcctccgc ctgcggagga 180
tgcacgtgtg cggcgggtca ctgctcagcc cccagtgggt gctcacagct gcccactgct 240
tctccgggtc cctgaactca tccgactacc aggtgcacct gggggaactg gagatcactt 300
tgtctcccca cttctccacc gtgaggcaga tcatcctgca ctccagcccc tcaggacagc 360
cggggaccag cggggacatc gccctggtgg agctcagtgt ccccgtgacc ctctccagcc 420
ggatcctgcc cgtctgcctc ccggaggcct cagatgactt ctgccctggg atccggtgct 480
gggtgaccgg ctggggctat acgcgggagg gagagcctct gccacccccg tacagcctgc 540
gggaggtgaa agtctccgtg gtggacacag agacctgccg ccgggactat cccggccccg 600
ggggcagcat ccttcagccc gacatgctgt gtgcccgggg ccccggggat gcctgccagg 660
acgactccgg ggggcctctg gtctgccagg tgaacggtgc ctgggtgcag gctggcattg 720

tgagctgggg tgagggctgc ggccgcccca acaggccggg agtctacact cgtgtccctg 780
cctacgtgaa ctggatccgc cgccacatca cagcatcagg gggctcagag tctgggtacc 840
ccaggctccc cctcctggct ggcttcttcc tccccggcct cttccttctg ctagtctcct 900
gtgtcctgct ggccaagtgc ctgctgcacc catctgcgga tggtactccc ttccccgccc 960
ctgactgatg gcaggaatcc aagtgcattt cttaaataag ttactattta ttccgctccg 1020
ccccctccct ctcccttgag aagctgagtc ttctgcatca gattattgca acatttaacc 1080
tgaatttaaa agcacacgaa acaaaaaaaa aaaaaaaaaa aaaa 1124

<210> 62
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<223> tryptase gamma 1

<400> 62
Met Ala Leu Gly Ala Cys Gly Leu Leu Leu Leu Leu Ala Val Pro Gly
1 5 10 15
Val Ser Leu Arg Thr Leu Gln Pro Gly Cys Gly Arg Pro Gln Val Ser
20 25 30
Asp Ala Gly Gly Arg Ile Val Gly Gly His Ala Ala Pro Ala Gly Ala
35 40 45
Trp Pro Trp Gln Ala Ser Leu Arg Leu Arg Arg Met His Val Cys Gly
50 55 60
Gly Ser Leu Leu Ser Pro Gln Trp Val Leu Thr Ala Ala His Cys Phe
65 70 75 80
Ser Gly Ser Leu Asn Ser Ser Asp Tyr Gln Val His Leu Gly Glu Leu
85 90 95
Glu Ile Thr Leu Ser Pro His Phe Ser Thr Val Arg Gln Ile Ile Leu
100 105 110
His Ser Ser Pro Ser Gly Gln Pro Gly Thr Ser Gly Asp Ile Ala Leu
115 120 125
Val Glu Leu Ser Val Pro Val Thr Leu Ser Ser Arg Ile Leu Pro Val
130 135 140
Cys Leu Pro Glu Ala Ser Asp Asp Phe Cys Pro Gly Ile Arg Cys Trp
145 150 155 160
Val Thr Gly Trp Gly Tyr Thr Arg Glu Gly Glu Pro Leu Pro Pro Pro
165 170 175
Tyr Ser Leu Arg Glu Val Lys Val Ser Val Val Asp Thr Glu Thr Cys
180 185 190
Arg Arg Asp Tyr Pro Gly Pro Gly Gly Ser Ile Leu Gln Pro Asp Met
195 200 205
Leu Cys Ala Arg Gly Pro Gly Asp Ala Cys Gln Asp Asp Ser Gly Gly
210 215 220
Pro Leu Val Cys Gln Val Asn Gly Ala Trp Val Gln Ala Gly Ile Val
225 230 235 240
Ser Trp Gly Glu Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
245 250 255
Arg Val Pro Ala Tyr Val Asn Trp Ile Arg Arg His Ile Thr Ala Ser
260 265 270
Gly Gly Ser Glu Ser Gly Tyr Pro Arg Leu Pro Leu Leu Ala Gly Phe
275 280 285
Phe Leu Pro Gly Leu Phe Leu Leu Leu Val Ser Cys Val Leu Leu Ala
290 295 300
Lys Cys Leu Leu His Pro Ser Ala Asp Gly Thr Pro Phe Pro Ala Pro
305 310 315 320

Asp

<210> 63
<211> 1459
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK14

<400> 63
gcacctagca gatcccaagc tggggaatgc cagttctggc accaaccttc ctgctccctg 60
ctggggcctc tgctccccca tctctcagga gtcgaaagtg agaaagcaag acatcaagga 120
gggacctgtg ccctgctcca catcctccca cctgccgccc gcagagcctg caggccccgc 180
ccccctcgtc tctggtccct acctctctgc tgtgtcttca tgtccctgag ggtcttgggc 240
tctgggacct ggccctcagc ccctaaaatg ttcctcctgc tgacagcact tcaagtcctg 300
gctatagcca tgacacagag ccaagaggat gagaacaaga taattggtgg ccatacgtgc 360
acccggagct cccagccgtg gcaggcggcc ctgctggcgg gtcccaggcg ccgcttcctc 420
tgcggaggcg ccctgctttc aggccagtgg gtcatcactg ctgctcactg cggccgcccg 480
atccttcagg ttgccctggg caagcacaac ctgaggaggt gggaggccac ccagcaggtg 540
ctgcgcgtgg ttcgtcaggt gacgcacccc aactacaact cccggaccca cgacaacgac 600
ctcatgctgc tgcagctaca gcagcccgca cggatcggga gggcagtcag gcccattgag 660
gtcacccagg cctgtgccag ccccgggacc tcctgccgag tgtcaggctg gggaactata 720
tccagcccca tcgccaggta ccccgcctct ctgcaatgcg tgaacatcaa catctccccg 780
gatgaggtgt gccagaaggc ctatcctaga accatcacgc ctggcatggt ctgtgcagga 840
gttccccagg gcgggaagga ctcttgtcag ggtgactctg ggggacccct ggtgtgcaga 900
ggacagctcc agggcctcgt gtcttgggga atggagcgct gcgccctgcc tggctacccc 960
ggtgtctaca ccaacctgtg caagtacaga agctggattg aggaaacgat gcgggacaaa 1020
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ggacccagga gtccaggccc cagcccctcc tccctcagac ccaggagtcc aggcccccag 1140
cccctcctcc ctcagacccg ggagtccagg cccccagccc ctcctccctc agacccagga 1200
gccccagtcc ccagcatcct gatctttact ccggctctga tctctccttt cccagagcag 1260
ttgcttcagg cgttttctcc ccaccaagcc cccacccttg ctgtgtcacc atcactactc 1320
aagaccggag gcacagaggg caggagcaca gacccccttaa accggcattg tattccaaag 1380
acgacaattt ttaacacgct tagtgtctct aaaaaccgaa taaataatga caataaaaat 1440
ggaatcatcc taaattgta 1459

<210> 64
<211> 251
<212> PRT
<213> Homo sapiens

<220>
<223> Kallikrein-14 precursor S01.029

<400> 64
Met Phe Leu Leu Leu Thr Ala Leu Gln Val Leu Ala Ile Ala Met Thr
 1   5   10   15
Gln Ser Gln Glu Asp Glu Asn Lys Ile Ile Gly Gly His Thr Cys Thr
            20   25   30
Arg Ser Ser Gln Pro Trp Gln Ala Ala Leu Leu Ala Gly Pro Arg Arg
        35   40   45
Arg Phe Leu Cys Gly Gly Ala Leu Leu Ser Gly Gln Trp Val Ile Thr

    50   55   60

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Ala Ala His Cys Gly Arg Pro Ile Leu Gln Val Ala Leu Gly Lys His
65                  70                  75                  80
Asn Leu Arg Arg Trp Glu Ala Thr Gln Gln Val Leu Arg Val Val Arg
                85                  90                  95
Gln Val Thr His Pro Asn Tyr Asn Ser Arg Thr His Asp Asn Asp Leu
            100                 105                 110
Met Leu Leu Gln Leu Gln Gln Pro Ala Arg Ile Gly Arg Ala Val Arg
        115                 120                 125
Pro Ile Glu Val Thr Gln Ala Cys Ala Ser Pro Gly Thr Ser Cys Arg
    130                 135                 140
Val Ser Gly Trp Gly Thr Ile Ser Ser Pro Ile Ala Arg Tyr Pro Ala
145                 150                 155                 160
Ser Leu Gln Cys Val Asn Ile Asn Ile Ser Pro Asp Glu Val Cys Gln
                165                 170                 175
Lys Ala Tyr Pro Arg Thr Ile Thr Pro Gly Met Val Cys Ala Gly Val
            180                 185                 190
Pro Gln Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
        195                 200                 205
Val Cys Arg Gly Gln Leu Gln Gly Leu Val Ser Trp Gly Met Glu Arg
    210                 215                 220
Cys Ala Leu Pro Gly Tyr Pro Gly Val Tyr Thr Asn Leu Cys Lys Tyr
225                 230                 235                 240
Arg Ser Trp Ile Glu Glu Thr Met Arg Asp Lys
                245                 250
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<210> 65
<211> 3008
<212> DNA
<213> Homo sapiens

<220>
<223> hyaluronan-binding serine protease (HGF activator-like protein)

<400> 65
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cctgaatcct tggagactga cattttccc ccctaaaggc atagacaaca aaagaaattt 60
tattgagagg aaaacacaag tccttaaact gcaaagatgt ttgccaggat gtctgatctc 120
catgttctgc tgttaatggc tctggtggga aagacagcct gtgggttctc cctgatgtct 180
ttattggaaa gcctggaccc agactggacc cctgaccagt atgattacag ctacgaggat 240
tataatcagg aagagaacac cagtagcaca cttacccacg ctgagaatcc tgactggtac 300
tacactgagg accaagctga tccatgccag cccaaccccc gtgaacacgg tggggactgc 360
ctcgtccatg ggagcacctt cacatgcagc tgcctggctc ctttctctgg gaataagtgt 420
cagaaagtgc aaaatacgtg caaggacaac ccatgtggcc ggggccaatg tctcattacc 480
cagagtcctc cctactaccg ctgtgtctgt aaacaccctt acacaggtcc cagctgctcc 540
caagtggttc ctgtatgcag gccaaacccc tgccagaatg gggctacctg ctcccggcat 600
aagcggagat ccaagttcac ctgtgcctgt cccgaccagt tcaaggggaa attctgtgaa 660
ataggttctg atgactgcta tgttggcgat ggctactctt accgagggaa aatgaatagg 720
acagtcaacc agcatgcgtg cctttactgg aactcccacc tcctcttgca ggagaattac 780
aacatgttta tggaggatgc tgaaacccat gggattgggg aacacaattt ctgcagaaac 840
ccagatgcgg acgaaaagcc ctggtgcttt attaaagtta ccaatgacaa ggtgaaatgg 900
gaatactgtg atgtctcagc ctgctcagcc caggacgttg cctacccaga ggaaagcccc 960
actgagccat caaccaagct tccggggttt gactcctgtg gaaagactga gatagcagag 1020
aggaagatca agagaatcta tggaggcttt aagagcacgg cgggcaagca cccatggcag 1080
gcgtccctcc agtcctcgct gcctctgacc atctccatgc cccagggcca cttctgtggt 1140
ggggcgctga tccacccctg ctgggtgctc actgctgccc actgcaccga cataaaaacc 1200
agacatctaa aggtggtgct aggggaccag gacctgaaga aagaagaatt tcatgagcag 1260
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agctttaggg tggagaagat attcaagtac agccactaca atgaaagaga tgagattccc 1320
cacaatgata ttgcattgct caagttaaag ccagtggatg gtcactgtgc tctagaatcc 1380
aaatacgtga agactgtgtg cttgcctgat gggtcctttc cctctgggag tgagtgccac 1440
atctctggct ggggtgttac agaaacagga aaagggtccc gccagctcct ggatgccaaa 1500
gtcaagctga ttgccaacac tttgtgcaac tcccgccaac tctatgacca catgattgat 1560
gacagtatga tctgtgcagg aaatcttcag aaacctgggc aagacacctg ccagggtgac 1620
tctggaggcc ccctgacctg tgagaaggac ggcacctact acgtctatgg gatagtgagc 1680
tggggcctgg agtgtgggaa gaggccaggg gtctacaccc aagttaccaa attcctgaat 1740
tggatcaaag ccaccatcaa aagtgaaagt ggcttctaag gtactgtctt ctggacctca 1800
gagcccactc tccttggcac cctgacaccg ggaggcctca tggccaacaa tggacacctc 1860
cagagcctcc aggggaccac acagtagact atccctactc taagcagaga caactgccac 1920
ccagcctggg ccttcccaga ccagcatttg cacaatatca ccaggcttct tctgcctccc 1980
ttggtaaccc aaggaatgat ggaatcaaca caacatagta tgtttgcttt ccttacccaa 2040
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cagacactcg aggcactcaa cagaatcagc catccacgtc taggtatcag agaggaccac 2220
aaatacaaca ttctccatct gctttcagag ttattatttt aataaaggaa gatctgggat 2280
gggctggtgg gccattccag cttgccgaaa tcaaagccat ctgaagcctg tctctggtga 2340
acaaacttcc tctctggcct ctcaggaatc agggtggcat ggctcacaac agcagggcct 2400
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ctccagcctc cactgcttct gccccccgct gctgaaatca aacatacccc aagttaaaat 2520
gaagctcccc caccccccact cccggccccg gttcccacag gacacgctaa gaagcacagg 2580
gagcatttaa caggctcacc ctccctttcc ttttcccctc ttctaccctc cccaagaaaa 2640
agggccttca aggcaggaat gagaaagcaa agccaatctc tcatttagac ctggcttctt 2700
tcttctgaac aaagtagggt tcaaaatgca gactgtcata tccagcgagt ccctgaccct 2760
ttctgcgaat gtaacgagca agcagtcagc acagcctggg ctgccctggc ccgggattga 2820
tgtagccccg gtaggtttgc ctctgcagaa ctaatggctg tgacttcaga gaaagccctg 2880
caggaagttt aacctgcgtg tcatctgcct ggtcatctca gacccatgaa attaggcgcc 2940
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ttgaaaag                                                        3008
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<210> 66
<211> 560
<212> PRT
<213> Homo sapiens

<220>
<223> hyaluronan-binding serine protease (HGF activator-like protein)

<400> 66

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Met Phe Ala Arg Met Ser Asp Leu His Val Leu Leu Leu Met Ala Leu
 1               5                  10                  15
Val Gly Lys Thr Ala Cys Gly Phe Ser Leu Met Ser Leu Leu Glu Ser
            20                  25                  30
Leu Asp Pro Asp Trp Thr Pro Asp Gln Tyr Asp Tyr Ser Tyr Glu Asp
        35                  40                  45
Tyr Asn Gln Glu Glu Asn Thr Ser Ser Thr Leu Thr His Ala Glu Asn
    50                  55                  60
Pro Asp Trp Tyr Tyr Thr Glu Asp Gln Ala Asp Pro Cys Gln Pro Asn
65                  70                  75                  80
Pro Cys Glu His Gly Gly Asp Cys Leu Val His Gly Ser Thr Phe Thr
                85                  90                  95
Cys Ser Cys Leu Ala Pro Phe Ser Gly Asn Lys Cys Gln Lys Val Gln
            100                 105                 110
Asn Thr Cys Lys Asp Asn Pro Cys Gly Arg Gly Gln Cys Leu Ile Thr
        115                 120                 125
Gln Ser Pro Pro Tyr Tyr Arg Cys Val Cys Lys His Pro Tyr Thr Gly
```

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    130                 135                 140
Pro Ser Cys Ser Gln Val Val Pro Val Cys Arg Pro Asn Pro Cys Gln
145                 150                 155                 160
Asn Gly Ala Thr Cys Ser Arg His Lys Arg Arg Ser Lys Phe Thr Cys
                165                 170                 175
Ala Cys Pro Asp Gln Phe Lys Gly Lys Phe Cys Glu Ile Gly Ser Asp
            180                 185                 190
Asp Cys Tyr Val Gly Asp Gly Tyr Ser Tyr Arg Gly Lys Met Asn Arg
        195                 200                 205
Thr Val Asn Gln His Ala Cys Leu Tyr Trp Asn Ser His Leu Leu Leu
    210                 215                 220
Gln Glu Asn Tyr Asn Met Phe Met Glu Asp Ala Glu Thr His Gly Ile
225                 230                 235                 240
Gly Glu His Asn Phe Cys Arg Asn Pro Asp Ala Asp Glu Lys Pro Trp
                245                 250                 255
Cys Phe Ile Lys Val Thr Asn Asp Lys Val Lys Trp Glu Tyr Cys Asp
            260                 265                 270
Val Ser Ala Cys Ser Ala Gln Asp Val Ala Tyr Pro Glu Glu Ser Pro
        275                 280                 285
Thr Glu Pro Ser Thr Lys Leu Pro Gly Phe Asp Ser Cys Gly Lys Thr
    290                 295                 300
Glu Ile Ala Glu Arg Lys Ile Lys Arg Ile Tyr Gly Gly Phe Lys Ser
305                 310                 315                 320
Thr Ala Gly Lys His Pro Trp Gln Ala Ser Leu Gln Ser Ser Leu Pro
                325                 330                 335
Leu Thr Ile Ser Met Pro Gln Gly His Phe Cys Gly Gly Ala Leu Ile
            340                 345                 350
His Pro Cys Trp Val Leu Thr Ala Ala His Cys Thr Asp Ile Lys Thr
        355                 360                 365
Arg His Leu Lys Val Val Leu Gly Asp Gln Asp Leu Lys Lys Glu Glu
    370                 375                 380
Phe His Glu Gln Ser Phe Arg Val Glu Lys Ile Phe Lys Tyr Ser His
385                 390                 395                 400
Tyr Asn Glu Arg Asp Glu Ile Pro His Asn Asp Ile Ala Leu Leu Lys
                405                 410                 415
Leu Lys Pro Val Asp Gly His Cys Ala Leu Glu Ser Lys Tyr Val Lys
            420                 425                 430
Thr Val Cys Leu Pro Asp Gly Ser Phe Pro Ser Gly Ser Glu Cys His
        435                 440                 445
Ile Ser Gly Trp Gly Val Thr Glu Thr Gly Lys Gly Ser Arg Gln Leu
    450                 455                 460
Leu Asp Ala Lys Val Lys Leu Ile Ala Asn Thr Leu Cys Asn Ser Arg
465                 470                 475                 480
Gln Leu Tyr Asp His Met Ile Asp Asp Ser Met Ile Cys Ala Gly Asn
                485                 490                 495
Leu Gln Lys Pro Gly Gln Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro
            500                 505                 510
Leu Thr Cys Glu Lys Asp Gly Thr Tyr Tyr Val Tyr Gly Ile Val Ser
        515                 520                 525
Trp Gly Leu Glu Cys Gly Lys Arg Pro Gly Val Tyr Thr Gln Val Thr
    530                 535                 540
Lys Phe Leu Asn Trp Ile Lys Ala Thr Ile Lys Ser Glu Ser Gly Phe
545                 550                 555                 560
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<210> 67
<211> 2124

<212> DNA
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 4 transcript variant 1

<400> 67
aatcaagctg cccaaagtcc cccaatcact cctggaatac acagagagag gcagcagctt 60
gctcagcgga caaggatgct gggcgtgagg gaccaaggcc tgccctgcac tcgggcctcc 120
tccagccagt gctgaccagg gacttctgac ctgctggcca gccaggacct gtgtggggag 180
gccctcctgc tgccttgggg tgacaatctc agctccaggc tacagggaga ccgggaggat 240
cacagagcca gcatgttaca ggatcctgac agtgatcaac ctctgaacag cctcgatgtc 300
aaaccccctgc gcaaaccccg tatccccatg gagaccttca gaaaggtggg gatccccatc 360
atcatagcac tactgagcct ggcgagtatc atcattgtgg ttgtcctcat caaggtgatt 420
ctggataaat actacttcct ctgcgggcag cctctccact tcatcccgag gaagcagctg 480
tgtgacggag agctggactg tcccttgggg gaggacgagg agcactgtgt caagagcttc 540
cccgaagggc ctgcagtggc agtccgcctc tccaaggacc gatccacact gcaggtgctg 600
gactcggcca cagggaactg gttctctgcc tgtttcgaca acttcacaga agctctcgct 660
gagacagcct gtaggcagat gggctacagc agcaaaccca ctttcagagc tgtggagatt 720
ggcccagacc aggatctgga tgttgttgaa atcacagaaa acagccagga gcttcgcatg 780
cggaactcaa gtgggccctg tctctcaggc tccctggtct ccctgcactg tcttgcctgt 840
gggaagagcc tgaagacccc ccgtgtggtg ggtggggagg aggcctctgt ggattcttgg 900
ccttggcagg tcagcatcca gtacgacaaa cagcacgtct gtggagggag catcctggac 960
ccccactggg tcctcacggc agcccactgc ttcaggaaac ataccgatgt gttcaactgg 1020
aaggtgcggg caggctcaga caaactgggc agcttcccat ccctggctgt ggccaagatc 1080
atcatcattg aattcaaccc catgtacccc aaagacaatg acatcgccct catgaagctg 1140
cagttcccac tcactttctc aggcacagtc aggcccatct gtctgccctt ctttgatgag 1200
gagctcactc cagccacccc actctggatc attggatggg gctttacgaa gcagaatgga 1260
gggaagatgt ctgacatact gctgcaggcg tcagtccagg tcattgacag cacacggtgc 1320
aatgcagacg atgcgtacca gggggaagtc accgagaaga tgatgtgtgc aggcatcccg 1380
gaaggggggtg tggacacctg ccagggtgac agtggtgggc ccctgatgta ccaatctgac 1440
cagtggcatg tggtgggcat cgttagctgg ggctatggct gcgggggccc gagcacccca 1500
ggagtataca ccaaggtctc agcctatctc aactggatct acaatgtctg gaaggctgag 1560
ctgtaatgct gctgcccctt tgcagtgctg ggagccgctt ccttcctgcc ctgcccacct 1620
ggggatcccc caaagtcaga cacagagcaa gagtcccctt gggtacaccc ctctgcccac 1680
agcctcagca tttcttggag cagcaaaggg cctcaattcc tgtaagagac cctcgcagcc 1740
cagaggcgcc cagaggaagt cagcagccct agctcggcca cacttggtgc tcccagcatc 1800
ccagggagag acacagccca ctgaacaagg tctcaggggt attgctaagc caagaaggaa 1860
ctttcccaca ctactgaatg gaagcaggct gtcttgtaaa agcccagatc actgtgggct 1920
ggagaggaga aggaaagggt ctgcgccagc cctgtccgtc ttcacccatc cccaagccta 1980
ctagagcaag aaaccagttg taatataaaa tgcactgccc tactgttggt atgactaccg 2040
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atctctggaa aaaaaaaaaa aaaa 2124

<210> 68
<211> 437
<212> PRT
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 4 isoform 1

<400> 68
Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val
 1   5   10   15
Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val
            20   25   30

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Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile
            35                  40                  45
Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys
        50                  55                  60
Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu
65                  70                  75                  80
Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe
                85                  90                  95
Pro Glu Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr
            100                 105                 110
Leu Gln Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe
        115                 120                 125
Asp Asn Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly
    130                 135                 140
Tyr Ser Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln
145                 150                 155                 160
Asp Leu Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met
                165                 170                 175
Arg Asn Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His
            180                 185                 190
Cys Leu Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly
        195                 200                 205
Glu Glu Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr
    210                 215                 220
Asp Lys Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val
225                 230                 235                 240
Leu Thr Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp
                245                 250                 255
Lys Val Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala
            260                 265                 270
Val Ala Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp
        275                 280                 285
Asn Asp Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly
    290                 295                 300
Thr Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
305                 310                 315                 320
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly
                325                 330                 335
Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val Ile Asp
            340                 345                 350
Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu Val Thr Glu
        355                 360                 365
Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val Asp Thr Cys Gln
    370                 375                 380
Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser Asp Gln Trp His Val
385                 390                 395                 400
Val Gly Ile Val Ser Trp Gly Tyr Gly Cys Gly Gly Pro Ser Thr Pro
                405                 410                 415
Gly Val Tyr Thr Lys Val Ser Ala Tyr Leu Asn Trp Ile Tyr Asn Val
            420                 425                 430
Trp Lys Ala Glu Leu
        435
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<210> 69
<211> 1983
<212> DNA

<213> Homo sapiens

<220>
<223> transmembrane protease, serine 4 transcript variant 2

<400> 69
aatcaagctg cccaaagtcc cccaatcact cctggaatac acagagagag gcagcagctt 60
gctcagcgga caaggatgct gggcgtgagg gaccaaggcc tgccctgcac tcgggcctcc 120
tccagccagt gctgaccagg gacttctgac ctgctggcca gccaggacct gtgtggggag 180
gccctcctgc tgccttgggg tgacaatctc agctccaggc tacagggaga ccgggaggat 240
cacagagcca gcatggatcc tgacagtgat caacctctga acagcctcga tgtcaaaccc 300
ctgcgcaaac cccgtatccc catggagacc ttcagaaagg tggggatccc catcatcata 360
gcactactga gcctggcgag tatcatcatt gtggttgtcc tcatcaaggt gattctggat 420
aaatactact tcctctgcgg gcagcctctc cacttcatcc cgaggaagca gctgtgtgac 480
ggagagctgg actgtccctt gggggaggac gaggagcact gtgtcaagag cttccccgaa 540
gggcctgcag tggcagtccg cctctccaag gaccgatcca cactgcaggt gctggactcg 600
gccacaggga actggttctc tgcctgtttc gacaacttca cagaagctct cgctgagaca 660
gcctgtaggc agatgggcta cagcagcaaa cccactttca gagctgtgga gattggccca 720
gaccaggatc tggatgttgt tgaaatcaca gaaaacagcc aggagcttcg catgcggaac 780
tcaagtgggc cctgtctctc aggctccctg gtctccctgc actgtcttgc ctgtgggaag 840
agcctgaaga ccccccgtgt ggtgggtggg gaggaggcct ctgtggattc ttggccttgg 900
caggtcagca tccagtacga caaacagcac gtctgtggag ggagcatcct ggacccccac 960
tgggtcctca cggcagccca ctgcttcagg aaacataccg atgtgttcaa ctggaaggtg 1020
cgggcaggct cagacaaact gggcagcttc ccatccctgg ctgtggccaa gatcatcatc 1080
attgaattca accccatgta ccccaaagac aatgacatcg ccctcatgaa gctgcagttc 1140
ccactcactt tctcaggcac agtcaggccc atctgtctgc ccttctttga tgaggagctc 1200
actccagcca ccccactctg gatcattgga tggggcttta cgaagcagaa tggagggtga 1260
cagtggtggg cccctgatgt accaatctga ccagtggcat gtggtgggca tcgttagctg 1320
gggctatggc tgcgggggcc cgagcacccc aggagtatac accaaggtct cagcctatct 1380
caactggatc tacaatgtct ggaaggctga gctgtaatgc tgctgccccc ttgcagtgct 1440
gggagccgct tccttcctgc cctgcccacc tggggatccc ccaaagtcag acacagagca 1500
agagtccccc tgggtacacc cctctgccca cagcctcagc atttcttgga gcagcaaagg 1560
gcctcaattc ctgtaagaga ccctcgcagc ccagaggcgc ccagaggaag tcagcagccc 1620
tagctcggcc acacttggtg ctcccagcat cccagggaga gacacagccc actgaacaag 1680
gtctcagggg tattgctaag ccaagaagga actttcccac actactgaat ggaagcaggc 1740
tgtcttgtaa aagcccagat cactgtgggc tggagaggag aaggaaaggg tctgcgccag 1800
ccctgtccgt cttcacccat ccccaagcct actagagcaa gaaaccagtt gtaatataaa 1860
atgcactgcc ctactgttgg tatgactacc gttacctact gttgtcattg ttattacagc 1920
tatggccact attattaaag agctgtgtaa catctctgga aaaaaaaaaa aaaaaaaaaa 1980
aaa 1983

<210> 70
<211> 335
<212> PRT
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 4 isoform 2

<400> 70
Met Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val Lys Pro
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Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val Gly Ile
            20   25   30
Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile Val Val
        35   40   45
Val Leu Ile Lys Val Ile Leu Asp Lys Tyr Tyr Phe Leu Cys Gly Gln

```
    50                  55                  60
Pro Leu His Phe Ile Pro Arg Lys Gln Leu Cys Asp Gly Glu Leu Asp
65                  70                  75                  80
Cys Pro Leu Gly Glu Asp Glu Glu His Cys Val Lys Ser Phe Pro Glu
                85                  90                  95
Gly Pro Ala Val Ala Val Arg Leu Ser Lys Asp Arg Ser Thr Leu Gln
            100                 105                 110
Val Leu Asp Ser Ala Thr Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn
        115                 120                 125
Phe Thr Glu Ala Leu Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser
    130                 135                 140
Ser Lys Pro Thr Phe Arg Ala Val Glu Ile Gly Pro Asp Gln Asp Leu
145                 150                 155                 160
Asp Val Val Glu Ile Thr Glu Asn Ser Gln Glu Leu Arg Met Arg Asn
                165                 170                 175
Ser Ser Gly Pro Cys Leu Ser Gly Ser Leu Val Ser Leu His Cys Leu
            180                 185                 190
Ala Cys Gly Lys Ser Leu Lys Thr Pro Arg Val Val Gly Gly Glu Glu
        195                 200                 205
Ala Ser Val Asp Ser Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys
    210                 215                 220
Gln His Val Cys Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr
225                 230                 235                 240
Ala Ala His Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val
                245                 250                 255
Arg Ala Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala
            260                 265                 270
Lys Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
        275                 280                 285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr Val
    290                 295                 300
Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro Ala Thr
305                 310                 315                 320
Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn Gly Gly
                325                 330                 335
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<210> 71
<211> 855
<212> DNA
<213> Homo sapiens

<220>
<223> tryptase delta 1

<400> 71
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aggcccacga tgctcctcct tgctccccag atgctgagcc tgctgctgct ggcgctgccc 60
gtcctggcga gcccggccta cgtggccccc gccccaggcc aggccctgca gcaaacgggc 120
attgttgggg ggcaggaggc ccccaggagc aagtggccct ggcaggtgag cctgagagtc 180
cgcggcccat actggatgca cttctgcggg ggctccctca tccacccccа gtgggtgcta 240
accgcggcgc actgcgtgga accggacatc aaggatctgg ccgccctcag ggtgcaactg 300
cgggagcagc acctctacta ccaggaccag ctgctgccgg tcagcaggat catcgtgcac 360
ccacagttct acatcatcca gaccggggcg gacatcgccc tgctggagct ggaggagccc 420
gtgaacatct ccagccacat ccacacggtc acgctgcccc ctgcctcgga gaccttcccc 480
ccggggatgc cgtgctgggt cactggctgg ggcgacgtgg acaataatgt gcacctgccg 540
ccgccatacc cgctgaagga ggtggaagtc cccgtagtgg aaaaccacct ttgcaacgcg 600
gaatatcaca ccggcctcca tacgggccac agctttcaaa tcgtccgcga tgacatgctg 660
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tgtgcgggga gcgaaaatca cgactcctgc cagggtgact ctggagggcc cctggtctgc 720
aaggtgaatg gcacctaact gcaggcgggc gtggtcagct gggaggagag ctgtgcccag 780
cccaaccggc ctggcatcta cacccgtgtc acctactact tggactggat ccaccactat 840
gtccccaaga agccc 855

<210> 72
<211> 242
<212> PRT
<213> Homo sapiens

<220>
<223> tryptase delta 1

<400> 72
Met Leu Leu Leu Ala Pro Gln Met Leu Ser Leu Leu Leu Leu Ala Leu
 1   5   10   15
Pro Val Leu Ala Ser Pro Ala Tyr Val Ala Pro Ala Pro Gly Gln Ala
            20   25   30
Leu Gln Gln Thr Gly Ile Val Gly Gly Gln Glu Ala Pro Arg Ser Lys
        35   40   45
Trp Pro Trp Gln Val Ser Leu Arg Val Arg Gly Pro Tyr Trp Met His
    50   55   60
Phe Cys Gly Gly Ser Leu Ile His Pro Gln Trp Val Leu Thr Ala Ala
65   70   75   80
His Cys Val Glu Pro Asp Ile Lys Asp Leu Ala Ala Leu Arg Val Gln
                85   90   95
Leu Arg Glu Gln His Leu Tyr Tyr Gln Asp Gln Leu Leu Pro Val Ser
            100   105   110
Arg Ile Ile Val His Pro Gln Phe Tyr Ile Ile Gln Thr Gly Ala Asp
        115   120   125
Ile Ala Leu Leu Glu Leu Glu Glu Pro Val Asn Ile Ser Ser His Ile
    130   135   140
His Thr Val Thr Leu Pro Pro Ala Ser Glu Thr Phe Pro Pro Gly Met
145   150   155   160
Pro Cys Trp Val Thr Gly Trp Gly Asp Val Asp Asn Asn Val His Leu
                165   170   175
Pro Pro Pro Tyr Pro Leu Lys Glu Val Glu Val Pro Val Val Glu Asn
            180   185   190
His Leu Cys Asn Ala Glu Tyr His Thr Gly Leu His Thr Gly His Ser
        195   200   205
Phe Gln Ile Val Arg Asp Asp Met Leu Cys Ala Gly Ser Glu Asn His
    210   215   220
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Val Asn
225   230   235   240
Gly Thr

<210> 73
<211> 1462
<212> DNA
<213> Homo sapiens

<220>
<223> Marapsin

<400> 73

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ctgtctcaaa aaattaaaaa aaataataat aataataatg aatgaagctg gacggacttc 60
gcgtgcaccg cggtcagctc ggggtctgct gggggggtctg ggtcagctca gggtccagga 120
accgaggcca acggcacccc gtgctgcgct ggggtgaggg gtctgccctg gggtctcggg 180
gttcagggct aggtcacgga ggagtcggct ctgggcgctt ccttcctgag gagaggagct 240
gggcaggccg ggccgacggg ttgggccgca tagccgggcc tgtgctcatc tccagcataa 300
aactccactt catggagcct gcacctcgct cgtgctccaa cgcttctgcc accgccgacc 360
acggccctgc gccccagcca ggcctgagga catgaggcgg ccggcggcgg tgccgctcct 420
gctgctgctg tgttttgggt ctcagagggc caaggcagca acagcctgtg gtcgccccag 480
gatgctgaac cgaatggtgg gcgggcagga cacgcaggag ggcgagtggc cctggcaagt 540
cagcatccag cgcaacggaa gccacttctg cgggggcagc ctcatcgcgg agcagtgggt 600
cctgacggct gcgcactgct tccgcaacac ctctgagacg tccctgtacc aggtcctgct 660
gggggcaagg cagctagtgc agccgggacc acacgctatg tatgcccggg tgaggcaggt 720
ggagagcaac cccctgtacc agggcacggc ctccagcgct gacgtggccc tggtggagct 780
ggaggcacca gtgcccttca ccaattacat cctccccgtg tgcctgcctg acccctcggt 840
gatctttgag acgggcatga actgctgggt cactggctgg ggcagcccca gtgaggaaga 900
cctcctgccc gaaccgcgga tcctgcagaa actcgctgtg cccatcatcg acacacccaa 960
gtgcaacctg ctctacagca aagacaccga gtttggctac caacccaaaa ccatcaagaa 1020
tgacatgctg tgcgccggct tcgaggaggg caagaaggat gcctgcaagg gcgactcggg 1080
cggccccctg gtgtgcctcg tgggtcagtc gtggctgcag gcgggggtga tcagctgggg 1140
tgagggctgt gcccgccaga accgcccagg tgtctacatc cgtgtcaccg cccaccacaa 1200
ctggatccat cggatcatcc ccaaactgca gttccagcca gcgaggttgg gcggccagaa 1260
gtgagacccc cggggccagg agccccttga gcagagctct gcacccagcc tgcccgccca 1320
caccatcctg ctggtcctcc cagcgctgct gttgcacctg tgagccccac cagactcatt 1380
tgtaaatagc gctccttcct cccctctcaa atacccttat tttatttatg tttctcccaa 1440
taaaaaccca gcctgtgtgc ca                                          1462
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<210> 74
<211> 290
<212> PRT
<213> Homo sapiens

<220>
<223> Marapsin

<400> 74

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Met Arg Arg Pro Ala Ala Val Pro Leu Leu Leu Leu Leu Cys Phe Gly
 1               5                  10                  15
Ser Gln Arg Ala Lys Ala Ala Thr Ala Cys Gly Arg Pro Arg Met Leu
            20                  25                  30
Asn Arg Met Val Gly Gly Gln Asp Thr Gln Glu Gly Glu Trp Pro Trp
        35                  40                  45
Gln Val Ser Ile Gln Arg Asn Gly Ser His Phe Cys Gly Gly Ser Leu
    50                  55                  60
Ile Ala Glu Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asn Thr
65                  70                  75                  80
Ser Glu Thr Ser Leu Tyr Gln Val Leu Leu Gly Ala Arg Gln Leu Val
                85                  90                  95
Gln Pro Gly Pro His Ala Met Tyr Ala Arg Val Arg Gln Val Glu Ser
            100                 105                 110
Asn Pro Leu Tyr Gln Gly Thr Ala Ser Ser Ala Asp Val Ala Leu Val
        115                 120                 125
Glu Leu Glu Ala Pro Val Pro Phe Thr Asn Tyr Ile Leu Pro Val Cys
    130                 135                 140
Leu Pro Asp Pro Ser Val Ile Phe Glu Thr Gly Met Asn Cys Trp Val
145                 150                 155                 160
Thr Gly Trp Gly Ser Pro Ser Glu Glu Asp Leu Leu Pro Glu Pro Arg
                165                 170                 175
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Ile Leu Gln Lys Leu Ala Val Pro Ile Ile Asp Thr Pro Lys Cys Asn
            180                 185                 190
Leu Leu Tyr Ser Lys Asp Thr Glu Phe Gly Tyr Gln Pro Lys Thr Ile
        195                 200                 205
Lys Asn Asp Met Leu Cys Ala Gly Phe Glu Glu Gly Lys Lys Asp Ala
    210                 215                 220
Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Val Gly Gln Ser
225                 230                 235                 240
Trp Leu Gln Ala Gly Val Ile Ser Trp Gly Glu Gly Cys Ala Arg Gln
                245                 250                 255
Asn Arg Pro Gly Val Tyr Ile Arg Val Thr Ala His His Asn Trp Ile
            260                 265                 270
His Arg Ile Ile Pro Lys Leu Gln Phe Gln Pro Ala Arg Leu Gly Gly
        275                 280                 285
Gln Lys
    290
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<210> 75
<211> 1755
<212> DNA
<213> Homo sapiens

<220>
<223> Tryptase homologue 2

<400> 75

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aacgtgtgct ctgcagggag cccagaccag agtccaagcc ctaggcagtg ccacccttac 120
ccagcccagc cttgaagaca gaatgagagg ggtttcctgt ctccaggtcc tgctccttct 180
ggtgctggga gctgctggga ctcagggaag gaagtctgca gcctgcgggc agccccgcat 240
gtccagtcgg atcgttgggg gccgggatgg ccgggacgga gagtggccgt ggcaggcgag 300
catccagcat cgtggggcac acgtgtgcgg ggggtcgctc atcgcccccc agtgggtgct 360
gacagcggcg cactgcttcc ccaggagggc actgccagct gagtaccgcg tgcgcctggg 420
ggcgctgcgt ctgggctcca cctcgccccg cacgctctcg gtgcccgtgc gacgggtgct 480
gctgcccccg gactactccg aggacggggc ccgcggcgac ctggcactgc tgcagctgcg 540
tcgcccggtg cccctgagcg ctcgcgtcca acccgtctgc ctgcccgtgc ccggcgcccg 600
cccgccgccc ggcacaccat gccgggtcac cggctggggc agcctccgcc caggagtgcc 660
cctcccagag tggcgaccgc tacaaggagt aagggtgccg ctgctggact cgcgcacctg 720
cgacggcctc taccacgtgg gcgcggacgt gccccaggct gagcgcattg tgctgcctgg 780
gagtctgtgt gccggctacc cccagggcca caaggacgcc tgccagggtg attctggggg 840
acctctgacc tgcctgcagt ctgggagctg ggtcctggtg ggcgtggtga gctggggcaa 900
gggttgtgcc ctgcccaacc gtccaggggt ctacaccagt gtggccacat atagcccctg 960
gattcaggct cgcgtcagct tctaatgcta gccggtgagg ctgacctgga gccagctgct 1020
ggggtccctc agcctcctgg ttcatccagg cacctgccta taccccacat cccttctgcc 1080
tcgaggccaa gatgcctaaa aaagctaaag gccaccccac cccccaccca ccacctcctg 1140
cctcctctcc tctttgggga tcaccagctc tgactccacc aaccctcatc caggaatctg 1200
ccatgagtcc cagggagtca cactccccac tcccttcctg gcttgtattt acttttcttg 1260
gccctggcca gggctgggcg caaggcacgc agtgatgggc aaaccaattg ctgcccatct 1320
ggcctgtgtg cccatctttt tctggagaaa gtcagattca cagcatgaca gagatttgac 1380
accagggaga tcctccatag ctggctttga ggacacgggg accacagcca tgagcggcct 1440
ctaagagctg agagacagcc ggcagggaat cggaaccctc agacccacag ccgcaaggca 1500
ctggattctg gcagcaccct gaaggagctg ggaagtaagt tcttccccag cctccagata 1560
agagccccgc cggccaatcc cttcatttca acctaaagag accctaagca gagaacctag 1620
ctgagccact cctgacctac aaagttgtga cttaataaat gtgtgctttg aacccaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaa                                                  1755
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<210> 76
<211> 284
<212> PRT
<213> Homo sapiens

<220>
<223> Tryptase homologue 2

<400> 76
Met Arg Gly Val Ser Cys Leu Gln Val Leu Leu Leu Leu Val Leu Gly
 1   5   10   15
Ala Ala Gly Thr Gln Gly Arg Lys Ser Ala Ala Cys Gly Gln Pro Arg
            20   25   30
Met Ser Ser Arg Ile Val Gly Gly Arg Asp Gly Arg Asp Gly Glu Trp
        35   40   45
Pro Trp Gln Ala Ser Ile Gln His Pro Gly Ala His Val Cys Gly Gly
    50   55   60
Ser Leu Ile Ala Pro Gln Trp Val Leu Thr Ala Ala His Cys Phe Pro
65   70   75   80
Arg Arg Ala Leu Pro Ala Glu Tyr Arg Val Arg Leu Gly Ala Leu Arg
                85   90   95
Leu Gly Ser Thr Ser Pro Arg Thr Leu Ser Val Pro Val Arg Arg Val
            100   105   110
Leu Leu Pro Pro Asp Tyr Ser Glu Asp Gly Ala Arg Gly Asp Leu Ala
        115   120   125
Leu Leu Gln Leu Arg Arg Pro Val Pro Leu Ser Ala Arg Val Gln Pro
    130   135   140
Val Cys Leu Pro Val Pro Gly Ala Arg Pro Pro Pro Gly Thr Pro Cys
145   150   155   160
Arg Val Thr Gly Trp Gly Ser Leu Arg Pro Gly Val Pro Leu Pro Glu
                165   170   175
Trp Arg Pro Leu Gln Gly Val Arg Val Pro Leu Leu Asp Ser Arg Thr
            180   185   190
Cys Asp Gly Leu Tyr His Val Gly Ala Asp Val Pro Gln Ala Glu Arg
        195   200   205
Ile Val Leu Pro Gly Ser Leu Cys Ala Gly Tyr Pro Gln Gly His Lys
    210   215   220
Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Thr Cys Leu Gln Ser
225   230   235   240
Gly Ser Trp Val Leu Val Gly Val Val Ser Trp Gly Lys Gly Cys Ala
                245   250   255
Leu Pro Asn Arg Pro Gly Val Tyr Thr Ser Val Ala Thr Tyr Ser Pro
            260   265   270
Trp Ile Gln Ala Arg Val Thr Ser Asn Ala Ser Arg
        275   280

<210> 77
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<223> Tryptase homologue 3

<400> 77

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cgcctgagga gacgccaccg atgtggaggg agcctgctca gccgccgctg ggtgctctcg 120
gctgcgcact gcttcgctcc ccagggtgac tcaggtggac ccttggtctg tgacaaggat 180
ggactgtggt atcaggttgg aatcgtgagc tggggaatgg actgcggtca acccaatcgg 240
cctggtgtct acaccaacat cagtgtgtac ttccactgga tccggagggt gatgtcccac 300
agtacaccca ggccaaaccc c                                           321

<210> 78
<211> 107
<212> PRT
<213> Homo sapiens

<220>
<223> Tryptase homologue 3

<400> 78
Ala Leu Val Ala Gly Gly Val Glu Ser Ala Arg Gly Arg Trp Pro Trp
 1               5                  10                  15
Gln Ala Ser Leu Arg Leu Arg Arg Arg His Arg Cys Gly Gly Ser Leu
            20                  25                  30
Leu Ser Arg Arg Trp Val Leu Ser Ala Ala His Cys Phe Ala Pro Gln
        35                  40                  45
Gly Asp Ser Gly Gly Pro Leu Val Cys Asp Lys Asp Gly Leu Trp Tyr
    50                  55                  60
Gln Val Gly Ile Val Ser Trp Gly Met Asp Cys Gly Gln Pro Asn Arg
65                  70                  75                  80
Pro Gly Val Tyr Thr Asn Ile Ser Val Tyr Phe His Trp Ile Arg Arg
                85                  90                  95
Val Met Ser His Ser Thr Pro Arg Pro Asn Pro
            100                 105


<210> 79
<211> 2468
<212> DNA
<213> Homo sapiens

<220>

<223> transmembrane protease, serine 3 transcript variant A

<400> 79
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ccatctacat ttttgggact cgggaattat gaggtagagg tggaggcgga gccggatgtc 180
agaggtcctg aaatagtcac catgggggaa aatgatccgc ctgctgttga agccccccttc 240
tcattccgat cgctttttgg ccttgatgat ttgaaaataa gtcctgttgc accagatgca 300
gatgctgttg ctgcacagat cctgtcactg ctgccattga agtttttttcc aatcatcgtc 360
attgggatca ttgcattgat attagcactg gccattggtc tgggcatcca cttcgactgc 420
tcagggaagt acagatgtcg ctcatccttt aagtgtatcg agctgatagc tcgatgtgac 480
ggagtctcgg attgcaaaga cggggaggac gagtaccgct gtgtccgggt gggtggtcag 540
aatgccgtgc tccaggtgtt cacagctgct tcgtggaaga ccatgtgctc cgatgactgg 600
aagggtcact acgcaaatgt tgcctgtgcc caactgggtt tcccaagcta tgtgagttca 660
gataacctca gagtgagctc gctggagggg cagttccggg aggagtttgt gtccatcgat 720
cacctcttgc cagatgacaa ggtgactgca ttacaccact cagtatatgt gagggaggga 780
tgtgcctctg gccacgtggt taccttgcag tgcacagcct gtggtcatag aaggggctac 840
agctcacgca tcgtgggtgg aaacatgtcc ttgctctcgc agtggccctg gcaggccagc 900
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```
cttcagttcc agggctacca cctgtgcggg ggctctgtca tcacgcccct gtggatcatc 960
actgctgcac actgtgttta tgacttgtac ctccccaagt catggaccat ccaggtgggt 1020

ctagtttccc tgttggacaa tccagcccca tcccacttgg tggagaagat tgtctaccac 1080
agcaagtaca agccaaagag gctgggcaat gacatcgccc ttatgaagct ggccgggcca 1140
ctcacgttca atgaaatgat ccagcctgtg tgcctgccca actctgaaga gaacttcccc 1200
gatggaaaag tgtgctggac gtcaggatgg ggggccacag aggatggagc aggtgacgcc 1260
tcccctgtcc tgaaccacgc ggccgtccct ttgatttcca acaagatctg caaccacagg 1320
gacgtgtacg gtggcatcat ctccccctcc atgctctgcg cgggctacct gacgggtggc 1380
gtggacagct gccaggggga cagcgggggg cccctggtgt gtcaagagag gaggctgtgg 1440
aagttagtgg gagcgaccag ctttggcatc ggctgcgcag aggtgaacaa gcctggggtg 1500
tacacccgtg tcacctcctt cctggactgg atccacgagc agatggagag agacctaaaa 1560
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ttgcctcagc ttccccagta gctgggacca caggtgcccg ccaccacacc caactaattt 1920
ttgtattttt agtagagaca gggtttcacc atgttggcca ggctgctctc aaacccctga 1980
cctcaaatga tgtgcctgct tcagcctccc acagtgctgg gattacaggc atgggccacc 2040
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agggcggcct ttcccactgg tccatctggt tttctctcca ggggtcttgc aaaattcctg 2160
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gcaccagccc agaagtgcag aactgcagtc actgcacgtt ttcatctcta gggaccagaa 2280
ccaaacccac cctttctact tccaagactt attttcacat gtggggaggt taatctagga 2340
atgactcgtt taaggcctat tttcatgatt tctttgtagc atttggtgct tgacgtatta 2400
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aaaaaaaa                                                          2468
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<210> 80
<211> 454
<212> PRT
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 isoform 1

<400> 80

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 1               5                  10                  15
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
            20                  25                  30
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
        35                  40                  45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
    50                  55                  60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
65                  70                  75                  80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
                85                  90                  95
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
            100                 105                 110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
        115                 120                 125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
    130                 135                 140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
```

```
145                 150                 155                 160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
                165                 170                 175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
            180                 185                 190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
        195                 200                 205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
    210                 215                 220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
225                 230                 235                 240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
                245                 250                 255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
            260                 265                 270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
        275                 280                 285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
    290                 295                 300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met Ile
305                 310                 315                 320
Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly Lys
                325                 330                 335
Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala Gly Asp
            340                 345                 350
Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn Lys
        355                 360                 365
Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser Met
    370                 375                 380
Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly Asp
385                 390                 395                 400
Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu Val
                405                 410                 415
Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly
            420                 425                 430
Val Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met
        435                 440                 445
Glu Arg Asp Leu Lys Thr
    450
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<210> 81
<211> 2554
<212> DNA
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 transcript variant B

<400> 81
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tgtctttctg ggggatacta ttcaacccat agcacatccc ctcatccccc atggaataac 180
cgggtcagag gtggagcagg taggactgaa ctagagaatg tgccccttgg tgggtggccc 240
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aaggatagtt aaatttgtaa gtttcatggc actccaagtc aggttctggg gctttctgct 360
cttccttttt ctggttatca gatgcagatg ctgttgctgc acagatcctg tcactgctgc 420

```
cattgaagtt ttttccaatc atcgtcattg ggatcattgc attgatatta gcactggcca 480
ttggtctggg catccacttc gactgctcag ggaagtacag atgtcgctca tcctttaagt 540
gtatcgagct gatagctcga tgtgacggag tctcggattg caaagacggg gaggacgagt 600
accgctgtgt ccgggtgggt ggtcagaatg ccgtgctcca ggtgttcaca gctgcttcgt 660
ggaagaccat gtgctccgat gactggaagg gtcactacgc aaatgttgcc tgtgcccaac 720
tgggtttccc aagctatgtg agttcagata acctcagagt gagctcgctg gaggggcagt 780
tccgggagga gtttgtgtcc atcgatcacc tcttgccaga tgacaaggtg actgcattac 840
accactcagt atatgtgagg gagggatgtg cctctggcca cgtggttacc ttgcagtgca 900
cagcctgtgg tcatagaagg ggctacagct cacgcatcgt gggtggaaac atgtccttgc 960
tctcgcagtg gccctggcag gccagccttc agttccaggg ctaccacctg tgcgggggct 1020
ctgtcatcac gcccctgtgg atcatcactg ctgcacactg tgtttatgac ttgtacctcc 1080
ccaagtcatg gaccatccag gtgggtctag tttccctgtt ggacaatcca gccccatccc 1140
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tcgcccttat gaagctggcc gggccactca cgttcaatga aatgatccag cctgtgtgcc 1260
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ccacagagga tggagcaggt gacgcctccc ctgtcctgaa ccacgcggcc gtccctttga 1380
tttccaacaa gatctgcaac cacagggacg tgtacggtgg catcatctcc ccctccatgc 1440
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tggtgtgtca agagaggagg ctgtggaagt tagtgggagc gaccagcttt ggcatcggct 1560
gcgcagaggt gaacaagcct ggggtgtaca cccgtgtcac ctccttcctg gactggatcc 1620
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ttcctgaggt gatgaagaca gcccgatcct cccctggact cccgtgtagg aacctgcaca 1740
cgagcagaca cccttggagc tctgagttcc ggcaccagta gcaggcccga aagaggcacc 1800
cttccatctg attccagcac aaccttcaag ctgctttttg ttttttgttt ttttgaggtg 1860
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tgcccgccac cacacccaac taatttttgt atttttagta gagacagggt ttcaccatgt 2040
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tgctgggatt acaggcatgg gccaccacgc ctagcctcac gctcctttct gatcttcact 2160
aagaacaaaa gaagcagcaa cttgcaaggg cggcctttcc cactggtcca tctggttttc 2220
tctccagggg tcttgcaaaa ttcctgacga gataagcagt tatgtgacct cacgtgcaaa 2280
gccaccaaca gccactcaga aaagacgcac cagcccagaa gtgcagaact gcagtcactg 2340
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tcacatgtgg ggaggttaat ctaggaatga ctcgtttaag gcctattttc atgatttctt 2460
tgtagcattt ggtgcttgac gtattattgt cctttgattc caaataatat gtttccttcc 2520
ctcaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa                             2554
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<210> 82
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 isoform 2

<400> 82

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Met Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala
 1               5                  10                  15
Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser
            20                  25                  30
Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu
        35                  40                  45
Leu Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg
    50                  55                  60
Glu Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys
65                  70                  75                  80
Gly His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser
```

```
                85                  90                  95
Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr
            100                 105                 110
His Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala
        115                 120                 125
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln
    130                 135                 140
Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val
145                 150                 155                 160
Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn
                165                 170                 175
Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met
            180                 185                 190
Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly
        195                 200                 205
Lys Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala Gly
    210                 215                 220
Asp Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn
225                 230                 235                 240
Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser
                245                 250                 255
Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly
            260                 265                 270
Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu
        275                 280                 285
Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro
    290                 295                 300
Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln
305                 310                 315                 320
Met Glu Arg Asp Leu Lys Thr
                325
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<210> 83
<211> 2135
<212> DNA
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 transcript variant C

<400> 83
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tgtatcgagc tgatagctcg atgtgacgga gtctcggatt gcaaagacgg ggaggacgag 180
taccgctgtg tccgggtggg tggtcagaat gccgtgctcc aggtgttcac agctgcttcg 240
tggaagacca tgtgctccga tgactggaag ggtcactacg caaatgttgc ctgtgcccaa 300
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ttccgggagg agtttgtgtc catcgatcac ctcttgccag atgacaaggt gactgcatta 420
caccactcag tatatgtgag ggagggatgt gcctctggcc acgtggttac cttgcagtgc 480
acagcctgtg gtcatagaag gggctacagc tcacgcatcg tgggtggaaa catgtccttg 540
ctctcgcagt ggccctggca ggccagcctt cagttccagg gctaccacct gtgcgggggc 600
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cccaagtcat ggaccatcca ggtgggtcta gtttccctgt tggacaatcc agccccatcc 720
cacttggtgg agaagattgt ctaccacagc aagtacaagc caaagaggct gggcaatgac 780
atcgccctta tgaagctggc cgggccactc acgttcaatg aaatgatcca gcctgtgtgc 840
ctgcccaact ctgaagagaa cttccccgat ggaaaagtgt gctggacgtc aggatggggg 900
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ctctgcgcgg gctacctgac gggtggcgtg gacagctgcc agggggacag cgggggggcc 1080
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tgcgcagagg tgaacaagcc tggggtgtac acccgtgtca cctccttcct ggactggatc 1200
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ccttccatct gattccagca caaccttcaa gctgcttttt gtttttgtt ttttgaggt 1440
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tccgcttccc tggttcaagc gattctcttg cctcagcttc cccagtagct gggaccacag 1560
gtgcccgcca ccacacccaa ctaatttttg tatttttagt agagacaggg tttcaccatg 1620
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agccaccaac agccactcag aaaagacgca ccagcccaga agtgcagaac tgcagtcact 1920
gcacgttttc atctctaggg accagaacca aacccaccct ttctacttcc aagacttatt 1980
ttcacatgtg gggaggttaa tctaggaatg actcgtttaa ggcctatttt catgatttct 2040
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cctcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa                           2135
```

<210> 84
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 isoform 2

<400> 84

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Met Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala
 1               5                  10                  15
Gln Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser
            20                  25                  30
Ser Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu
        35                  40                  45
Leu Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg
    50                  55                  60
Glu Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys
65                  70                  75                  80
Gly His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser
                85                  90                  95
Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr
            100                 105                 110
His Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala
        115                 120                 125
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln
    130                 135                 140
Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val
145                 150                 155                 160
Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn
                165                 170                 175
Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu Met
            180                 185                 190
Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp Gly
        195                 200                 205
```

```
Lys Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala Gly
    210                 215                 220
Asp Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser Asn
225                 230                 235                 240
Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro Ser
                245                 250                 255
Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln Gly
            260                 265                 270
Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys Leu
        275                 280                 285
Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys Pro
    290                 295                 300
Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln
305                 310                 315                 320
Met Glu Arg Asp Leu Lys Thr
                325
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<210> 85
<211> 1359
<212> DNA
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 transcript variant D

<400> 85
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ccatctacat ttttgggact cgggaattat gaggtagagg tggaggcgga gccggatgtc 180
agaggtcctg aaatagtcac catgggggaa aatgatccgc ctgctgttga agccccccttc 240
tcattccgat cgctttttgg ccttgatgat ttgaaaataa gtcctgttgc accagatgca 300
gatgctgttg ctgcacagat cctgtcactg ctgccattga agttttttcc aatcatcgtc 360
attgggatca ttgcattgat attagcactg gccattggtc tgggcatcca cttcgactgc 420
tcagggaagt acagatgtcg ctcatccttt aagtgtatcg agctgatagc tcgatgtgac 480
ggagtctcgg attgcaaaga cggggaggac gagtaccgct gtgtccgggt gggtggtcag 540
aatgccgtgc tccaggtgtt cacagctgct tcgtggaaga ccatgtgctc cgatgactgg 600
aagggtcact acgcaaatgt tgcctgtgcc caactgggtt tcccaagcta tgtgagttca 660
gataacctca gagtgagctc gctggagggg cagttccggg aggagtttgt gtccatcgat 720

cacctcttgc cagatgacaa ggtgactgca ttacaccact cagtatatgt gagggaggga 780
tgtgcctctg gccacgtggt taccttgcag tgcacagcct gtggtcatag aaggggctac 840
agctcacgca tcgtgggtgg aaacatgtcc ttgctctcgc agtggccctg gcaggccagc 900
cttcagttcc agggctacca cctgtgcggg ggctctgtca tcacgcccct gtggatcatc 960
actgctgcac actgtgttta tgacttgtac ctccccaagt catggaccat ccaggtgggt 1020
ctagtttccc tgttggacaa tccagcccca tcccacttgg tggagaagat tgtctaccac 1080
agcaagtaca agccaaagag gctgggcaat gacatcgccc ttatgaagct ggccgggcca 1140
ctcacgttca atggtacatc tgggtctcta tgtggttctg cagctcttcc tttgtttcaa 1200
gaggatttgc aattgctcat tgaagcattc ttatgatggc tgctttataa tccttgtcag 1260
atattaataa ttccaactcc tgattcatgt tggtgttggc atcagttgat tatcttttct 1320
cattaaaatt gtgatgctcc taaaaaaaaa aaaaaaaaa                        1359
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<210> 86
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<223> transmembrane protease, serine 3 isoform 3

<400> 86
Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe Arg
 1   5   10   15
Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala Pro Asp
            20   25   30
Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro Leu Lys Phe
        35   40   45
Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile Leu Ala Leu Ala
    50   55   60
Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly Lys Tyr Arg Cys Arg
65   70   75   80
Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala Arg Cys Asp Gly Val Ser
                85   90   95
Asp Cys Lys Asp Gly Glu Asp Glu Tyr Arg Cys Val Arg Val Gly Gly
            100   105   110
Gln Asn Ala Val Leu Gln Val Phe Thr Ala Ala Ser Trp Lys Thr Met
        115   120   125
Cys Ser Asp Asp Trp Lys Gly His Tyr Ala Asn Val Ala Cys Ala Gln
    130   135   140
Leu Gly Phe Pro Ser Tyr Val Ser Ser Asp Asn Leu Arg Val Ser Ser
145   150   155   160
Leu Glu Gly Gln Phe Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu
                165   170   175
Pro Asp Asp Lys Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu
            180   185   190
Gly Cys Ala Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly
        195   200   205
His Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu
    210   215   220
Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His
225   230   235   240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala Ala
                245   250   255
His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile Gln Val
            260   265   270
Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu Val Glu
        275   280   285
Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly Asn Asp
    290   295   300
Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Gly Thr Ser
305   310   315   320
Gly Ser Leu Cys Gly Ser Ala Ala Leu Pro Leu Phe Gln Glu Asp Leu
                325   330   335
Gln Leu Leu Ile Glu Ala Phe Leu
            340

<210> 87
<211> 1191
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK15 transcript variant 1

<400> 87
actgcagccg aaccctggtc cctcctccac aatgtggctt ctcctcactc tctccttcct 60
gctggcatcc acagcagccc aggatggtga caagttgctg gaaggtgacg agtgtgcacc 120
ccactcccag ccatggcaag tggctctcta cgagcgtgga cgctttaact gtggcgcttc 180
cctcatctcc ccacactggg tgctgtctgc ggcccactgc caaagccgct tcatgagagt 240
gcgcctggga gagcacaacc tgcgcaagcg cgatggccca gagcaactac ggaccacgtc 300
tcgggtcatt ccacacccgc gctacgaagc gcgcagccac cgcaacgaca tcatgttgct 360
gcgcctagtc cagcccgcac gcctgaaccc ccagtgagtc tcccagatac gttgcattgt 420
gccaacatca gcattatctc ggacacatct tgtgacaaga gctacccagg gcgcctgaca 480
aacaccatgg tgtgtgcagg cgcggagggc agaggcgcag aatcctgtga gggtgactct 540
gggggacccc tggtctgtgg gggcatcctg cagggcattg tgtcctgggg tgacgtccct 600
tgtgacaaca ccaccaagcc tggtgtctat accaaagtct gccactactt ggagtggatc 660
agggaaacca tgaagaggaa ctgactattc tagcctatct cctgtgcccc tgactgagca 720
gaagccccca cagctggcca gcagccccgc ctgacatgga acagaacgga gccatccccc 780
aagaccctgt ccaaggccca gatgttagcc aaggacttgt cccacctgag gacaaagctg 840
gcgctcaagg tcacctgttt aatgccaaga taacaaagcg ctgatccaag ttgctctgta 900
ggaatttctg tgacttttt ctggggtcaa agagaaaccc cgagacactg tacactgttc 960
cttttcaccc accacccga tccctaggtg aggagaagcg gcttgaagca gggctccatt 1020
cattcaacac acatgaccac ccgtgtgatc ttgaacaaga ggcccaatct cacttcgcct 1080
tggtttcctt atctgtaaaa tgagaccatc ttattgctga cttcaaaggg ctgttgtgag 1140
gattaaatga gatgattcgt ctgaactgat taaaatcgtg tctggcactg a 1191

<210> 88
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK15 isoform 1

<400> 88
Met Trp Leu Leu Leu Thr Leu Ser Phe Leu Leu Ala Ser Thr Ala Ala
1 5 10 15
Gln Asp Gly Asp Lys Leu Leu Glu Gly Asp Glu Cys Ala Pro His Ser
20 25 30
Gln Pro Trp Gln Val Ala Leu Tyr Glu Arg Gly Arg Phe Asn Cys Gly
35 40 45
Ala Ser Leu Ile Ser Pro His Trp Val Leu Ser Ala Ala His Cys Gln
50 55 60
Ser Arg Phe Met Arg Val Arg Leu Gly Glu His Asn Leu Arg Lys Arg
65 70 75 80
Asp Gly Pro Glu Gln Leu Arg Thr Thr Ser Arg Val Ile Pro His Pro
85 90 95
Arg Tyr Glu Ala Arg Ser His Arg Asn Asp Ile Met Leu Leu Arg Leu
100 105 110
Val Gln Pro Ala Arg Leu Asn Pro Gln
115 120

<210> 89
<211> 1172
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK15 transcript variant 2

<400> 89
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gctggcatcc acagcagccc aggatggtga caagttgctg gaaggtgacg agtgtgcacc 120
ccactcccag ccatggcaag tggctctcta cgagcgtgga cgctttaact gtggcgcttc 180
cctcatctcc ccacactggg tgctgtctgc ggcccactgc caaagccgct tcatgagagt 240
gcgcctggga gagcacaacc tgcgcaagcg cgatggccca gagcaactac ggaccacgtc 300
tcgggtcatt ccacacccgc gctacgaagc gcgcagccac cgcaacgaca tcatgttgct 360
gcgcctagtc cagcccgcac gcctgaaccc ccaggtgcgc cccgcggtgc tacccacgcg 420
ttgcccccac ccgggggagg cctgtgtggt gtctggctgg ggcctggtgt cccacaacga 480
gcctgggacc gctgggagcc cccggtcaca agggtgactc tgggggaccc ctggtctgtg 540
ggggcatcct gcagggcatt gtgtcctggg gtgacgtccc ttgtgacaac accaccaagc 600
ctggtgtcta taccaaagtc tgccactact tggagtggat cagggaaacc atgaagagga 660
actgactatt ctagcctatc tcctgtgccc ctgactgagc agaagccccc acagctggcc 720
agcagccccg cctgacatgg aacagaacgg agccatcccc caagaccctg tccaaggccc 780
agatgttagc caaggacttg tcccacctga ggacaaagct ggcgctcaag gtcacctgtt 840
taatgccaag ataacaaagc gctgatccaa gttgctctgt aggaatttct gtgacttttt 900
tctggggtca aagagaaacc ccgagacact gtacactgtt ccttttcacc caccaccccg 960
atccctaggt gaggagaagc ggcttgaagc agggctccat tcattcaaca cacatgacca 1020
cccgtgtgat cttgaacaag aggcccaatc tcacttcgcc ttggtttcct tatctgtaaa 1080
atgagaccat cttattgctg acttcaaagg gctgttgtga ggattaaatg agatgattcg 1140
tctgaactga ttaaaatcgt gtctggcact ga 1172

<210> 90
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK15 isoform 2

<400> 90
Met Trp Leu Leu Leu Thr Leu Ser Phe Leu Leu Ala Ser Thr Ala Ala
 1   5   10   15
Gln Asp Gly Asp Lys Leu Leu Glu Gly Asp Glu Cys Ala Pro His Ser
            20   25   30
Gln Pro Trp Gln Val Ala Leu Tyr Glu Arg Gly Arg Phe Asn Cys Gly
        35   40   45
Ala Ser Leu Ile Ser Pro His Trp Val Leu Ser Ala Ala His Cys Gln
    50   55   60
Ser Arg Phe Met Arg Val Arg Leu Gly Glu His Asn Leu Arg Lys Arg
65   70   75   80
Asp Gly Pro Glu Gln Leu Arg Thr Thr Ser Arg Val Ile Pro His Pro
                85   90   95
Arg Tyr Glu Ala Arg Ser His Arg Asn Asp Ile Met Leu Leu Arg Leu
            100   105   110
Val Gln Pro Ala Arg Leu Asn Pro Gln Val Arg Pro Ala Val Leu Pro
        115   120   125
Thr Arg Cys Pro His Pro Gly Glu Ala Cys Val Val Ser Gly Trp Gly
    130   135   140
Leu Val Ser His Asn Glu Pro Gly Thr Ala Gly Ser Pro Arg Ser Gln
145   150   155   160
Gly

<210> 91

<211> 1054
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK15 transcript variant 3

<400> 91

actgcagccg aaccctggtc cctcctccac aatgtggctt ctcctcactc tctccttcct 60
gctggcatcc acagcagccc aggatggtga caagttgctg gaaggtgacg agtgtgcacc 120
ccactcccag ccatggcaag tggctctcta cgagcgtgga cgctttaact gtggcgcttc 180
cctcatctcc ccacactggg tgctgtctgc ggcccactgc caaagccgct tcatgagagt 240
gcgcctggga gagcacaacc tgcgcaagcg cgatggccca gagcaactac ggaccacgtc 300
tcgggtcatt ccacacccgc gctacgaagc gcgcagccac cgcaacgaca tcatgttgct 360
gcgcctagtc cagcccgcac gcctgaaccc ccagggtgac tctgggggac ccctggtctg 420
tgggggcatc ctgcagggca ttgtgtcctg gggtgacgtc ccttgtgaca acaccaccaa 480
gcctggtgtc tataccaaag tctgccacta cttggagtgg atcagggaaa ccatgaagag 540
gaactgacta ttctagccta tctcctgtgc ccctgactga gcagaagccc ccacagctgg 600
ccagcagccc cgcctgacat ggaacagaac ggagccatcc cccaagaccc tgtccaaggc 660
ccagatgtta gccaaggact tgtcccacct gaggacaaag ctggcgctca aggtcacctg 720
tttaatgcca agataacaaa gcgctgatcc aagttgctct gtaggaattt ctgtgacttt 780
tttctggggt caaagagaaa ccccgagaca ctgtacactg ttccttttca cccaccaccc 840
cgatccctag gtgaggagaa gcggcttgaa gcagggctcc attcattcaa cacacatgac 900
cacccgtgtg atcttgaaca agaggcccaa tctcacttcg ccttggtttc cttatctgta 960
aaatgagacc atcttattgc tgacttcaaa gggctgttgt gaggattaaa tgagatgatt 1020
cgtctgaact gattaaaatc gtgtctggca ctga 1054

<210> 92
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK15 isoform 3

<400> 92
Met Trp Leu Leu Leu Thr Leu Ser Phe Leu Leu Ala Ser Thr Ala Ala
 1   5   10   15
Gln Asp Gly Asp Lys Leu Leu Glu Gly Asp Glu Cys Ala Pro His Ser
            20   25   30
Gln Pro Trp Gln Val Ala Leu Tyr Glu Arg Gly Arg Phe Asn Cys Gly
        35   40   45
Ala Ser Leu Ile Ser Pro His Trp Val Leu Ser Ala Ala His Cys Gln
    50   55   60
Ser Arg Phe Met Arg Val Arg Leu Gly Glu His Asn Leu Arg Lys Arg
65   70   75   80
Asp Gly Pro Glu Gln Leu Arg Thr Thr Ser Arg Val Ile Pro His Pro
                85   90   95
Arg Tyr Glu Ala Arg Ser His Arg Asn Asp Ile Met Leu Leu Arg Leu
            100   105   110

Val Gln Pro Ala Arg Leu Asn Pro Gln Gly Asp Ser Gly Gly Pro Leu
        115   120   125
Val Cys Gly Gly Ile Leu Gln Gly Ile Val Ser Trp Gly Asp Val Pro
    130   135   140
Cys Asp Asn Thr Thr Lys Pro Gly Val Tyr Thr Lys Val Cys His Tyr

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145                 150                 155                 160
Leu Glu Trp Ile Arg Glu Thr Met Lys Arg Asn
                165                 170
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<210> 93
<211> 1309
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK15 transcript variant 4

<400> 93

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gctggcatcc acagcagccc aggatggtga caagttgctg gaaggtgacg agtgtgcacc 120
ccactcccag ccatggcaag tggctctcta cgagcgtgga cgctttaact gtggcgcttc 180
cctcatctcc ccacactggg tgctgtctgc ggcccactgc caaagccgct tcatgagagt 240
gcgcctggga gagcacaacc tgcgcaagcg cgatggccca gagcaactac ggaccacgtc 300
tcgggtcatt ccacacccgc gctacgaagc gcgcagccac cgcaacgaca tcatgttgct 360
gcgcctagtc cagcccgcac gcctgaaccc ccaggtgcgc cccgcggtgc tacccacgcg 420
ttgcccccac ccgggggagg cctgtgtggt gtctggctgg ggcctggtgt cccacaacga 480
gcctgggacc gctgggagcc cccggtcaca agtgagtctc ccagatacgt tgcattgtgc 540
caacatcagc attatctcgg acacatcttg tgacaagagc tacccagggc gcctgacaaa 600
caccatggtg tgtgcaggcg cggagggcag aggcgcagaa tcctgtgagg gtgactctgg 660
gggacccctg gtctgtgggg gcatcctgca gggcattgtg tcctggggtg acgtcccttg 720
tgacaacacc accaagcctg gtgtctatac caaagtctgc cactacttgg agtggatcag 780
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agcccccaca gctggccagc agccccgcct gacatggaac agaacggagc catcccccaa 900
gaccctgtcc aaggcccaga tgttagccaa ggacttgtcc cacctgagga caaagctggc 960
gctcaaggtc acctgtttaa tgccaagata acaaagcgct gatccaagtt gctctgtagg 1020
aatttctgtg actttttttct ggggtcaaag agaaaccccg agacactgta cactgttcct 1080
tttcacccac caccccgatc cctaggtgag gagaagcggc ttgaagcagg gctccattca 1140
ttcaacacac atgaccaccc gtgtgatctt gaacaagagg cccaatctca cttcgccttg 1200
gtttccttat ctgtaaaatg agaccatctt attgctgact tcaaagggct gttgtgagga 1260
ttaaatgaga tgattcgtct gaactgatta aaatcgtgtc tggcactga              1309
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<210> 94
<211> 256
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK15 isoform 4

<400> 94

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Met Trp Leu Leu Leu Thr Leu Ser Phe Leu Leu Ala Ser Thr Ala Ala
 1               5                  10                  15
Gln Asp Gly Asp Lys Leu Leu Glu Gly Asp Glu Cys Ala Pro His Ser
            20                  25                  30
Gln Pro Trp Gln Val Ala Leu Tyr Glu Arg Gly Arg Phe Asn Cys Gly
        35                  40                  45
Ala Ser Leu Ile Ser Pro His Trp Val Leu Ser Ala Ala His Cys Gln
    50                  55                  60
Ser Arg Phe Met Arg Val Arg Leu Gly Glu His Asn Leu Arg Lys Arg
65                  70                  75                  80
Asp Gly Pro Glu Gln Leu Arg Thr Thr Ser Arg Val Ile Pro His Pro
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                85                  90                  95
Arg Tyr Glu Ala Arg Ser His Arg Asn Asp Ile Met Leu Leu Arg Leu
            100                 105                 110
Val Gln Pro Ala Arg Leu Asn Pro Gln Val Arg Pro Ala Val Leu Pro
        115                 120                 125
Thr Arg Cys Pro His Pro Gly Glu Ala Cys Val Val Ser Gly Trp Gly
    130                 135                 140
Leu Val Ser His Asn Glu Pro Gly Thr Ala Gly Ser Pro Arg Ser Gln
145                 150                 155                 160
Val Ser Leu Pro Asp Thr Leu His Cys Ala Asn Ile Ser Ile Ile Ser
                165                 170                 175
Asp Thr Ser Cys Asp Lys Ser Tyr Pro Gly Arg Leu Thr Asn Thr Met
            180                 185                 190
Val Cys Ala Gly Ala Glu Gly Arg Gly Ala Glu Ser Cys Glu Gly Asp
        195                 200                 205
Ser Gly Gly Pro Leu Val Cys Gly Gly Ile Leu Gln Gly Ile Val Ser
    210                 215                 220
Trp Gly Asp Val Pro Cys Asp Asn Thr Thr Lys Pro Gly Val Tyr Thr
225                 230                 235                 240
Lys Val Cys His Tyr Leu Glu Trp Ile Arg Glu Thr Met Lys Arg Asn
                245                 250                 255
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<210> 95
<211> 920
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA031 peptidase

<400> 95
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tggagctaaa ctgggctttc aacatcatca tgaagtttat cctcctctgg gccctcttga 120
atctgactgt tgctttggcc tttaatccag attacacagt cagctccact ccccttact 180
tggtctattt gaaatctgac tacttgccct gcgctggagt cctgatccac ccgctttggg 240
tgatcacagc tgcacactgc aatttaccaa agcttcgggt gatattgggg gttacaatcc 300
cagcagactc taatgaaaag catctgcaag tgattggcta tgagaagatg attcatcatc 360
cacacttctc agtcacttct attgatcatg acatcatgct aatcaagctg aaaacagagg 420
ctgaactcaa tgactatgtg aaattagcca acctgcccta ccaaactatc tctgaaaata 480
ccatgtgctc tgtctctacc tggagctaca atgtgtgtga tatctacaaa gagcccgatt 540
cactgcaaac tgtgaacatc tctgtaatct ccaagcctca gtgtcgcgat gcctataaaa 600
cctacaacat cacggaaaat atgctgtgtg tgggcattgt gccaggaagg aggcagccct 660
gcaaggaagt ttctgctgcc ccggcaatct gcaatgggat gcttcaagga atcctgtctt 720
ttgcggatgg atgtgttttg agagccgatg ttggcatcta tgccaaaatt ttttactata 780
taccctggat tgaaaatgta atccaaaata actgagctgt ggcagttgtg gaccatatga 840
cacagcttgt ccccatcgtt cacctttaga attaaatata aattaactcc tcaaaaaaaa 900
aaaaaaaaaa aaaaaaaaaa   920

<210> 96

<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA031 peptidase

<400> 96
Met Lys Phe Ile Leu Leu Trp Ala Leu Leu Asn Leu Thr Val Ala Leu
1 5 10 15
Ala Phe Asn Pro Asp Tyr Thr Val Ser Ser Thr Pro Pro Tyr Leu Val
20 25 30
Tyr Leu Lys Ser Asp Tyr Leu Pro Cys Ala Gly Val Leu Ile His Pro
35 40 45
Leu Trp Val Ile Thr Ala Ala His Cys Asn Leu Pro Lys Leu Arg Val
50 55 60
Ile Leu Gly Val Thr Ile Pro Ala Asp Ser Asn Glu Lys His Leu Gln
65 70 75 80
Val Ile Gly Tyr Glu Lys Met Ile His His Pro His Phe Ser Val Thr
85 90 95
Ser Ile Asp His Asp Ile Met Leu Ile Lys Leu Lys Thr Glu Ala Glu
100 105 110
Leu Asn Asp Tyr Val Lys Leu Ala Asn Leu Pro Tyr Gln Thr Ile Ser
115 120 125
Glu Asn Thr Met Cys Ser Val Ser Thr Trp Ser Tyr Asn Val Cys Asp
130 135 140
Ile Tyr Lys Glu Pro Asp Ser Leu Gln Thr Val Asn Ile Ser Val Ile
145 150 155 160
Ser Lys Pro Gln Cys Arg Asp Ala Tyr Lys Thr Tyr Asn Ile Thr Glu
165 170 175
Asn Met Leu Cys Val Gly Ile Val Pro Gly Arg Arg Gln Pro Cys Lys
180 185 190
Glu Val Ser Ala Ala Pro Ala Ile Cys Asn Gly Met Leu Gln Gly Ile
195 200 205
Leu Ser Phe Ala Asp Gly Cys Val Leu Arg Ala Asp Val Gly Ile Tyr
210 215 220
Ala Lys Ile Phe Tyr Tyr Ile Pro Trp Ile Glu Asn Val Ile Gln Asn
225 230 235 240
Asn

<210> 97
<211> 2393
<212> DNA
<213> Homo sapiens

<220>
<223> membrane-type mosaic serine protease

<400> 97
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gcaagaacac cttcagctgg agcatctcca gcccaggcat ctccagctgg gacacctcca 180
ggccgggcat ctccagccca ggcatctcca gcccaggcat ctccagctgg gacacctccg 240
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ggccgggcat ctccagccca ggcatctcca gcccgggcat ctccggctct ggcatcactt 360
tccaggtcct catccggcag gtcatcatcc gccaggtcag cctcggtgac aacctcccca 420
accagagtgt accttgttag agcaacacca gtgggggctg tacccatccg atcatctcct 480
gccaggtcag caccagcaac cagggccacc agggagagcc caggtacgag cctgcccaag 540
ttcacctggc gggagggcca gaagcagcta ccgctcatcg ggtgcgtgct cctcctcatt 600
gccctggtgg tttcgctcat catcctcttc cagttctggc agggccacac agggatcagg 660
cacaaggagc agagggagag ctgtcccaag cacgctgttc gctgtgacgg ggtggtggac 720

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tgcaagctga agagtgacga gctgggctgc gtgaggtttg actgggacaa gtctctgctt 780
aaaatctact ctgggtcctc ccatcagtgg cttcccatct gtagcagcaa ctggaatgac 840
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gttgcccaca gggattttgc caacagcttc tcaatcttga gatacaactc caccatccag 960
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ctcatgcggc tgtccaagcc cctgaccctg tccgctcaca tccaccctgc ttgcctcccc 1380
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tgtgagcaga acaaccgctg gtacctggca ggtgtcacca gctggggcac aggctgtggc 1680
cagagaaaca aacctggtgt gtacaccaaa gtgacagaag ttcttccctg gatttacagc 1740
aagatggagg taagatccct gcagcaggac actgcaccca gcaggctggg aacttcctca 1800
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tacaggccag gcaggcagtt gctgggcaga tgttctccca gaagtatttt tttgtgtaag 2040
gttgcaatgg actttgaaaa cgtttcagtt tctgcagagg attttgtgat agtctttgtt 2100
atcaagcatt tatgcatggg aatccgctct tcatggcctt tcccagctct gtttgtttta 2160
gtctttttga ttttcttttt gttgttgttg ttgtcttttt ttaaaaacac aagtgactcc 2220
attttaactc tgacaacttt cacagctgtc accagaatgc tccctgagaa ctaccattct 2280
ttccctttcc cacttaaaat atttcatcag aacctcacca ctatcataaa agagtataaa 2340
gtaataaaat aataaaaagc gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa        2393
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<210> 98
<211> 581
<212> PRT
<213> Homo Sapiens

<220>
<223> membrane-type mosaic serine protease

<400> 98

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Met Glu Arg Asp Ser His Gly Asn Ala Ser Pro Ala Arg Thr Pro Ser
 1               5                  10                  15
Ala Gly Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr Pro Pro Gly
            20                  25                  30
Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly
        35                  40                  45
Thr Pro Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser Pro Ala Gly Thr

    50                  55                  60
Pro Pro Gly Arg Ala Ser Pro Gly Arg Ala Ser Pro Ala Gln Ala Ser
65                  70                  75                  80
Pro Ala Arg Ala Ser Pro Ala Leu Ala Ser Leu Ser Arg Ser Ser Ser
                85                  90                  95
Gly Arg Ser Ser Ser Ala Arg Ser Ala Ser Val Thr Thr Ser Pro Thr
            100                 105                 110
Arg Val Tyr Leu Val Arg Ala Thr Pro Val Gly Ala Val Pro Ile Arg
        115                 120                 125
Ser Ser Pro Ala Arg Ser Ala Pro Ala Thr Arg Ala Thr Arg Glu Ser
    130                 135                 140
```

```
Pro Gly Thr Ser Leu Pro Lys Phe Thr Trp Arg Glu Gly Gln Lys Gln
145                 150                 155                 160
Leu Pro Leu Ile Gly Cys Val Leu Leu Leu Ile Ala Leu Val Val Ser
                165                 170                 175
Leu Ile Ile Leu Phe Gln Phe Trp Gln Gly His Thr Gly Ile Arg His
            180                 185                 190
Lys Glu Gln Arg Glu Ser Cys Pro Lys His Ala Val Arg Cys Asp Gly
        195                 200                 205
Val Val Asp Cys Lys Leu Lys Ser Asp Glu Leu Gly Cys Val Arg Phe
    210                 215                 220
Asp Trp Asp Lys Ser Leu Leu Lys Ile Tyr Ser Gly Ser Ser His Gln
225                 230                 235                 240
Trp Leu Pro Ile Cys Ser Ser Asn Trp Asn Asp Ser Tyr Ser Glu Lys
                245                 250                 255
Thr Cys Arg Gln Leu Gly Phe Glu Ser Ala His Arg Thr Thr Glu Val
            260                 265                 270
Ala His Arg Asp Phe Ala Asn Ser Phe Ser Ile Leu Arg Tyr Asn Ser
        275                 280                 285
Thr Ile Gln Glu Ser Leu His Arg Ser His Cys Pro Ser Gln Arg Tyr
    290                 295                 300
Ile Ser Leu Gln Cys Ser His Cys Gly Leu Arg Ala Met Thr Gly Arg
305                 310                 315                 320
Ile Val Gly Gly Ala Leu Ala Ser Asp Ser Lys Trp Pro Trp Gln Val
                325                 330                 335
Ser Leu His Phe Gly Thr Thr His Ile Cys Gly Gly Thr Leu Ile Asp
            340                 345                 350
Ala Gln Trp Val Leu Thr Ala Ala His Cys Phe Phe Val Thr Arg Glu
        355                 360                 365
Lys Val Leu Glu Gly Trp Lys Val Tyr Ala Gly Thr Ser Asn Leu His
    370                 375                 380
Gln Leu Pro Glu Ala Ala Ser Ile Ala Glu Ile Ile Ile Asn Ser Asn
385                 390                 395                 400
Tyr Thr Asp Glu Glu Asp Asp Tyr Asp Ile Ala Leu Met Arg Leu Ser
                405                 410                 415
Lys Pro Leu Thr Leu Ser Ala His Ile His Pro Ala Cys Leu Pro Met
            420                 425                 430
His Gly Gln Thr Phe Ser Leu Asn Glu Thr Cys Trp Ile Thr Gly Phe
        435                 440                 445
Gly Lys Thr Arg Glu Thr Asp Asp Lys Thr Ser Pro Phe Leu Arg Glu
    450                 455                 460
Val Gln Val Asn Leu Ile Asp Phe Lys Lys Cys Asn Asp Tyr Leu Val
465                 470                 475                 480
Tyr Asp Ser Tyr Leu Thr Pro Arg Met Met Cys Ala Gly Asp Leu His
                485                 490                 495
Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
            500                 505                 510
Glu Gln Asn Asn Arg Trp Tyr Leu Ala Gly Val Thr Ser Trp Gly Thr
        515                 520                 525
Gly Cys Gly Gln Arg Asn Lys Pro Gly Val Tyr Thr Lys Val Thr Glu
    530                 535                 540
Val Leu Pro Trp Ile Tyr Ser Lys Met Glu Val Arg Ser Leu Gln Gln
545                 550                 555                 560
Asp Thr Ala Pro Ser Arg Leu Gly Thr Ser Ser Gly Gly Asp Pro Gly
                565                 570                 575
Gly Ala Pro Arg Val
            580
```

<210> 99
<211> 148
<212> PRT
<213> Homo sapiens

<220>
<223> mername-AA038 peptidase

<400> 99
Cys Gly Lys Pro Lys Val Val Gly Lys Ile Tyr Gly Gly Arg Asp Ala
 1   5   10   15
Ala Ala Gly Gln Trp Pro Trp Gln Ala Ser Leu Leu Tyr Trp Gly Ser
            20   25   30
His Leu Cys Gly Ala Val Leu Ile Asp Ser Cys Trp Leu Val Ser Thr
        35   40   45
Thr His Cys Phe Leu Asn Lys Ser Gln Ala Pro Lys Asn Tyr Gln Val
    50   55   60
Leu Leu Gly Asn Ile Gln Leu Tyr His Gln Thr Gln His Thr Gln Lys
65   70   75   80
Met Ser Val His Arg Ile Ile Thr His Pro Asp Phe Glu Lys Leu His
                85   90   95
Pro Phe Gly Ser Asp Ile Ala Met Leu Gln Leu His Leu Pro Met Asn
            100   105   110
Phe Thr Ser Tyr Ile Val Pro Val Cys Leu Pro Ser Arg Asp Met Gln
        115   120   125
Leu Pro Ser Asn Val Ser Cys Trp Ile Thr Gly Trp Gly Met Ala Ile
    130   135   140
Leu Gly Gly Leu
145

<210> 100
<211> 712
<212> DNA
<213> Homo sapiens

<220>
<223> mername-AA128 peptidase

<400> 100
cacagagggc tccagcgtga ttgccactgg ttaatgacct gccacccccg ccccccaac 60
ctctggtgcc gtccaaggac tctgacccca gtgcagtgtc tgtagggaag aggagccatg 120
gggcttcggg caggccccat cctgcttctg ctgctgtggc tgctgccaga atgcggccac 180
tccaaggagg ccgggaggat tgtgggaggc caagacaccc aggaaggacg ctggccgtgg 240
caggttggcc tgtggttgac ctcagtgggg catgtatgtg ggggcttcct catccaccca 300
cgctgggtgc tcacagccgc ccactgcttc ctgagggtga ctccgggggg ccgctggtct 360
gccccatcaa tgatacgtgg atccaggccg gcattgtgag ctggggattc ggctgtgccc 420
ggcctttccg gcctggtgtc tacacccagg tgctaagcta cacagactgg attcagagaa 480
ccctggctga atctcactca ggcatgtctg gggcccgccc aggtgcccca ggatcccact 540
caggcacctc cagatcccac ccagtgctgc tgcttgagct gttgaccgta tgcttgcttg 600
ggtccctgtg aaccatgagc catggagtcc gggatcccct ttctggtagg attgatggaa 660
tctaataata aaaactgtag gtttttttatg tgaaaaaaaa aaaaaaaaaa aa   712

<210> 101
<211> 146
<212> PRT

<213> Homo sapiens

<220>
<223> mername-AA128 peptidase

<400> 101
Met Arg Pro Leu Gln Gly Gly Arg Glu Asp Cys Gly Arg Pro Arg His
 1   5   10   15
Pro Gly Arg Thr Leu Ala Val Ala Gly Trp Pro Val Val Asp Leu Ser
            20   25   30
Gly Ala Cys Met Trp Gly Leu Pro His Pro Pro Thr Leu Gly Ala His
        35   40   45
Ser Arg Pro Leu Leu Pro Glu Gly Asp Ser Gly Gly Pro Leu Val Cys
    50   55   60
Pro Ile Asn Asp Thr Trp Ile Gln Ala Gly Ile Val Ser Trp Gly Phe
65   70   75   80
Gly Cys Ala Arg Pro Phe Arg Pro Gly Val Tyr Thr Gln Val Leu Ser
                85   90   95
Tyr Thr Asp Trp Ile Gln Arg Thr Leu Ala Glu Ser His Ser Gly Met
            100   105   110
Ser Gly Ala Arg Pro Gly Ala Pro Gly Ser His Ser Gly Thr Ser Arg
        115   120   125
Ser His Pro Val Leu Leu Leu Glu Leu Leu Thr Val Cys Leu Leu Gly
    130   135   140
Ser Leu
145

<210> 102
<211> 800
<212> DNA
<213> Homo sapiens

<220>
<223> cationic trypsin (Homo sapiens-type 1) (cationic)

<400> 102
accaccatga atccactcct gatccttacc tttgtggcag ctgctcttgc tgccccctttt 60
gatgatgatg acaagatcgt tgggggctac aactgtgagg agaattctgt cccctaccag 120
gtgtccctga attctggcta ccacttctgt ggtggctccc tcatcaacga acagtgggtg 180
gtatcagcag gccactgcta caagtcccgc atccaggtga gactgggaga gcacaacatc 240
gaagtcctgg aggggaatga gcagttcatc aatgcagcca agatcatccg ccacccccaa 300
tacgacagga agactctgaa caatgacatc atgttaatca agctctcctc acgtgcagta 360
atcaacgccc gcgtgtccac catctctctg cccaccgccc ctccagccac tggcacgaag 420
tgcctcatct ctggctgggg caacactgcg agctctggcg ccgactaccc agacgagctg 480
cagtgcctgg acgctcctgt gctgagccag gctaagtgtg aagcctccta ccctggaaag 540
attaccagca acatgttctg tgtgggcttc cttgagggag gcaaggattc atgtcagggt 600
gattctggtg gccctgtggt ctgcaatgga cagctccaag gagttgtctc ctggggtgat 660
ggctgtgccc agaagaacaa gcctggagtc tacaccaagg tctacaacta tgtgaaatgg 720
attaagaaca ccatagctgc caatagctaa agcccccagt atctcttcag tctctatacc 780
aataaagtga ccctgttctc   800

<210> 103
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> cationic trypsin (Homo sapiens-type 1) (cationic)

<400> 103
Met Asn Pro Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Leu Ala Ala
 1   5   10   15
Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Asn Cys Glu Glu
            20   25   30
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys
        35   40   45
Gly Gly Ser Leu Ile Asn Glu Gln Trp Val Val Ser Ala Gly His Cys
    50   55   60
Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
65   70   75   80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
                85   90   95
Pro Gln Tyr Asp Arg Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys
            100   105   110
Leu Ser Ser Arg Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu
        115   120   125
Pro Thr Ala Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp
    130   135   140
Gly Asn Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
145   150   155   160
Leu Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro
                165   170   175
Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
            180   185   190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly
        195   200   205
Gln Leu Gln Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln Lys Asn
    210   215   220
Lys Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Lys Trp Ile Lys
225   230   235   240
Asn Thr Ile Ala Ala Asn Ser
                245

<210> 104
<211> 938
<212> DNA
<213> Homo sapiens

<220>
<223> Neutrophil elastase

<400> 104
gcacggaggg gcagagaccc cggagcccca gccccaccat gaccctcggc cgccgactcg 60
cgtgtctttt cctcgcctgt gtcctgccgg ccttgctgct ggggggcacc gcgctggcct 120
cggagattgt ggggggccgg cgagcgcggc cccacgcgtg gcccttcatg gtgtccctgc 180
agctgcgcgg aggccacttc tgcggcgcca ccctgattgc gcccaacttc gtcatgtcgg 240
ccgcgcactg cgtggcgaat gtaaacgtcc gcgcggtgcg ggtggtcctg ggagcccata 300
acctctcgcg gcgggagccc acccggcagg tgttcgccgt gcagcgcatc ttcgaaaacg 360
gctacgaccc cgtaaacttg ctcaacgaca tcgtgattct ccagctcaac gggtcggcca 420
ccatcaacgc caacgtgcag gtggcccagc tgccggctca gggacgccgc ctgggcaacg 480
gggtgcagtg cctggccatg ggctggggcc ttctgggcag gaaccgtggg atcgccagcg 540
tcctgcagga gctcaacgtg acggtggtga cgtccctctg ccgtcgcagc aacgtctgca 600

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ctctcgtgag gggccggcag gccggcgtct gtttcgggga ctccggcagc cccttggtct 660
gcaacgggct aatccacgga attgcctcct tcgtccgggg aggctgcgcc tcagggctct 720
accccgatgc ctttgccccg gtggcacagt ttgtaaactg gatcgactct atcatccaac 780
gctccgagga caacccctgt ccccaccccc gggacccgga cccggccagc aggacccact 840
gagaagggct gcccgggtca cctcagctgc ccacacccac actctccagc atctggcaca 900
ataaacattc tctgttttgt agaaaaaaaa aaaaaaaa                          938
```

<210> 105
<211> 267
<212> PRT
<213> Homo sapiens

<220>
<223> Neutrophil elastase

<400> 105

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Met Thr Leu Gly Arg Arg Leu Ala Cys Leu Phe Leu Ala Cys Val Leu
 1               5                  10                  15
Pro Ala Leu Leu Leu Gly Gly Thr Ala Leu Ala Ser Glu Ile Val Gly
            20                  25                  30
Gly Arg Arg Ala Arg Pro His Ala Trp Pro Phe Met Val Ser Leu Gln
        35                  40                  45
Leu Arg Gly Gly His Phe Cys Gly Ala Thr Leu Ile Ala Pro Asn Phe
    50                  55                  60
Val Met Ser Ala Ala His Cys Val Ala Asn Val Asn Val Arg Ala Val
65                  70                  75                  80
Arg Val Val Leu Gly Ala His Asn Leu Ser Arg Arg Glu Pro Thr Arg
                85                  90                  95
Gln Val Phe Ala Val Gln Arg Ile Phe Glu Asn Gly Tyr Asp Pro Val
            100                 105                 110
Asn Leu Leu Asn Asp Ile Val Ile Leu Gln Leu Asn Gly Ser Ala Thr
        115                 120                 125
Ile Asn Ala Asn Val Gln Val Ala Gln Leu Pro Ala Gln Gly Arg Arg
    130                 135                 140
Leu Gly Asn Gly Val Gln Cys Leu Ala Met Gly Trp Gly Leu Leu Gly
145                 150                 155                 160
Arg Asn Arg Gly Ile Ala Ser Val Leu Gln Glu Leu Asn Val Thr Val
                165                 170                 175
Val Thr Ser Leu Cys Arg Arg Ser Asn Val Cys Thr Leu Val Arg Gly
            180                 185                 190
Arg Gln Ala Gly Val Cys Phe Gly Asp Ser Gly Ser Pro Leu Val Cys
        195                 200                 205
Asn Gly Leu Ile His Gly Ile Ala Ser Phe Val Arg Gly Gly Cys Ala
    210                 215                 220
Ser Gly Leu Tyr Pro Asp Ala Phe Ala Pro Val Ala Gln Phe Val Asn
225                 230                 235                 240
Trp Ile Asp Ser Ile Ile Gln Arg Ser Glu Asp Asn Pro Cys Pro His
                245                 250                 255
Pro Arg Asp Pro Asp Pro Ala Ser Arg Thr His
            260                 265
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<210> 106
<211> 3895
<212> DNA
<213> Homo sapiens

<220>
<223> mannan-binding lectin-associated serine protease-3

<400> 106
attccggcac agggacacaa acaagctcac ccaacaaagc caagctggga ggaccaaggc 60
cgggcagccg ggagcaccca aggcaggaaa atgaggtggc tgcttctcta ttatgctctg 120
tgcttctccc tgtcaaaggc ttcagcccac accgtggagc taaacaatat gtttggccag 180
atccagtcgc ctggttatcc agactcctat cccagtgatt cagaggtgac ttggaatatc 240
actgtcccag atgggtttcg gatcaagctt tacttcatgc acttcaactt ggaatcctcc 300
tacctttgtg aatatgacta tgtgaaggta gaaactgagg accaggtgct ggcaaccttc 360
tgtggcaggg agaccacaga cacagagcag actcccggcc aggaggtggt cctctcccct 420
ggctccttca tgtccatcac tttccggtca gatttctcca atgaggagcg tttcacaggc 480
tttgatgccc actacatggc tgtggatgtg gacgagtgca aggagaggga ggacgaggag 540
ctgtcctgtg accactactg ccacaactac attggcggct actactgctc ctgccgcttc 600
ggctacatcc tccacacaga caacaggacc tgccgagtgg agtgcagtga caacctcttc 660
actcaaagga ctggggtgat caccagccct gacttcccaa acccttaccc caagagctct 720
gaatgcctgt ataccatcga gctggaggag ggtttcatgg tcaacctgca gtttgaggac 780
atatttgaca ttgaggacca tcctgaggtg ccctgccccc atgactacat caagatcaaa 840
gttggtccaa aagttttggg gcctttctgt ggagagaaag ccccagaacc catcagcacc 900
cagagccaca gtgtcctgat cctgttccat agtgacaact cgggagagaa ccggggctgg 960
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aaaatcgagc cctcccaagc caagtatttc ttcaaagacc aagtgctcgt cagctgtgac 1080
acaggctaca aagtgctgaa ggataatgtg gagatggaca cattccagat tgagtgtctg 1140
aaggatggga cgtggagtaa caagattccc acctgtaaaa ttgtagactg tagagcccca 1200
ggagagctgg aacacgggct gatcaccttc tctacaagga acaacctcac cacatacaag 1260
tctgagatca aatactcctg tcaggagccc tattacaaga tgctcaacaa taacacaggt 1320
atatatacct gttctgccca aggagtctgg atgaataaag tattggggag aagcctaccc 1380
acctgccttc cagagtgtgg tcagccctcc cgctccctgc caagcctggt caagaggatc 1440
attgggggcc gaaatgctga gcctggcctc ttcccgtggc aggccctgat agtggtggag 1500
gacacttcga gagtgccaaa tgacaagtgg tttgggagtg gggccctgct ctctgcgtcc 1560
tggatcctca cagcagctca tgtgctgcgc tcccagcgta gagacaccac ggtgatacca 1620
gtctccaagg agcatgtcac cgtctacctg ggcttgcatg atgtgcgaga caaatcgggg 1680
gcagtcaaca gctcagctgc ccgagtggtg ctccacccag acttcaacat ccaaaactac 1740
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gccggctggg gcatctccaa tcccaatgtg acagtggatg agatcatcag cagtggcaca 1920
cggaccttgt cagatgtcct gcagtatgtc aagttacccg tggtgcctca cgctgagtgc 1980
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tttgatgact tgagccagcg ctgggtggtg caaggcctgg tgtcctgggg gggacctgaa 2160
gaatgcggca gcaagcaggt ctatggagtc tacacaaagg tctccaatta cgtggactgg 2220
gtgtgggagc agatgggctt accacaaagt gttgtggagc cccaggtgga acggtgagct 2280
gacttacttc ctcggggcct gcctcccctg agcgaagcta caccgcactt ccgacagcac 2340
actccacatt acttatcaga ccatatggaa tggaacacac tgacctagcg gtggcttctc 2400
ctaccgagac agcccccagg accctgagag gcagagtgtg gtatagggaa aaggctccag 2460
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ccgagtaata caatgcagga gctcaaccaa ggcctctgtg ccaatcccag cactcctttc 2580
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tctcttagtg tgatcccttg gagcaccttc atgcctgggg tttctctccc aaaagcttct 2880
tgcagtctaa gccttatccc ttatgttccc cattaaagga atttcaaaag acatggagaa 2940
agttgggaag gtttgtgctg actgctggga gcagaatagc cgtgggaggc ccaccaagcc 3000
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attacctgga aaaagaaaag acccacactg tgtcctgctg tgcttttggg caggaaaatg 3240
gaagaaagag tggggtgggc acattagaag tcacccaaat cctgccaggc tgcctggcat 3300
ccctggggca tgagctgggc ggagaatcca ccccgcagga tgttcagagg gacccactcc 3360
ttcatttttc agagtcaaag gaatcagagg ctcacccatg gcaggcagtg aaaagagcca 3420
ggagtcctgg gttctagtcc ctgctctgcc cccaactggc tgtataacct ttgaaaaatc 3480
attttctttg tctgagtctc tggttctccg tcagcaacag gctggcataa ggtcccctgc 3540
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cacagggctg attgttctcc ttctccctgg agctctctct cctgaaaatc tccatcagag 3660
caaggcagcc agagaagccc ctgagaggga atgattggga agtgtccact ttctcaaccg 3720
gctcatcaaa cacactcctt tgtctatgaa tggcacatgt aaatgatgtt atattttgta 3780
tcttttatat catatgcttc accattctgt aaagggcctc tgcattgttg ctcccatcag 3840
gggtctcaag tggaaataaa ccctcgtgga taaccaaaaa aaaaaaaaaa aaaaa 3895

<210> 107
<211> 728
<212> PRT
<213> Homo sapiens

<220>
<223> mannan-binding lectin-associated serine protease-3

<400> 107
Met Arg Trp Leu Leu Leu Tyr Tyr Ala Leu Cys Phe Ser Leu Ser Lys
1 5 10 15
Ala Ser Ala His Thr Val Glu Leu Asn Asn Met Phe Gly Gln Ile Gln
20 25 30
Ser Pro Gly Tyr Pro Asp Ser Tyr Pro Ser Asp Ser Glu Val Thr Trp
35 40 45
Asn Ile Thr Val Pro Asp Gly Phe Arg Ile Lys Leu Tyr Phe Met His
50 55 60
Phe Asn Leu Glu Ser Ser Tyr Leu Cys Glu Tyr Asp Tyr Val Lys Val
65 70 75 80
Glu Thr Glu Asp Gln Val Leu Ala Thr Phe Cys Gly Arg Glu Thr Thr
85 90 95
Asp Thr Glu Gln Thr Pro Gly Gln Glu Val Val Leu Ser Pro Gly Ser
100 105 110
Phe Met Ser Ile Thr Phe Arg Ser Asp Phe Ser Asn Glu Glu Arg Phe
115 120 125
Thr Gly Phe Asp Ala His Tyr Met Ala Val Asp Val Asp Glu Cys Lys
130 135 140
Glu Arg Glu Asp Glu Glu Leu Ser Cys Asp His Tyr Cys His Asn Tyr
145 150 155 160
Ile Gly Gly Tyr Tyr Cys Ser Cys Arg Phe Gly Tyr Ile Leu His Thr
165 170 175
Asp Asn Arg Thr Cys Arg Val Glu Cys Ser Asp Asn Leu Phe Thr Gln
180 185 190
Arg Thr Gly Val Ile Thr Ser Pro Asp Phe Pro Asn Pro Tyr Pro Lys
195 200 205
Ser Ser Glu Cys Leu Tyr Thr Ile Glu Leu Glu Glu Gly Phe Met Val
210 215 220
Asn Leu Gln Phe Glu Asp Ile Phe Asp Ile Glu Asp His Pro Glu Val
225 230 235 240
Pro Cys Pro Tyr Asp Tyr Ile Lys Ile Lys Val Gly Pro Lys Val Leu
245 250 255
Gly Pro Phe Cys Gly Glu Lys Ala Pro Glu Pro Ile Ser Thr Gln Ser
260 265 270
His Ser Val Leu Ile Leu Phe His Ser Asp Asn Ser Gly Glu Asn Arg

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        275                 280                 285
Gly Trp Arg Leu Ser Tyr Arg Ala Ala Gly Asn Glu Cys Pro Glu Leu
    290                 295                 300
Gln Pro Pro Val His Gly Lys Ile Glu Pro Ser Gln Ala Lys Tyr Phe
305                 310                 315                 320
Phe Lys Asp Gln Val Leu Val Ser Cys Asp Thr Gly Tyr Lys Val Leu
                325                 330                 335
Lys Asp Asn Val Glu Met Asp Thr Phe Gln Ile Glu Cys Leu Lys Asp
            340                 345                 350
Gly Thr Trp Ser Asn Lys Ile Pro Thr Cys Lys Ile Val Asp Cys Arg
        355                 360                 365
Ala Pro Gly Glu Leu Glu His Gly Leu Ile Thr Phe Ser Thr Arg Asn
    370                 375                 380
Asn Leu Thr Thr Tyr Lys Ser Glu Ile Lys Tyr Ser Cys Gln Glu Pro
385                 390                 395                 400
Tyr Tyr Lys Met Leu Asn Asn Asn Thr Gly Ile Tyr Thr Cys Ser Ala
                405                 410                 415
Gln Gly Val Trp Met Asn Lys Val Leu Gly Arg Ser Leu Pro Thr Cys
            420                 425                 430
Leu Pro Glu Cys Gly Gln Pro Ser Arg Ser Leu Pro Ser Leu Val Lys
        435                 440                 445
Arg Ile Ile Gly Gly Arg Asn Ala Glu Pro Gly Leu Phe Pro Trp Gln
    450                 455                 460
Ala Leu Ile Val Val Glu Asp Thr Ser Arg Val Pro Asn Asp Lys Trp
465                 470                 475                 480
Phe Gly Ser Gly Ala Leu Leu Ser Ala Ser Trp Ile Leu Thr Ala Ala
                485                 490                 495
His Val Leu Arg Ser Gln Arg Arg Asp Thr Thr Val Ile Pro Val Ser
            500                 505                 510
Lys Glu His Val Thr Val Tyr Leu Gly Leu His Asp Val Arg Asp Lys
        515                 520                 525
Ser Gly Ala Val Asn Ser Ser Ala Ala Arg Val Val Leu His Pro Asp
    530                 535                 540
Phe Asn Ile Gln Asn Tyr Asn His Asp Ile Ala Leu Val Gln Leu Gln
545                 550                 555                 560
Glu Pro Val Pro Leu Gly Pro His Val Met Pro Val Cys Leu Pro Arg
                565                 570                 575
Leu Glu Pro Glu Gly Pro Ala Pro His Met Leu Gly Leu Val Ala Gly
            580                 585                 590
Trp Gly Ile Ser Asn Pro Asn Val Thr Val Asp Glu Ile Ile Ser Ser
        595                 600                 605
Gly Thr Arg Thr Leu Ser Asp Val Leu Gln Tyr Val Lys Leu Pro Val
    610                 615                 620
Val Pro His Ala Glu Cys Lys Thr Ser Tyr Glu Ser Arg Ser Gly Asn
625                 630                 635                 640
Tyr Ser Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Tyr Glu Gly Gly
                645                 650                 655
Lys Asp Thr Cys Leu Gly Asp Ser Gly Gly Ala Phe Val Ile Phe Asp
            660                 665                 670
Asp Leu Ser Gln Arg Trp Val Val Gln Gly Leu Val Ser Trp Gly Gly
        675                 680                 685
Pro Glu Glu Cys Gly Ser Lys Gln Val Tyr Gly Val Tyr Thr Lys Val
    690                 695                 700
Ser Asn Tyr Val Asp Trp Val Trp Glu Gln Met Gly Leu Pro Gln Ser
705                 710                 715                 720
Val Val Glu Pro Gln Val Glu Arg
                725
```

<210> 108
<211> 924
<212> DNA
<213> Homo sapiens

<220>
<223> cathepsin G

<400> 108
gcacagcagc aactgactgg gcagcctttc aggaaagatg cagccactcc tgcttctgct 60
ggcctttctc ctacccactg gggctgaggc aggggagatc atcggaggcc gggagagcag 120
gccccactcc cgcccctaca tggcgtatct tcagatccag agtccagcag gtcagagcag 180
atgtggaggg ttcctggtgc gagaagactt tgtgctgaca gcagctcatt gctggggaag 240
caatataaat gtcaccctgg gcgcccacaa tatccagaga cgggaaaaca cccagcaaca 300
catcactgcg cgcagagcca tccgccaccc tcaatataat cagcggacca tccagaatga 360
catcatgtta ttgcagctga gcagaagagt cagacggaat cgaaacgtga acccagtggc 420
tctgcctaga gcccaggagg gactgagacc cgggacgctg tgcactgtgg ccggctgggg 480
cagggtcagc atgaggaggg gaacagatac actccgagag gtgcagctga gagtgcagag 540
ggataggcag tgcctccgca tcttcggttc ctacgacccc cgaaggcaga tttgtgtggg 600
ggaccggcgg gaacggaagg ctgccttcaa gggggattcc ggaggccccc tgctgtgtaa 660
caatgtggcc cacggcatcg tctcctatgg aaagtcgtca ggggttcctc cagaagtctt 720
caccagggtc tcaagtttcc tgccctggat aaggacaaca atgagaagct tcaaactgct 780
ggatcagatg gagacccccc tgtgactgac tcttcttctc ggggacacag gccagctcca 840
cagtgttgcc agagccttaa taaacgtcca cagagtataa ataaccaatt cctcatttgt 900
tcattaaacg tcattcagta ctta 924

<210> 109
<211> 255
<212> PRT
<213> Homo sapiens

<220>
<223> cathepsin G

<400> 109
Met Gln Pro Leu Leu Leu Leu Leu Ala Phe Leu Leu Pro Thr Gly Ala
 1   5   10   15
Glu Ala Gly Glu Ile Ile Gly Gly Arg Glu Ser Arg Pro His Ser Arg
            20   25   30
Pro Tyr Met Ala Tyr Leu Gln Ile Gln Ser Pro Ala Gly Gln Ser Arg
        35   40   45
Cys Gly Gly Phe Leu Val Arg Glu Asp Phe Val Leu Thr Ala Ala His
    50   55   60
Cys Trp Gly Ser Asn Ile Asn Val Thr Leu Gly Ala His Asn Ile Gln
65   70   75   80
Arg Arg Glu Asn Thr Gln Gln His Ile Thr Ala Arg Arg Ala Ile Arg
                85   90   95
His Pro Gln Tyr Asn Gln Arg Thr Ile Gln Asn Asp Ile Met Leu Leu
            100   105   110
Gln Leu Ser Arg Arg Val Arg Arg Asn Arg Asn Val Asn Pro Val Ala
        115   120   125
Leu Pro Arg Ala Gln Glu Gly Leu Arg Pro Gly Thr Leu Cys Thr Val
    130   135   140
Ala Gly Trp Gly Arg Val Ser Met Arg Arg Gly Thr Asp Thr Leu Arg
145   150   155   160

```
Glu Val Gln Leu Arg Val Gln Arg Asp Arg Gln Cys Leu Arg Ile Phe
                165                 170                 175
Gly Ser Tyr Asp Pro Arg Arg Gln Ile Cys Val Gly Asp Arg Arg Glu
            180                 185                 190
Arg Lys Ala Ala Phe Lys Gly Asp Ser Gly Gly Pro Leu Leu Cys Asn
        195                 200                 205
Asn Val Ala His Gly Ile Val Ser Tyr Gly Lys Ser Ser Gly Val Pro
    210                 215                 220
Pro Glu Val Phe Thr Arg Val Ser Ser Phe Leu Pro Trp Ile Arg Thr
225                 230                 235                 240
Thr Met Arg Ser Phe Lys Leu Leu Asp Gln Met Glu Thr Pro Leu
                245                 250                 255
```

<210> 110
<211> 1001
<212> DNA
<213> Homo sapiens

<220>
<223> myeloblastin (proteinase 3)

<400> 110
```
cgtgggtgca ccctggaccc caccatggct caccggcccc ccagccctgc cctggcgtcc 60
gtgctgctgg ccttgctgct gagcggtgct gcccgagctg cggagatcgt gggcgggcac 120
gaggcgcagc cacactcccg gccctacatg gcctccctgc agatgcgggg gaacccgggc 180
agccacttct gcggaggcac cttgatccac cccagcttcg tgctgacggc cgcgcactgc 240
ctgcgggaca taccccagcg cctggtgaac gtggtgctcg gagcccacaa cgtgcggacg 300
caggagccca cccagcagca cttctcggtg gctcaggtgt ttctgaacaa ctacgacgcg 360
gagaacaaac tgaacgacgt tctcctcatc cagctgagca gcccagccaa cctcagtgcc 420
tccgtcgcca cagtccagct gccacagcag gaccagccag tgccccacgg cacccagtgc 480
ctggccatgg gctggggccg cgtgggtgcc cacgaccccc cagcccaggt cctgcaggag 540
ctcaatgtca ccgtggtcac cttcttctgc cggccacata acatttgcac tttcgtccct 600
cgccgcaagg ccggcatctg cttcggagac tcaggtggcc ccctgatctg tgatggcatc 660
atccaaggaa tagactcctt cgtgatctgg ggatgtgcca cccgcctttt ccctgacttc 720
ttcacgcggg tagccctcta cgtggactgg atccgttcca cgctgcgccg tgtggaggcc 780
aagggccgcc cctgaaccgc ccctcccaca gcgctggccg ggaccccgag cctggctcca 840
aaccctcgag gcggatcttt ggacagaagc agctcttccc cgaacactgt ggcgtccggg 900
acggccccac ccgtcccccc acactccctc ccacggggct ccgggagaca ggccggccct 960
gcacctcacc ccaccgtgac ctcaataaac gttgaaactc c                    1001
```

<210> 111
<211> 256
<212> PRT
<213> Homo sapiens

<220>
<223> myeloblastin (proteinase 3)

<400> 111
```
Met Ala His Arg Pro Pro Ser Pro Ala Leu Ala Ser Val Leu Leu Ala
 1               5                  10                  15
Leu Leu Leu Ser Gly Ala Ala Arg Ala Ala Glu Ile Val Gly Gly His
            20                  25                  30

Glu Ala Gln Pro His Ser Arg Pro Tyr Met Ala Ser Leu Gln Met Arg
        35                  40                  45
```

```
Gly Asn Pro Gly Ser His Phe Cys Gly Gly Thr Leu Ile His Pro Ser
    50                  55                  60
Phe Val Leu Thr Ala Ala His Cys Leu Arg Asp Ile Pro Gln Arg Leu
65                  70                  75                  80
Val Asn Val Val Leu Gly Ala His Asn Val Arg Thr Gln Glu Pro Thr
                85                  90                  95
Gln Gln His Phe Ser Val Ala Gln Val Phe Leu Asn Asn Tyr Asp Ala
            100                 105                 110
Glu Asn Lys Leu Asn Asp Val Leu Leu Ile Gln Leu Ser Ser Pro Ala
        115                 120                 125
Asn Leu Ser Ala Ser Val Ala Thr Val Gln Leu Pro Gln Gln Asp Gln
    130                 135                 140
Pro Val Pro His Gly Thr Gln Cys Leu Ala Met Gly Trp Gly Arg Val
145                 150                 155                 160
Gly Ala His Asp Pro Pro Ala Gln Val Leu Gln Glu Leu Asn Val Thr
                165                 170                 175
Val Val Thr Phe Phe Cys Arg Pro His Asn Ile Cys Thr Phe Val Pro
            180                 185                 190
Arg Arg Lys Ala Gly Ile Cys Phe Gly Asp Ser Gly Gly Pro Leu Ile
        195                 200                 205
Cys Asp Gly Ile Ile Gln Gly Ile Asp Ser Phe Val Ile Trp Gly Cys
    210                 215                 220
Ala Thr Arg Leu Phe Pro Asp Phe Phe Thr Arg Val Ala Leu Tyr Val
225                 230                 235                 240
Asp Trp Ile Arg Ser Thr Leu Arg Arg Val Glu Ala Lys Gly Arg Pro
                245                 250                 255
```

<210> 112
<211> 878
<212> DNA
<213> Homo sapiens

<220>
<223> granzyme A

<400> 112
cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtcgtttctc tcctgctaat tcctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactcctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctcactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttgtta agaaagagtt tccctatcca tgctatgacc 360
cagccacacg cgaaggtgac cttaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaaccatgt 480
gccaagttgc agggtggggg aggactcaca atagtgcatc ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
accctgtgat tggaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc cctttgttgt gcgagggtgt tttccgaggg gtcacttcct 720
ttggccttga aaataaatgc ggagaccctc gtgggcctgg tgtctatatt cttctctcaa 780
agaaacacct caactggata attatgacta tcaagggagc agtttaaata accgtttcct 840
ttcatttact gtggcttctt aatcttttca caaataaa   878

<210> 113
<211> 262
<212> PRT
<213> Homo sapiens

<220>
<223> granzyme A

<400> 113
Met Arg Asn Ser Tyr Arg Phe Leu Ala Ser Ser Leu Ser Val Val Val
1 5 10 15
Ser Leu Leu Leu Ile Pro Glu Asp Val Cys Glu Lys Ile Ile Gly Gly
20 25 30
Asn Glu Val Thr Pro His Ser Arg Pro Tyr Met Val Leu Leu Ser Leu
35 40 45
Asp Arg Lys Thr Ile Cys Ala Gly Ala Leu Ile Ala Lys Asp Trp Val
50 55 60
Leu Thr Ala Ala His Cys Asn Leu Asn Lys Arg Ser Gln Val Ile Leu
65 70 75 80
Gly Ala His Ser Ile Thr Arg Glu Glu Pro Thr Lys Gln Ile Met Leu
85 90 95
Val Lys Lys Glu Phe Pro Tyr Pro Cys Tyr Asp Pro Ala Thr Arg Glu
100 105 110
Gly Asp Leu Lys Leu Leu Gln Leu Thr Glu Lys Ala Lys Ile Asn Lys
115 120 125
Tyr Val Thr Ile Leu His Leu Pro Lys Lys Gly Asp Asp Val Lys Pro
130 135 140
Gly Thr Met Cys Gln Val Ala Gly Trp Gly Arg Thr His Asn Ser Ala
145 150 155 160
Ser Trp Ser Asp Thr Leu Arg Glu Val Asn Ile Thr Ile Ile Asp Arg
165 170 175
Lys Val Cys Asn Asp Arg Asn His Tyr Asn Phe Asn Pro Val Ile Gly
180 185 190
Met Asn Met Val Cys Ala Gly Ser Leu Arg Gly Gly Arg Asp Ser Cys
195 200 205
Asn Gly Asp Ser Gly Ser Pro Leu Leu Cys Glu Gly Val Phe Arg Gly
210 215 220
Val Thr Ser Phe Gly Leu Glu Asn Lys Cys Gly Asp Pro Arg Gly Pro
225 230 235 240
Gly Val Tyr Ile Leu Leu Ser Lys Lys His Leu Asn Trp Ile Ile Met
245 250 255
Thr Ile Lys Gly Ala Val
260

<210> 114
<211> 947
<212> DNA
<213> Homo sapiens

<220>
<223> granzyme M

<400> 114
ggctcggggc cggggccagc acccacactg ggtctccaca gcggcatgga ggcctgcgtg 60
tcttcactgc tggtgctggc cctgggggcc ctgtcagtag gcagctcctt tgggacccag 120
atcatcgggg gccgggaggt gatcccccac tcgcgcccgt acatggcctc actgcagaga 180
aatggctccc acctgtgcgg gggtgtcctg gtgcacccaa agtgggtgct gacggctgcc 240
cactgcctgg cccagcggat ggcccagctg aggctggtgc tggggctcca caccctggac 300
agccccggtc tcaccttcca catcaaggca gccatccagc accctcgcta caagcccgtc 360

```
cctgccctgg agaacgacct cgcgctgctt cagctggacg ggaaagtgaa gcccagccgg 420
accatccggc cgttggccct gcccagtaag cgccaggtgg tggcagcagg gactcggtgc 480
agcatggccg gctgggggct gacccaccag ggcgggcgcc tgtcccgggt gctgcgggag 540
ctggacctcc aagtgctgga cacccgcatg tgtaacaaca gccgcttctg gaacggcagc 600
ctctccccca gcatggtctg cctggcggcc gactccaagg accaggctcc ctgcaagggt 660
gactcgggcg ggcccctggt gtgtggcaaa ggccgggtgt tggccggagt cctgtccttc 720
agctccaggg tctgcactga catcttcaag cctcccgtgg ccaccgctgt ggcgccttac 780
gtgtcctgga tcaggaaggt caccggccga tcggcctgat gccctggggt gatggggacc 840
ccctcgctgt ctccacagga cccttccct ccaggggtgc agtggggtgg gtgaggacgg 900
gtgggaggga cagggaggga ccaataaatc ataatgaaga aacgctc               947
```

<210> 115
<211> 257
<212> PRT
<213> Homo sapiens

<220>
<223> granzyme M

<400> 115

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Met Glu Ala Cys Val Ser Ser Leu Leu Val Leu Ala Leu Gly Ala Leu
 1               5                  10                  15
Ser Val Gly Ser Ser Phe Gly Thr Gln Ile Ile Gly Gly Arg Glu Val
            20                  25                  30
Ile Pro His Ser Arg Pro Tyr Met Ala Ser Leu Gln Arg Asn Gly Ser
        35                  40                  45
His Leu Cys Gly Gly Val Leu Val His Pro Lys Trp Val Leu Thr Ala
    50                  55                  60
Ala His Cys Leu Ala Gln Arg Met Ala Gln Leu Arg Leu Val Leu Gly
65                  70                  75                  80
Leu His Thr Leu Asp Ser Pro Gly Leu Thr Phe His Ile Lys Ala Ala
                85                  90                  95
Ile Gln His Pro Arg Tyr Lys Pro Val Pro Ala Leu Glu Asn Asp Leu
            100                 105                 110
Ala Leu Leu Gln Leu Asp Gly Lys Val Lys Pro Ser Arg Thr Ile Arg
        115                 120                 125
Pro Leu Ala Leu Pro Ser Lys Arg Gln Val Val Ala Ala Gly Thr Arg
    130                 135                 140
Cys Ser Met Ala Gly Trp Gly Leu Thr His Gln Gly Gly Arg Leu Ser
145                 150                 155                 160
Arg Val Leu Arg Glu Leu Asp Leu Gln Val Leu Asp Thr Arg Met Cys
                165                 170                 175
Asn Asn Ser Arg Phe Trp Asn Gly Ser Leu Ser Pro Ser Met Val Cys
            180                 185                 190
Leu Ala Ala Asp Ser Lys Asp Gln Ala Pro Cys Lys Gly Asp Ser Gly
        195                 200                 205
Gly Pro Leu Val Cys Gly Lys Gly Arg Val Leu Ala Gly Val Leu Ser
    210                 215                 220
Phe Ser Ser Arg Val Cys Thr Asp Ile Phe Lys Pro Pro Val Ala Thr
225                 230                 235                 240
Ala Val Ala Pro Tyr Val Ser Trp Ile Arg Lys Val Thr Gly Arg Ser
                245                 250                 255
Ala
```

<210> 116

<211> 784
<212> DNA
<213> Homo sapiens

<220>
<223> chymase (human-type)

<400> 116
agcatttgct caggcagcct ctctgggaag atgctgcttc ttcctctccc cctgctgctc 60
tttctcttgt gctccagagc tgaagctggg gagatcatcg ggggcacaga atgcaagcca 120
cattcccgcc cctacatggc ctacctggaa attgtaactt ccaacggtcc ctcaaaattt 180
tgtggtggtt tccttataag acggaacttt gtgctgacgg ctgctcattg tgcaggaagg 240
tctataacag tcacccttgg agcccataac ataacagagg aagaagacac atggcagaag 300
cttgaggtta taaagcaatt ccgtcatcca aaatataaca cttctactct tcaccacgat 360
atcatgttac taaagttgaa ggagaaagcc agcctgaccc tggctgtggg gacactcccc 420
ttcccatcac aattcaactt tgtcccacct gggagaatgt gccgggtggc tggctgggga 480
agaacaggtg tgttgaagcc gggctcagac actctgcaag aggtgaagct gagactcatg 540
gatccccagg cctgcagcca cttcagagac tttgaccaca atcttcagct gtgtgtgggc 600
aatcccagga agacaaaatc tgcatttaag ggagactctg ggggccctct tctgtgtgct 660
ggggtggccc agggcatcgt atcctatgga cggtcggatg caaagccccc tgctgtcttc 720
acccgaatct cccattaccg gccctggatc aaccagatcc tgcaggcaaa ttaatcctgg 780
atcc 784

<210> 117
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> chymase (human-type)

<400> 117
Met Leu Leu Leu Pro Leu Pro Leu Leu Leu Phe Leu Leu Cys Ser Arg
 1   5   10   15
Ala Glu Ala Gly Glu Ile Ile Gly Gly Thr Glu Cys Lys Pro His Ser
            20   25   30
Arg Pro Tyr Met Ala Tyr Leu Glu Ile Val Thr Ser Asn Gly Pro Ser
        35   40   45
Lys Phe Cys Gly Gly Phe Leu Ile Arg Arg Asn Phe Val Leu Thr Ala
    50   55   60
Ala His Cys Ala Gly Arg Ser Ile Thr Val Thr Leu Gly Ala His Asn
65   70   75   80
Ile Thr Glu Glu Glu Asp Thr Trp Gln Lys Leu Glu Val Ile Lys Gln
                85   90   95
Phe Arg His Pro Lys Tyr Asn Thr Ser Thr Leu His His Asp Ile Met
            100   105   110
Leu Leu Lys Leu Lys Glu Lys Ala Ser Leu Thr Leu Ala Val Gly Thr
        115   120   125
Leu Pro Phe Pro Ser Gln Phe Asn Phe Val Pro Pro Gly Arg Met Cys
    130   135   140
Arg Val Ala Gly Trp Gly Arg Thr Gly Val Leu Lys Pro Gly Ser Asp
145   150   155   160
Thr Leu Gln Glu Val Lys Leu Arg Leu Met Asp Pro Gln Ala Cys Ser
                165   170   175
His Phe Arg Asp Phe Asp His Asn Leu Gln Leu Cys Val Gly Asn Pro
            180   185   190
Arg Lys Thr Lys Ser Ala Phe Lys Gly Asp Ser Gly Gly Pro Leu Leu

```
        195                 200                 205
Cys Ala Gly Val Ala Gln Gly Ile Val Ser Tyr Gly Arg Ser Asp Ala
    210                 215                 220
Lys Pro Pro Ala Val Phe Thr Arg Ile Ser His Tyr Arg Pro Trp Ile
225                 230                 235                 240
Asn Gln Ile Leu Gln Ala Asn
                245
```

<210> 118
<211> 1194
<212> DNA
<213> Homo sapiens

<220>
<223> tryptase alpha (1)

<400> 118
ataaatgggg aggggagagc ccactgggta gaaggaacag ggagcggcca ggatgctgaa 60
tctgctgctg ctggcgctgc ccgtcctggc gagccgcgcc tacgcggccc ctgccccagg 120
ccaggccctg cagcgagtgg gcatcgtcgg gggtcaggag gcccccagga gcaagtggcc 180
ctggcaggtg agcctgagag tccacggccc atactggatg cacttctgcg ggggctccct 240
catccacccc cagtgggtgc tgaccgcagc gcactgcgtg ggaccggacg tcaaggatct 300
ggccgccctc agggtgcaac tgcgggagca gcacctctac taccaggacc agctgctgcc 360
ggtcagcagg atcatcgtgc acccacagtt ctacaccgcc cagatcggag cggacatcgc 420
cctgctggag ctggaggagc cggtgaacgt ctccagccac gtccacacgg tcaccctgcc 480
ccctgcctca gagaccttcc ccccggggat gccgtgctgg gtcactggct ggggcgatgt 540
ggacaatgat gagcgcctcc caccgccatt tcctctgaag caggtgaagg tccccataat 600
ggaaaaccac atttgtgacg caaaatacca ccttggcgcc tacacgggag acgacgtccg 660
catcgtccgt gacgacatgc tgtgtgccgg gaacacccgg agggactcat gccagggcga 720
ctccggaggg cccctggtgt gcaaggtgaa tggcacctgg ctgcaggcgg gcgtggtcag 780
ctggggcgag ggctgtgccc agcccaaccg gcctggcatc tacacccgtg tcacctacta 840
cttggactgg atccaccact atgtccccaa aaagccgtga gtcaggcctg ggttggccac 900
ctgggtcact ggaggaccaa cccctgctgt ccaaaacacc actgcttcct acccaggtgg 960
cgactgcccc ccacaccttc cctgccccgt cctgagtgcc ccttcctgtc ctaagccccc 1020
tgctctcttc tgagcccctt cccctgtcct gaggaccctt ccctatcctg agcccccttc 1080
cctgtcctaa gcctgacgcc tgcaccgggc cctccagccc tcccctgccc agatagctgg 1140
tggtgggcgc taatcctcct gagtgctgga cctcattaaa gtgcatggaa atca 1194

<210> 119
<211> 275
<212> PRT
<213> Homo sapiens

<220>
<223> tryptase alpha (1)

<400> 119
```
Met Leu Asn Leu Leu Leu Leu Ala Leu Pro Val Leu Ala Ser Arg Ala
 1               5                  10                  15
Tyr Ala Ala Pro Ala Pro Gly Gln Ala Leu Gln Arg Val Gly Ile Val
            20                  25                  30
Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp Pro Trp Gln Val Ser Leu
        35                  40                  45
Arg Val His Gly Pro Tyr Trp Met His Phe Cys Gly Gly Ser Leu Ile
    50                  55                  60
His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro Asp Val
```

```
65                  70                  75                  80
Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His Leu Tyr
                85                  90                  95
Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His Pro Gln
            100                 105                 110
Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu Leu Glu
        115                 120                 125
Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu Pro Pro
    130                 135                 140
Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr Gly Trp
145                 150                 155                 160
Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro Leu Lys
                165                 170                 175
Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala Lys Tyr
            180                 185                 190

His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg Asp Asp
        195                 200                 205
Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly Asp Ser
    210                 215                 220
Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln Ala Gly
225                 230                 235                 240
Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro Gly Ile
                245                 250                 255
Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr Val Pro
            260                 265                 270
Lys Lys Pro
        275
```

<210> 120
<211> 1074
<212> DNA
<213> Homo sapiens

<220>
<223> granzyme K

<400> 120
```
gatcaacaca tttcatctgg gcttcttaaa tctaaatctt taaaatgact aagttttctt 60
ccttttctct gtttttccta atagttgggg cttatatgac tcatgtgtgt ttcaatatgg 120
aaattattgg agggaaagaa gtgtcacctc attccaggcc atttatggcc tccatccagt 180
atggcggaca tcacgtttgt ggaggtgttc tgattgatcc acagtgggtg ctgacagcag 240
cccactgcca atatcggttt accaaaggcc agtctcccac tgtggtttta ggcgcacact 300
ctctctcaaa gaatgaggcc tccaaacaaa cactggagat caaaaaattt ataccattct 360
caagagttac atcagatcct caatcaaatg atatcatgct ggttaagctt caaacagccg 420
caaaactcaa taaacatgtc aagatgctcc acataagatc caaaacctct cttagatctg 480
gaaccaaatg caaggttact ggctggggag ccaccgatcc agattcatta agaccttctg 540
acaccctgcg agaagtcact gttactgtcc taagtcgaaa actttgcaac agccaaagtt 600
actacaacgg cgacccttt atcaccaaag acatggtctg tgcaggagat gccaaaggcc 660
agaaggattc ctgtaagggt gactcagggg gccccttgat ctgtaaaggt gtcttccacg 720
ctatagtctc tggaggtcat gaatgtggtg ttgccacaaa gcctggaatc tacaccctgt 780
taaccaagaa ataccagact tggatcaaaa gcaaccttgt cccgcctcat acaaattaag 840
ttacaaataa ttttattgga tgcacttgct tctttttcc taatatgctc gcaggttaga 900
gttgggtgta agtaaagcag agcacatatg gggtccattt ttgcacttgt aagtcatttt 960
attaaggaat caagttcttt ttcacttgta tcactgatgt atttctacca tgctggtttt 1020
attctaaata aaatttagaa gactcaaaaa aaaaaaaaaa aaaaaaaaaa aaaa       1074
```

<210> 121
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<223> granzyme K

<400> 121
Met Thr Lys Phe Ser Ser Phe Ser Leu Phe Phe Leu Ile Val Gly Ala
 1   5   10   15
Tyr Met Thr His Val Cys Phe Asn Met Glu Ile Ile Gly Gly Lys Glu
            20   25   30
Val Ser Pro His Ser Arg Pro Phe Met Ala Ser Ile Gln Tyr Gly Gly
        35   40   45
His His Val Cys Gly Gly Val Leu Ile Asp Pro Gln Trp Val Leu Thr
    50   55   60
Ala Ala His Cys Gln Tyr Arg Phe Thr Lys Gly Gln Ser Pro Thr Val
65   70   75   80
Val Leu Gly Ala His Ser Leu Ser Lys Asn Glu Ala Ser Lys Gln Thr
                85   90   95
Leu Glu Ile Lys Lys Phe Ile Pro Phe Ser Arg Val Thr Ser Asp Pro
            100   105   110
Gln Ser Asn Asp Ile Met Leu Val Lys Leu Gln Thr Ala Ala Lys Leu
        115   120   125
Asn Lys His Val Lys Met Leu His Ile Arg Ser Lys Thr Ser Leu Arg
    130   135   140
Ser Gly Thr Lys Cys Lys Val Thr Gly Trp Gly Ala Thr Asp Pro Asp
145   150   155   160
Ser Leu Arg Pro Ser Asp Thr Leu Arg Glu Val Thr Val Thr Val Leu
                165   170   175
Ser Arg Lys Leu Cys Asn Ser Gln Ser Tyr Tyr Asn Gly Asp Pro Phe
            180   185   190
Ile Thr Lys Asp Met Val Cys Ala Gly Asp Ala Lys Gly Gln Lys Asp
        195   200   205
Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Ile Cys Lys Gly Val Phe
    210   215   220
His Ala Ile Val Ser Gly Gly His Glu Cys Gly Val Ala Thr Lys Pro
225   230   235   240
Gly Ile Tyr Thr Leu Leu Thr Lys Lys Tyr Gln Thr Trp Ile Lys Ser
                245   250   255
Asn Leu Val Pro Pro His Thr Asn
            260

<210> 122
<211> 1047
<212> DNA
<213> Homo sapiens

<220>
<223> granzyme H

<400> 122
ggagtcaaca ccaacagctc tgacctgggc agccttcctg agaaaatgca gccattcctc 60
ctcctgttgg cctttcttct gacccctggg gctgggacag aggagatcat cgggggccat 120

gaggccaagc cccactcccg cccctacatg gcctttgttc agtttctgca agagaagagt 180
cggaagaggt gtggcggcat cctagtgaga aaggactttg tgctgacagc tgctcactgc 240
cagggaagct ccataaatgt caccttgggg gcccacaata tcaaggaaca ggagcggacc 300
cagcagttta tccctgtgaa aagacccatc ccccatccag cctataatcc taagaacttc 360
tccaacgaca tcatgctact gcagctggag agaaaggcca agtggaccac agctgtgcgg 420
cctctcaggc tacctagcag caaggcccag gtgaagccag ggcagctgtg cagtgtggct 480
ggctggggtt atgtctcaat gagcacttta gcaaccacac tgcaggaagt gttgctgaca 540
gtgcagaagg actgccagtg tgaacgtctc ttccatggca attacagcag agccactgag 600
atttgtgtgg gggatccaaa gaagacacag accggtttca agggggactc cgggggccc 660
ctcgtgtgta aggacgtagc ccaaggtatt ctctcctatg gaaacaaaaa agggacacct 720
ccaggagtct acatcaaggt ctcacacttc ctgccctgga taaagagaac aatgaagcgc 780
ctctaacagc aggcatgaga ctaaccttcc tctgggcctg accatctctg ggacagaggc 840
aagaatcccc aaggggtggg cagtcagggt tgcaggactg taataaatgg atctctggtg 900
tagaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aaaaaaaaaa aaaaaaa 1047

<210> 123
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<223> granzyme H

<400> 123
Met Gln Pro Phe Leu Leu Leu Leu Ala Phe Leu Leu Thr Pro Gly Ala
1 5 10 15
Gly Thr Glu Glu Ile Ile Gly Gly His Glu Ala Lys Pro His Ser Arg
20 25 30
Pro Tyr Met Ala Phe Val Gln Phe Leu Gln Glu Lys Ser Arg Lys Arg
35 40 45
Cys Gly Gly Ile Leu Val Arg Lys Asp Phe Val Leu Thr Ala Ala His
50 55 60
Cys Gln Gly Ser Ser Ile Asn Val Thr Leu Gly Ala His Asn Ile Lys
65 70 75 80
Glu Gln Glu Arg Thr Gln Gln Phe Ile Pro Val Lys Arg Pro Ile Pro
85 90 95
His Pro Ala Tyr Asn Pro Lys Asn Phe Ser Asn Asp Ile Met Leu Leu
100 105 110
Gln Leu Glu Arg Lys Ala Lys Trp Thr Thr Ala Val Arg Pro Leu Arg
115 120 125
Leu Pro Ser Ser Lys Ala Gln Val Lys Pro Gly Gln Leu Cys Ser Val
130 135 140
Ala Gly Trp Gly Tyr Val Ser Met Ser Thr Leu Ala Thr Thr Leu Gln
145 150 155 160
Glu Val Leu Leu Thr Val Gln Lys Asp Cys Gln Cys Glu Arg Leu Phe
165 170 175
His Gly Asn Tyr Ser Arg Ala Thr Glu Ile Cys Val Gly Asp Pro Lys
180 185 190
Lys Thr Gln Thr Gly Phe Lys Gly Asp Ser Gly Gly Pro Leu Val Cys
195 200 205
Lys Asp Val Ala Gln Gly Ile Leu Ser Tyr Gly Asn Lys Lys Gly Thr
210 215 220
Pro Pro Gly Val Tyr Ile Lys Val Ser His Phe Leu Pro Trp Ile Lys
225 230 235 240
Arg Thr Met Lys Arg Leu

245

<210> 124
<211> 865
<212> DNA
<213> Homo sapiens

<220>
<223> chymotrypsin B

<400> 124
ccctgccagc ggcaccatgg ctttcctctg gctcctctcc tgctgggccc tcctgggtac 60
caccttcggc tgcggggtcc ccgccatcca ccctgtgctc agcggcctgt ccaggatcgt 120
gaatggggag gacgccgtcc ccggctcctg gccctggcag gtgtccctgc aggacaaaac 180
cggcttccac ttctgcgggg gctccctcat cagcgaggac tgggtggtca ccgctgccca 240
ctgcggggtc aggacctccg acgtggtcgt ggctggggag tttgaccagg gctctgacga 300
ggagaacatc caggtcctga agatcgccaa ggtcttcaag aaccccaagt tcagcattct 360
gaccgtgaac aatgacatca ccctgctgaa gctggccaca cctgcccgct tctcccagac 420
agtgtccgcc gtgtgcctgc ccagcgccga cgacgacttc cccgcgggga cactgtgtgc 480
caccacaggc tggggcaaga ccaagtacaa cgccaacaag acccctgaca agctgcagca 540
ggcagccctg cccctcctgt ccaatgccga atgcaagaag tcctggggca ggaggatcac 600
cgacgtgatg atctgtgccg gggccagtgg cgtctcctcc tgcatgggcg actctggcgg 660
tcccctggtc tgccaaaagg atggagcctg gaccctggtg ggcattgtgt cctggggcag 720
cgacacctgc tccacctcca gccctggcgt gtacgcccgt gtcaccaagc tcataccttg 780
ggtgcagaag atcctggctg ccaactgagc ccgcggctcc ctccgaccct gctccccaca 840
gagcctcagt aaacccatgg aacac 865

<210> 125
<211> 263
<212> PRT
<213> Homo sapiens

<220>
<223> chymotrypsin B

<400> 125
Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
 1   5   10   15
Phe Gly Cys Gly Val Pro Ala Ile His Pro Val Leu Ser Gly Leu Ser
            20   25   30
Arg Ile Val Asn Gly Glu Asp Ala Val Pro Gly Ser Trp Pro Trp Gln
        35   40   45
Val Ser Leu Gln Asp Lys Thr Gly Phe His Phe Cys Gly Gly Ser Leu
    50   55   60
Ile Ser Glu Asp Trp Val Val Thr Ala Ala His Cys Gly Val Arg Thr
65   70   75   80
Ser Asp Val Val Val Ala Gly Glu Phe Asp Gln Gly Ser Asp Glu Glu
                85   90   95
Asn Ile Gln Val Leu Lys Ile Ala Lys Val Phe Lys Asn Pro Lys Phe
            100   105   110
Ser Ile Leu Thr Val Asn Asn Asp Ile Thr Leu Leu Lys Leu Ala Thr
        115   120   125
Pro Ala Arg Phe Ser Gln Thr Val Ser Ala Val Cys Leu Pro Ser Ala
    130   135   140
Asp Asp Asp Phe Pro Ala Gly Thr Leu Cys Ala Thr Thr Gly Trp Gly

```
145                 150                 155                 160
Lys Thr Lys Tyr Asn Ala Asn Lys Thr Pro Asp Lys Leu Gln Gln Ala
                165                 170                 175
Ala Leu Pro Leu Leu Ser Asn Ala Glu Cys Lys Lys Ser Trp Gly Arg
            180                 185                 190
Arg Ile Thr Asp Val Met Ile Cys Ala Gly Ala Ser Gly Val Ser Ser
        195                 200                 205
Cys Met Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Asp Gly Ala
    210                 215                 220
Trp Thr Leu Val Gly Ile Val Ser Trp Gly Ser Asp Thr Cys Ser Thr
225                 230                 235                 240
Ser Ser Pro Gly Val Tyr Ala Arg Val Thr Lys Leu Ile Pro Trp Val
                245                 250                 255
Gln Lys Ile Leu Ala Ala Asn
            260
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<210> 126
<211> 952
<212> DNA
<213> Homo sapiens

<220>
<223> pancreatic elastase

<400> 126
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acagcaccca ggaccttccg gaaaccaatg cccgcgtagt cggagggact gaggccggga 120
ggaattcctg gccctctcag atttccctcc agtaccggtc tggaggttcc cggtatcaca 180
cctgtggagg gacccttatc agacagaact gggtgatgac agctgctcac tgcgtggatt 240
accagaagac tttccgcgtg gtggctggag accataacct gagccagaat gatggcactg 300
agcagtacgt gagtgtgcag aagatcgtgg tgcatccata ctggaacagc gataacgtgg 360
ctgccggcta tgacatcgcc ctgctgcgcc tggcccagag cgttaccctc aatagctatg 420
tccagctggg tgttctgccc caggagggag ccatcctggc taacaacagt ccctgctaca 480
tcacaggctg gggcaagacc aagaccaatg ggcagctggc ccagaccctg cagcaggctt 540
acctgccctc tgtggactac gccatctgct ccagctcctc ctactggggc tccactgtga 600
agaacaccat ggtgtgtgct ggtggagatg gagttcgctc tggatgccag ggtgactctg 660
ggggcccccc ccattgcttg gtgaatggca agtattctgt ccatggagtg accagctttg 720
tgtccagccg gggctgtaat gtctccagga agcctacagt cttcacccag gtctctgctt 780
acatctcctg gataaataat gtcatcgcct ccaactgaac attttcctga gtccaacgac 840
cttcccaaaa tggttcttag atctgcaata ggacttgcga tcaaaaagta aaacacattc 900
tgaaagacta ttgagccatt gatagaaaag caaataaaac tagatataca tt          952
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<210> 127
<211> 258
<212> PRT
<213> Homo sapiens

<220>
<223> pancreatic elastase

<400> 127
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Met Leu Val Leu Tyr Gly His Ser Thr Gln Asp Leu Pro Glu Thr Asn
 1               5                  10                  15
Ala Arg Val Val Gly Gly Thr Glu Ala Gly Arg Asn Ser Trp Pro Ser
            20                  25                  30
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Gln Ile Ser Leu Gln Tyr Arg Ser Gly Gly Ser Arg Tyr His Thr Cys
        35                  40                  45
Gly Gly Thr Leu Ile Arg Gln Asn Trp Val Met Thr Ala Ala His Cys
    50                  55                  60
Val Asp Tyr Gln Lys Thr Phe Arg Val Val Ala Gly Asp His Asn Leu
65                  70                  75                  80
Ser Gln Asn Asp Gly Thr Glu Gln Tyr Val Ser Val Gln Lys Ile Val
                85                  90                  95
Val His Pro Tyr Trp Asn Ser Asp Asn Val Ala Ala Gly Tyr Asp Ile
            100                 105                 110
Ala Leu Leu Arg Leu Ala Gln Ser Val Thr Leu Asn Ser Tyr Val Gln
        115                 120                 125
Leu Gly Val Leu Pro Gln Glu Gly Ala Ile Leu Ala Asn Asn Ser Pro
    130                 135                 140
Cys Tyr Ile Thr Gly Trp Gly Lys Thr Lys Thr Asn Gly Gln Leu Ala
145                 150                 155                 160
Gln Thr Leu Gln Gln Ala Tyr Leu Pro Ser Val Asp Tyr Ala Ile Cys
                165                 170                 175
Ser Ser Ser Ser Tyr Trp Gly Ser Thr Val Lys Asn Thr Met Val Cys
            180                 185                 190
Ala Gly Gly Asp Gly Val Arg Ser Gly Cys Gln Gly Asp Ser Gly Gly
        195                 200                 205
Pro Leu His Cys Leu Val Asn Gly Lys Tyr Ser Val His Gly Val Thr
    210                 215                 220
Ser Phe Val Ser Ser Arg Gly Cys Asn Val Ser Arg Lys Pro Thr Val
225                 230                 235                 240
Phe Thr Gln Val Ser Ala Tyr Ile Ser Trp Ile Asn Asn Val Ile Ala
                245                 250                 255
Ser Asn
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<210> 128
<211> 963
<212> DNA
<213> Homo sapiens

<220>
<223> pancreatic endopeptidase E (A)

<400> 128
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tcctatcatc acaaaactca tgatgctccg gctgctcagt tccctcctcc ttgtggccgt 60
tgcctcaggc tatggcccac cttcctctca ctcttccagc cgcgttgtcc atggtgagga 120
tgcggtcccc tacagctggc cctggcaggt ttccctgcag tatgagaaaa gtggaagctt 180
ctaccacacg tgtggcggta gcctcatcgc ccccgattgg gttgtgactg ccggccactg 240
catctcgagg gatctgacct accaggtggt gttgggtgag tacaaccttg ctgtgaagga 300
gggccccgag caggtgatcc ccatcaactc tgaggagctg tttgtgcatc cactctggaa 360
ccgctcgtgt gtggcctgtg gcaatgacat cgccctcatc aagctctcac gcagcgccca 420
gctgggagat gccgtccagc tcgcctcact ccctcccgct ggtgacatcc ttcccaacaa 480
gacaccctgc tacatcaccg gctggggccg tctctatacc aatgggccac tcccagacaa 540
gctgcagcag gcccggctgc ccgtggtgga ctataagcac tgctccaggt ggaactggtg 600
gggttccacc gtgaagaaaa ccatggtgtg tgctggaggg tacatccgct ccggctgcaa 660
cggtgactct ggaggacccc tcaactgccc cacagaggat ggtggctggc aggtccacgg 720
tgtgaccagc tttgtttctg gctttggctg caacttcatc tggaagccca cggtgttcac 780
tcgagtctcc gccttcatcg actggattga ggagaccata gcaagccact agaaccaagg 840
cccagctggc agtgctgatc gatcccacat cctgaataaa gaataaaagat ctctcagaaa 900
attccaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
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aaa 963

<210> 129
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<223> pancreatic endopeptidase E (A)

<400> 129
Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser
1 5 10 15
Gly Tyr Gly Pro Pro Ser Ser His Ser Ser Ser Arg Val Val His Gly
20 25 30
Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
35 40 45
Glu Lys Ser Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
50 55 60
Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Arg Asp Leu Thr
65 70 75 80
Tyr Gln Val Val Leu Gly Glu Tyr Asn Leu Ala Val Lys Glu Gly Pro
85 90 95
Glu Gln Val Ile Pro Ile Asn Ser Glu Glu Leu Phe Val His Pro Leu
100 105 110
Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys
115 120 125
Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu
130 135 140
Pro Pro Ala Gly Asp Ile Leu Pro Asn Lys Thr Pro Cys Tyr Ile Thr
145 150 155 160
Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln
165 170 175
Gln Ala Arg Leu Pro Val Val Asp Tyr Lys His Cys Ser Arg Trp Asn
180 185 190
Trp Trp Gly Ser Thr Val Lys Lys Thr Met Val Cys Ala Gly Gly Tyr
195 200 205
Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro
210 215 220
Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser
225 230 235 240
Gly Phe Gly Cys Asn Phe Ile Trp Lys Pro Thr Val Phe Thr Arg Val
245 250 255
Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His
260 265 270

<210> 130
<211> 914
<212> DNA
<213> Homo sapiens

<220>
<223> pancreatic elastase II (IIA)

<400> 130
ttttacagaa ctcccacgga cacaccatga taaggacgct gctgctgtcc actttggtgg 60

ctggagccct cagttgtggg gaccccactt acccacctta tgtgactagg gtggttggcg 120
gtgaagaagc gaggcccaac agctggccct ggcaggtctc cctgcagtac agctccaatg 180
gcaagtggta ccacacctgc ggagggtccc tgatagccaa cagctgggtc ctgacggctg 240
cccactgcat cagctcctcc aggacctacc gcgtggggct gggccggcac aacctctacg 300
ttgcggagtc cggctcgctg gcagtcagtg tctctaagat tgtggtgcac aaggactgga 360
actccaacca aatctccaaa gggaacgaca ttgccctgct caaactggct aaccccgtct 420
ccctcaccga caagatccag ctggcctgcc tccctcctgc cggcaccatt ctacccaaca 480
actacccctg ctacgtcacg ggctggggaa ggctgcagac caacggggct gttcctgatg 540
tcctgcagca gggccggttg ctggttgtgg actatgccac ctgctccagc tctgcctggt 600
ggggcagcag cgtgaaaacc agtatgatct gtgctggggg tgatggcgtg atctccagct 660
gcaacggaga ctctggcggg ccactgaact gtcaggcgtc tgacggccgg tggcaggtgc 720
acggcatcgt cagcttcggg tctcgcctcg gctgcaacta ctaccacaag ccctccgtct 780
tcacgcgggt ctccaattac atcgactgga tcaattcggt gattgcaaat aactaaccaa 840
aagaagtccc tgggactgtt tcagacttgg aaaggtcaca gaaggaaaat aatataataa 900
agtgacaact atgc 914

<210> 131
<211> 269
<212> PRT
<213> Homo sapiens

<220>
<223> pancreatic elastase II (IIA)

<400> 131
Met Ile Arg Thr Leu Leu Leu Ser Thr Leu Val Ala Gly Ala Leu Ser
1 5 10 15
Cys Gly Asp Pro Thr Tyr Pro Pro Tyr Val Thr Arg Val Val Gly Gly
20 25 30
Glu Glu Ala Arg Pro Asn Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
35 40 45
Ser Ser Asn Gly Lys Trp Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
50 55 60

Asn Ser Trp Val Leu Thr Ala Ala His Cys Ile Ser Ser Ser Arg Thr
65 70 75 80
Tyr Arg Val Gly Leu Gly Arg His Asn Leu Tyr Val Ala Glu Ser Gly
85 90 95
Ser Leu Ala Val Ser Val Ser Lys Ile Val Val His Lys Asp Trp Asn
100 105 110
Ser Asn Gln Ile Ser Lys Gly Asn Asp Ile Ala Leu Leu Lys Leu Ala
115 120 125
Asn Pro Val Ser Leu Thr Asp Lys Ile Gln Leu Ala Cys Leu Pro Pro
130 135 140
Ala Gly Thr Ile Leu Pro Asn Asn Tyr Pro Cys Tyr Val Thr Gly Trp
145 150 155 160
Gly Arg Leu Gln Thr Asn Gly Ala Val Pro Asp Val Leu Gln Gln Gly
165 170 175
Arg Leu Leu Val Val Asp Tyr Ala Thr Cys Ser Ser Ser Ala Trp Trp
180 185 190
Gly Ser Ser Val Lys Thr Ser Met Ile Cys Ala Gly Gly Asp Gly Val
195 200 205
Ile Ser Ser Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Gln Ala
210 215 220
Ser Asp Gly Arg Trp Gln Val His Gly Ile Val Ser Phe Gly Ser Arg
225 230 235 240
Leu Gly Cys Asn Tyr Tyr His Lys Pro Ser Val Phe Thr Arg Val Ser

245 250 255
Asn Tyr Ile Asp Trp Ile Asn Ser Val Ile Ala Asn Asn
260 265

<210> 132
<211> 3696
<212> DNA
<213> Homo sapiens

<220>
<223> Enteropeptidase

<400> 132
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attggtagtg ctctgtgctg gattaattgc agtatcctgc ctgacaatca aggaatccca 180
acgaggtgca gcacttggac agagtcatga agccagagcg acatttaaaa taacatccgg 240
agttacatat aatcctaatt tgcaagacaa actctcagtg gatttcaaag ttcttgcttt 300
tgaccttcag caaatgatag atgagatctt tctatcaagc aatctgaaga atgaatataa 360
gaactcaaga gttttacaat ttgaaaatgg cagcattata gtcgtatttg acctttttctt 420
tgcccagtgg gtgtcagatc aaaatgtaaa agaagaactg attcaaggcc ttgaagcaaa 480
taaatccagc caactggtca ctttccatat tgatttgaac agcgttgata tcctagacaa 540
gctaacaacc accagtcatc tggcaactcc aggaaatgtc tcaatagagt gcctgcctgg 600
ttcaagtcct tgtactgatg ctctaacgtg tataaaagct gatttatttt gtgatggaga 660
agtaaactgt ccagatggtt ctgacgaaga caataaaatg tgtgccacag tttgtgatgg 720
aagatttttg ttaactggat catctgggtc tttccaggct actcattatc caaaaccttc 780
tgaaacaagt gttgtctgcc agtggatcat acgtgtaaac caaggacttt ccattaaact 840
gagcttcgat gattttaata catattatac agatatatta gatatttatg aaggtgtagg 900
atcaagcaag attttaagag cttctatttg ggaaactaat cctggcacaa taagaatttt 960
ttccaaccaa gttactgcca cctttcttat agaatctgat gaaagtgatt atgttggctt 1020
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taactttgag gatggctttt gtttctgggt ccaggatcta aatgatgata atgaatggga 1140
aaggattcag ggaagcacct tttctccttt tactggaccc aattttgacc acacttttgg 1200
caatgcttca ggattttaca tttctacccc aactggacca ggagggagac aagaacgagt 1260
ggggctttta agcctccctt tggaccccac tttggagcca gcttgcctta gtttctggta 1320
tcatatgtat ggtgaaaatg tccataaatt aagcattaat atcagcaatg accaaaatat 1380
ggagaagaca gttttccaaa aggaaggaaa ttatggagac aattggaatt atggacaagt 1440
aaccctaaat gaaacagtta aatttaaggt tgcttttaat gcttttaaaa acaagatcct 1500
gagtgatatt gcgttggatg acattagcct aacatatggg atttgcaatg ggagtcttta 1560
tccagaacca actttggtgc caactcctcc accagaactt cctacggact gtggaggacc 1620
ttttgagctg tgggagccaa atacaacatt cagttctacg aactttccaa acagctaccc 1680
taatctggct ttctgtgttt ggattttaaa tgcacaaaaa ggaaagaata tacaacttca 1740
ttttcaagaa tttgacttag aaaatattaa cgatgtagtt gaaataagag atggtgaaga 1800
agctgattcc ttgctcttag ctgtgtacac agggcctggc ccagtaaagg atgtgttctc 1860
taccaccaac agaatgactg tgcttctcat cactaacgat gtgttggcaa gaggagggtt 1920
taaagcaaac tttactactg gctatcactt ggggattcca gagccatgca aggcagacca 1980
ttttcaatgt aaaaatggag agtgtgttcc actggtgaat ctctgtgacg gtcatctgca 2040
ctgtgaggat ggctcagatg aagcagattg tgtgcgtttt ttcaatggca caacgaacaa 2100
caatggttta gtgcggttca gaatccagag catatggcat acagcttgtg ctgagaactg 2160
gaccacccag atttcaaatg atgtttgtca actgctggga ctagggagtg gaaactcatc 2220
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ccacttaata ctaacaccca gtcaacagtg tttacaggat tccttgattc ggttacagtg 2340
taaccataaa tcttgtggaa aaaaactggc agctcaagac atcaccccaa agattgttgg 2400
aggaagtaat gccaaagaag gggcctggcc ctgggttgtg ggtctgtatt atggcggccg 2460
actgctctgc ggcgcatctc tcgtcagcag tgactggctg gtgtccgccg cacactgcgt 2520
gtatgggaga aacttagagc catccaagtg gacagcaatc ctaggcctgc atatgaaatc 2580

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aaatctgacc tctcctcaaa cagtccctcg attaatagat gaaattgtca taaaccctca 2640
ttacaatagg cgaagaaagg acaacgacat tgccatgatg catctggaat ttaaagtgaa 2700
ttacacagat tacatacaac ctatttgttt accggaagaa aatcaagttt ttcctccagg 2760
aagaaattgt tctattgctg gttgggggac ggttgtatat caaggtacta ctgcaaacat 2820
attgcaagaa gctgatgttc ctcttctatc aaatgagaga tgccaacagc agatgccaga 2880
atataacatt actgaaaata tgatatgtgc aggctatgaa gaaggaggaa tagattcttg 2940
tcaggggat tcaggaggac cattaatgtg ccaagaaaac aacaggtggt tccttgctgg 3000
tgtgacctca tttggataca agtgtgccct gcctaatcgc cccggagtgt atgccagggt 3060
ctcaaggttt accgaatgga tacaaagttt tctacattag cgcatttctt aaactaaaca 3120
ggaaagtcgc attattttcc cattctactc tagaaagcat ggaaattaag tgtttcgtac 3180
aaaaatttta aaaagttacc aaaggttttt attcttacct atgtcaatga aatgctaggg 3240
ggccagggaa acaaaatttt aaaaataata aaattcacca tagcaataca gaataacttt 3300
aaaataccat taaatacatt tgtatttcat tgtgaacagg tatttcttca cagatctcat 3360
ttttaaaatt cttaatgatt atttttatta cttactgttg tttaaaggga tgttatttta 3420
aagcatatac catacactta agaaatttga gcagaattta aaaaagaaag aaaataaatt 3480
gtttttccca aagtatgtca ctgttggaaa taaactgcca taaattttct agttccagtt 3540
tagtttgctg ctattagcag aaactcaatt gtttctctgt cttttctatc aaaattttca 3600
acatatgcat aaccttagta ttttcccaac caatagaaac tatttattgt aagcttatgt 3660
cacaggcctg gactaaattg attttacgtt cctctt                          3696
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<210> 133
<211> 1019
<212> PRT
<213> Homo sapiens

<220>
<223> Enteropeptidase

<400> 133

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Met Gly Ser Lys Arg Gly Ile Ser Ser Arg His His Ser Leu Ser Ser
 1               5                  10                  15
Tyr Glu Ile Met Phe Ala Ala Leu Phe Ala Ile Leu Val Val Leu Cys
            20                  25                  30
Ala Gly Leu Ile Ala Val Ser Cys Leu Thr Ile Lys Glu Ser Gln Arg
        35                  40                  45
Gly Ala Ala Leu Gly Gln Ser His Glu Ala Arg Ala Thr Phe Lys Ile
    50                  55                  60
Thr Ser Gly Val Thr Tyr Asn Pro Asn Leu Gln Asp Lys Leu Ser Val
65                  70                  75                  80
Asp Phe Lys Val Leu Ala Phe Asp Leu Gln Gln Met Ile Asp Glu Ile
                85                  90                  95
Phe Leu Ser Ser Asn Leu Lys Asn Glu Tyr Lys Asn Ser Arg Val Leu
            100                 105                 110
Gln Phe Glu Asn Gly Ser Ile Ile Val Val Phe Asp Leu Phe Phe Ala
        115                 120                 125
Gln Trp Val Ser Asp Gln Asn Val Lys Glu Glu Leu Ile Gln Gly Leu
    130                 135                 140
Glu Ala Asn Lys Ser Ser Gln Leu Val Thr Phe His Ile Asp Leu Asn
145                 150                 155                 160
Ser Val Asp Ile Leu Asp Lys Leu Thr Thr Thr Ser His Leu Ala Thr
                165                 170                 175
Pro Gly Asn Val Ser Ile Glu Cys Leu Pro Gly Ser Ser Pro Cys Thr
            180                 185                 190
Asp Ala Leu Thr Cys Ile Lys Ala Asp Leu Phe Cys Asp Gly Glu Val
        195                 200                 205
Asn Cys Pro Asp Gly Ser Asp Glu Asp Asn Lys Met Cys Ala Thr Val
    210                 215                 220
```

```
Cys Asp Gly Arg Phe Leu Leu Thr Gly Ser Ser Gly Ser Phe Gln Ala
225                 230                 235                 240
Thr His Tyr Pro Lys Pro Ser Glu Thr Ser Val Val Cys Gln Trp Ile
                245                 250                 255
Ile Arg Val Asn Gln Gly Leu Ser Ile Lys Leu Ser Phe Asp Asp Phe
            260                 265                 270
Asn Thr Tyr Tyr Thr Asp Ile Leu Asp Ile Tyr Glu Gly Val Gly Ser
        275                 280                 285
Ser Lys Ile Leu Arg Ala Ser Ile Trp Glu Thr Asn Pro Gly Thr Ile
    290                 295                 300
Arg Ile Phe Ser Asn Gln Val Thr Ala Thr Phe Leu Ile Glu Ser Asp
305                 310                 315                 320
Glu Ser Asp Tyr Val Gly Phe Asn Ala Thr Tyr Thr Ala Phe Asn Ser
                325                 330                 335
Ser Glu Leu Asn Asn Tyr Glu Lys Ile Asn Cys Asn Phe Glu Asp Gly
            340                 345                 350
Phe Cys Phe Trp Val Gln Asp Leu Asn Asp Asp Asn Glu Trp Glu Arg
        355                 360                 365
Ile Gln Gly Ser Thr Phe Ser Pro Phe Thr Gly Pro Asn Phe Asp His
    370                 375                 380
Thr Phe Gly Asn Ala Ser Gly Phe Tyr Ile Ser Thr Pro Thr Gly Pro
385                 390                 395                 400
Gly Gly Arg Gln Glu Arg Val Gly Leu Leu Ser Leu Pro Leu Asp Pro
                405                 410                 415
Thr Leu Glu Pro Ala Cys Leu Ser Phe Trp Tyr His Met Tyr Gly Glu
            420                 425                 430
Asn Val His Lys Leu Ser Ile Asn Ile Ser Asn Asp Gln Asn Met Glu
        435                 440                 445
Lys Thr Val Phe Gln Lys Glu Gly Asn Tyr Gly Asp Asn Trp Asn Tyr
    450                 455                 460
Gly Gln Val Thr Leu Asn Glu Thr Val Lys Phe Lys Val Ala Phe Asn
465                 470                 475                 480
Ala Phe Lys Asn Lys Ile Leu Ser Asp Ile Ala Leu Asp Asp Ile Ser
                485                 490                 495
Leu Thr Tyr Gly Ile Cys Asn Gly Ser Leu Tyr Pro Glu Pro Thr Leu
            500                 505                 510
Val Pro Thr Pro Pro Pro Glu Leu Pro Thr Asp Cys Gly Gly Pro Phe
        515                 520                 525
Glu Leu Trp Glu Pro Asn Thr Thr Phe Ser Ser Thr Asn Phe Pro Asn
    530                 535                 540
Ser Tyr Pro Asn Leu Ala Phe Cys Val Trp Ile Leu Asn Ala Gln Lys
545                 550                 555                 560
Gly Lys Asn Ile Gln Leu His Phe Gln Glu Phe Asp Leu Glu Asn Ile
                565                 570                 575
Asn Asp Val Val Glu Ile Arg Asp Gly Glu Glu Ala Asp Ser Leu Leu
            580                 585                 590
Leu Ala Val Tyr Thr Gly Pro Gly Pro Val Lys Asp Val Phe Ser Thr
        595                 600                 605
Thr Asn Arg Met Thr Val Leu Leu Ile Thr Asn Asp Val Leu Ala Arg
    610                 615                 620
Gly Gly Phe Lys Ala Asn Phe Thr Thr Gly Tyr His Leu Gly Ile Pro
625                 630                 635                 640
Glu Pro Cys Lys Ala Asp His Phe Gln Cys Lys Asn Gly Glu Cys Val
                645                 650                 655
Pro Leu Val Asn Leu Cys Asp Gly His Leu His Cys Glu Asp Gly Ser
            660                 665                 670
Asp Glu Ala Asp Cys Val Arg Phe Phe Asn Gly Thr Thr Asn Asn Asn
```

```
        675                 680                 685
Gly Leu Val Arg Phe Arg Ile Gln Ser Ile Trp His Thr Ala Cys Ala
    690                 695                 700
Glu Asn Trp Thr Thr Gln Ile Ser Asn Asp Val Cys Gln Leu Leu Gly
705                 710                 715                 720
Leu Gly Ser Gly Asn Ser Ser Lys Pro Ile Phe Ser Thr Asp Gly Gly
                725                 730                 735
Pro Phe Val Lys Leu Asn Thr Ala Pro Asp Gly His Leu Ile Leu Thr
            740                 745                 750
Pro Ser Gln Gln Cys Leu Gln Asp Ser Leu Ile Arg Leu Gln Cys Asn
        755                 760                 765
His Lys Ser Cys Gly Lys Lys Leu Ala Ala Gln Asp Ile Thr Pro Lys
    770                 775                 780
Ile Val Gly Gly Ser Asn Ala Lys Glu Gly Ala Trp Pro Trp Val Val
785                 790                 795                 800
Gly Leu Tyr Tyr Gly Gly Arg Leu Leu Cys Gly Ala Ser Leu Val Ser
                805                 810                 815
Ser Asp Trp Leu Val Ser Ala Ala His Cys Val Tyr Gly Arg Asn Leu
            820                 825                 830
Glu Pro Ser Lys Trp Thr Ala Ile Leu Gly Leu His Met Lys Ser Asn
        835                 840                 845
Leu Thr Ser Pro Gln Thr Val Pro Arg Leu Ile Asp Glu Ile Val Ile
    850                 855                 860
Asn Pro His Tyr Asn Arg Arg Arg Lys Asp Asn Asp Ile Ala Met Met
865                 870                 875                 880
His Leu Glu Phe Lys Val Asn Tyr Thr Asp Tyr Ile Gln Pro Ile Cys
                885                 890                 895
Leu Pro Glu Glu Asn Gln Val Phe Pro Pro Gly Arg Asn Cys Ser Ile
            900                 905                 910
Ala Gly Trp Gly Thr Val Val Tyr Gln Gly Thr Thr Ala Asn Ile Leu
        915                 920                 925
Gln Glu Ala Asp Val Pro Leu Leu Ser Asn Glu Arg Cys Gln Gln Gln
    930                 935                 940
Met Pro Glu Tyr Asn Ile Thr Glu Asn Met Ile Cys Ala Gly Tyr Glu
945                 950                 955                 960
Glu Gly Gly Ile Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met
                965                 970                 975
Cys Gln Glu Asn Asn Arg Trp Phe Leu Ala Gly Val Thr Ser Phe Gly
            980                 985                 990
Tyr Lys Cys Ala Leu Pro Asn Arg Pro Gly Val Tyr Ala Arg Val Ser
        995                 1000                1005
Arg Phe Thr Glu Trp Ile Gln Ser Phe Leu His
    1010                1015
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<210> 134
<211> 917
<212> DNA
<213> Homo sapiens

<220>
<223> chymotrypsin C

<400> 134
cagccagtcc tgagcaccta accatgttgg gcatcactgt cctcgctgcg ctcttggcct 60
gtgcctccag ctgtggggtg cccagcttcc cgcccaacct atccgcccga gtggtgggag 120
gagaggatgc ccggccccac agctggccct ggcagatctc cctccagtac ctcaagaacg 180

```
acacgtggag gcatacgtgt ggcgggactt tgattgctag caacttcgtc ctcactgccg 240
cccactgcat cagcaacacc cggacctacc gtgtggccgt gggaaagaac aacctggagg 300
tggaagacga agaaggatcc ctgtttgtgg gtgtggacac catccacgtc cacaagagat 360
ggaatgccct cctgttgcgc aatgatattg ccctcatcaa gcttgcagag catgtggagc 420
tgagtgacac catccaggtg gcctgcctgc cagagaagga ctccctgctc cccaaggact 480
acccctgcta tgtcaccggc tggggccgcc tctggaccaa cggccccatt gctgataagc 540
tgcagcaggg cctgcagccc gtggtggatc acgccacgtg ctccaggatt gactggtggg 600
gcttcagggt gaagaaaacc atggtgtgcg ctgggggcga tggcgtcatc tcagcctgca 660
atggggactc cggtggccca ctgaactgcc agttggagaa cggttcctgg gaggtgtttg 720
gcatcgtcag ctttggctcc cggcggggct gcaacacccg caagaagccg gtagtctaca 780
cccgggtgtc cgcctacatc gactggatca acgagaaaat gcagctgtga tttgttgctg 840
ggagcggcgg cagcgagtcc ctgcaacagc aataaacttc cttctcctcg ggccacctga 900
aaaaaaaaaa aaaaaaa                                                 917

<210> 135
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<223> chymotrypsin C

<400> 135
Met Leu Gly Ile Thr Val Leu Ala Ala Leu Leu Ala Cys Ala Ser Ser
 1               5                  10                  15
Cys Gly Val Pro Ser Phe Pro Pro Asn Leu Ser Ala Arg Val Val Gly
            20                  25                  30
Gly Glu Asp Ala Arg Pro His Ser Trp Pro Trp Gln Ile Ser Leu Gln
        35                  40                  45
Tyr Leu Lys Asn Asp Thr Trp Arg His Thr Cys Gly Gly Thr Leu Ile
    50                  55                  60
Ala Ser Asn Phe Val Leu Thr Ala Ala His Cys Ile Ser Asn Thr Arg
65                  70                  75                  80
Thr Tyr Arg Val Ala Val Gly Lys Asn Asn Leu Glu Val Glu Asp Glu
                85                  90                  95
Glu Gly Ser Leu Phe Val Gly Val Asp Thr Ile His Val His Lys Arg
            100                 105                 110
Trp Asn Ala Leu Leu Leu Arg Asn Asp Ile Ala Leu Ile Lys Leu Ala
        115                 120                 125
Glu His Val Glu Leu Ser Asp Thr Ile Gln Val Ala Cys Leu Pro Glu
    130                 135                 140
Lys Asp Ser Leu Leu Pro Lys Asp Tyr Pro Cys Tyr Val Thr Gly Trp
145                 150                 155                 160
Gly Arg Leu Trp Thr Asn Gly Pro Ile Ala Asp Lys Leu Gln Gln Gly
                165                 170                 175
Leu Gln Pro Val Val Asp His Ala Thr Cys Ser Arg Ile Asp Trp Trp
            180                 185                 190
Gly Phe Arg Val Lys Lys Thr Met Val Cys Ala Gly Gly Asp Gly Val
        195                 200                 205
Ile Ser Ala Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Gln Leu
    210                 215                 220
Glu Asn Gly Ser Trp Glu Val Phe Gly Ile Val Ser Phe Gly Ser Arg
225                 230                 235                 240
Arg Gly Cys Asn Thr Arg Lys Lys Pro Val Val Tyr Thr Arg Val Ser
                245                 250                 255
Ala Tyr Ile Asp Trp Ile Asn Glu Lys Met Gln Leu
            260                 265
```

<210> 136
<211> 1938
<212> DNA
<213> Homo sapoens

<220>
<223> Prostasin

<400> 136
gactttggtg gcaagaggag ctggcggagc ccagccagtg ggcggggcca ggggaggggc 60
gggcaggtag gtgcagccac tcctgggagg accctgcgtg gccagacggt gctggtgact 120
cgtccacact gctcgcttcg gatactccag gcgtctcccg ttgcggccgc tccctgcctt 180
agaggccagc cttggacact tgctgccccc ttccagcccg gattctggga tccttccctc 240
tgagccaaca tctgggtcct gccttcgaca ccaccccaag gcttcctacc ttgcgtgcct 300
ggagtctgcc ccaggggccc ttgtcctggg ccatggccca gaagggggtc ctggggcctg 360
ggcagctggg ggctgtggcc attctgctct atcttggatt actccggtcg gggacaggag 420
cggaaggggc agaagctccc tgcggtgtgg ccccccaagc acgcatcaca ggtggcagca 480
gtgcagtcgc cggtcagtgg ccctggcagg tcagcatcac ctatgaaggc gtccatgtgt 540
gtggtggctc tctcgtgtct gagcagtggg tgctgtcagc tgctcactgc ttccccagcg 600
agcaccacaa ggaagcctat gaggtcaagc tgggggccca ccagctagac tcctactccg 660
aggacgccaa ggtcagcacc ctgaaggaca tcatccccca ccccagctac ctccaggagg 720
gctcccaggg cgacattgca ctcctccaac tcagcagacc catcaccttc tcccgctaca 780
tccggcccat ctgcctccct gcagccaacg cctccttccc caacggcctc cactgcactg 840
tcactggctg gggtcatgtg gccccctcag tgagcctcct gacgcccaag ccactgcagc 900
aactcgaggt gcctctgatc agtcgtgaga cgtgtaactg cctgtacaac atcgacgcca 960
agcctgagga gccgcacttt gtccaagagg acatggtgtg tgctggctat gtggaggggg 1020
gcaaggacgc ctgccagggt gactctgggg gcccactctc ctgccctgtg gagggtctct 1080
ggtacctgac gggcattgtg agctggggag atgcctgtgg ggcccgcaac aggcctggtg 1140
tgtacactct ggcctccagc tatgcctcct ggatccaaag caaggtgaca gaactccagc 1200
ctcgtgtggt gccccaaacc caggagtccc agcccgacag caacctctgt ggcagccacc 1260
tggccttcag ctctgcccca gcccagggct tgctgaggcc catccttttc ctgcctctgg 1320
gcctggctct gggcctcctc tccccatggc tcagcgagca ctgagctggc cctacttcca 1380
ggatggatgc atcacactca aggacaggag cctggtcctt ccctgatggc ctttggaccc 1440
agggcctgac ttgagccact ccttccttca ggactctgcg ggaggctggg gccccatctt 1500
gatctttgag cccattcttc tgggtgtgct ttttgggacc atcactgaga gtcaggagtt 1560
ttactgcctg tagcaatggc cagagcctct ggcccctcac ccaccatgga ccagcccatt 1620
ggccgagctc ctggggagct cctgggaccc ttggctatga aaatgagccc tggctcccac 1680
ctgtttctgg aagactgctc ccggcccgcc tgcccagact gatgagcaca tctctctgcc 1740
ctctccctgt gttctgggct ggggccacct ttgtgcagct tcgaggacag gaaaggcccc 1800
aatcttgccc actggccgct gagcgccccc gagccctgac tcctggactc cggaggactg 1860
agcccccacc ggaactgggc tggcgcttgg atctggggtg ggagtaacag ggcagaaatg 1920
attaaaatgt ttgagcac 1938

<210> 137
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<223> Prostasin

<400> 137
Met Ala Gln Lys Gly Val Leu Gly Pro Gly Gln Leu Gly Ala Val Ala
 1   5   10   15
Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala Glu Gly

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            20                  25                  30
Ala Glu Ala Pro Cys Gly Val Ala Pro Gln Ala Arg Ile Thr Gly Gly
        35                  40                  45
Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile Thr Tyr
    50                  55                  60
Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln Trp Val
65                  70                  75                  80
Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu Ala Tyr
                85                  90                  95
Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu Asp Ala
            100                 105                 110
Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr Leu Gln
        115                 120                 125
Glu Gly Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg Pro Ile
    130                 135                 140
Thr Phe Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala Asn Ala
145                 150                 155                 160
Ser Phe Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly His Val
                165                 170                 175
Ala Pro Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln Leu Glu
            180                 185                 190
Val Pro Leu Ile Ser Arg Glu Thr Cys Asn Cys Leu Tyr Asn Ile Asp
        195                 200                 205
Ala Lys Pro Glu Glu Pro His Phe Val Gln Glu Asp Met Val Cys Ala
    210                 215                 220
Gly Tyr Val Glu Gly Gly Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly
225                 230                 235                 240
Pro Leu Ser Cys Pro Val Glu Gly Leu Trp Tyr Leu Thr Gly Ile Val

                245                 250                 255
Ser Trp Gly Asp Ala Cys Gly Ala Arg Asn Arg Pro Gly Val Tyr Thr
            260                 265                 270
Leu Ala Ser Ser Tyr Ala Ser Trp Ile Gln Ser Lys Val Thr Glu Leu
        275                 280                 285
Gln Pro Arg Val Val Pro Gln Thr Gln Glu Ser Gln Pro Asp Ser Asn
    290                 295                 300
Leu Cys Gly Ser His Leu Ala Phe Ser Ser Ala Pro Ala Gln Gly Leu
305                 310                 315                 320
Leu Arg Pro Ile Leu Phe Leu Pro Leu Gly Leu Ala Leu Gly Leu Leu
                325                 330                 335
Ser Pro Trp Leu Ser Glu His
            340
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<210> 138
<211> 874
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 1

<400> 138
agttcctcca cctgctggcc cctggacacc tctgtcacca tgtggttcct ggttctgtgc 60
ctcgccctgt ccctgggggg gactggtgct gcgcccccga ttcagtcccg gattgtggga 120
ggctgggagt gtgagcagca ttcccagccc tggcaggcgg ctctgtacca tttcagcact 180
ttccagtgtg ggggcatcct ggtgcaccgc cagtgggtgc tcacagctgc tcattgcatc 240

agcgacaatt accagctctg gctgggtcgc cacaacttgt ttgacgacga aaacacagcc 300
cagtttgttc atgtcagtga gagcttccca caccctggct tcaacatgag cctcctggag 360
aaccacaccc gccaagcaga cgaggactac agccacgacc tcatgctgct ccgcctgaca 420
gagcctgctg ataccatcac agatgctgtg aaggtcgtgg agttgcccac cgaggaaccc 480
gaagtgggga gcacctgttt ggcttccggc tggggcagca tcgaaccaga gaatttctca 540
tttccagatg atctccagtg tgtggacctc aaaatcctgc ctaatgatga gtgcaaaaaa 600
gcccacgtcc agaaggtgac agacttcatg ctgtgtgtcg gacacctgga aggtggcaaa 660
gacacctgtg tgggtgattc aggggggccg ctgatgtgtg atggtgtgct ccaaggtgtc 720
acatcatggg gctacgtccc ttgtggcacc cccaataagc cttctgtcgc cgtcagagtg 780
ctgtcttatg tgaagtggat cgaggacacc atagcggaga actcctgaac gcccagccct 840
gtcccctacc cccagtaaaa tcaaatgtgc atcc 874

<210> 139
<211> 262
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 1

<400> 139
Met Trp Phe Leu Val Leu Cys Leu Ala Leu Ser Leu Gly Gly Thr Gly
1 5 10 15
Ala Ala Pro Pro Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30
Gln His Ser Gln Pro Trp Gln Ala Ala Leu Tyr His Phe Ser Thr Phe
35 40 45
Gln Cys Gly Gly Ile Leu Val His Arg Gln Trp Val Leu Thr Ala Ala
50 55 60
His Cys Ile Ser Asp Asn Tyr Gln Leu Trp Leu Gly Arg His Asn Leu
65 70 75 80
Phe Asp Asp Glu Asn Thr Ala Gln Phe Val His Val Ser Glu Ser Phe
85 90 95
Pro His Pro Gly Phe Asn Met Ser Leu Leu Glu Asn His Thr Arg Gln
100 105 110
Ala Asp Glu Asp Tyr Ser His Asp Leu Met Leu Leu Arg Leu Thr Glu
115 120 125
Pro Ala Asp Thr Ile Thr Asp Ala Val Lys Val Val Glu Leu Pro Thr
130 135 140
Glu Glu Pro Glu Val Gly Ser Thr Cys Leu Ala Ser Gly Trp Gly Ser
145 150 155 160
Ile Glu Pro Glu Asn Phe Ser Phe Pro Asp Asp Leu Gln Cys Val Asp
165 170 175
Leu Lys Ile Leu Pro Asn Asp Glu Cys Lys Lys Ala His Val Gln Lys
180 185 190
Val Thr Asp Phe Met Leu Cys Val Gly His Leu Glu Gly Gly Lys Asp
195 200 205
Thr Cys Val Gly Asp Ser Gly Gly Pro Leu Met Cys Asp Gly Val Leu
210 215 220
Gln Gly Val Thr Ser Trp Gly Tyr Val Pro Cys Gly Thr Pro Asn Lys
225 230 235 240
Pro Ser Val Ala Val Arg Val Leu Ser Tyr Val Lys Trp Ile Glu Asp
245 250 255
Thr Ile Ala Glu Asn Ser
260

<210> 140
<211> 2855
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK2 transcript variant 1

<400> 140
agccccaaac tcaccacctg gccgtggaca cctgtgtcag catgtgggac ctggttctct 60
ccatcgcctt gtctgtgggg tgcactggtg ccgtgccccc catccagtct cggattgtgg 120
gaggctggga gtgtgagaag cattcccaac cctggcaggt ggctgtgtac agtcatggat 180
gggcacactg tgggggtgtc ctggtgcacc cccagtgggt gctcacagct gcccattgcc 240
taaagaagaa tagccaggtc tggctgggtc ggcacaacct gtttgagcct gaagacacag 300
gccagagggt ccctgtcagc cacagcttcc cacacccgct ctacaatatg agccttctga 360
agcatcaaag ccttagacca gatgaagact ccagccatga cctcatgctg ctccgcctgt 420
cagagcctgc caagatcaca gatgttgtga aggtcctggg cctgcccacc caggagccag 480
cactggggac cacctgctac gcctcaggct ggggcagcat cgaaccagag gagttcttgc 540
gccccaggag tcttcagtgt gtgagcctcc atctcctgtc caatgacatg tgtgctagag 600
cttactctga gaaggtgaca gagttcatgt tgtgtgctgg gctctggaca ggtggtaaag 660
acacttgtgg gggtgattct gggggtccac ttgtctgtaa tggtgtgctt caaggtatca 720
catcatgggg ccctgagcca tgtgccctgc ctgaaaagcc tgctgtgtac accaaggtgg 780
tgcattaccg gaagtggatc aaggacacca tcgcagccaa cccctgagtg cccctgtccc 840
acccctacct ctagtaaatt taagtccacc tcacgttctg gcatcacttg gcctttctgg 900
atgctggaca cctgaagctt ggaactcacc tggccgaagc tcgagcctcc tgagtcctac 960
tgacctgtgc tttctggtgt ggagtccagg gctgctagga aaaggaatgg gcagacacag 1020
gtgtatgcca atgtttctga aatgggtata atttcgtcct ctccttcgga acactggctg 1080
tctctgaaga cttctcgctc agtttcagtg aggacacaca caaagacgtg ggtgaccatg 1140
ttgtttgtgg ggtgcagaga tgggaggggt ggggcccacc ctggaagagt ggacagtgac 1200
acaaggtgga cactctctac agatcactga ggataagctg gagccacaat gcatgaggca 1260
cacacacagc aaggatgacg ctgtaaacat agcccacgct gtcctggggg cactgggaag 1320
cctagataag gccgtgagca gaaagaaggg gaggatcctc ctatgttgtt gaaggaggga 1380
ctagggggag aaactgaaag ctgattaatt acaggaggtt tgttcaggtc ccccaaacca 1440
ccgtcagatt tgatgatttc ctagcaggac ttacagaaat aaagagctat catgctgtgg 1500
tttattatgg tttgttacat tgatgggata catactgaaa tcagcaaaca aaacagatgt 1560
atagattaga gtgtggagaa aacagaggaa aacttgcagt tacgaagact ggcaacttgg 1620
ctttactaag ttttcagact ggcaggaagt caaacctatt aggctgagga ccttgtggag 1680
tgtagctgat ccagctgata gaggaactag ccaggtgggg gcctttccct ttggatgggg 1740
ggcatatctg acagttattc tctccaagtg gagacttacg gacagcatat aattctccct 1800
gcaaggatgt atgataatat gtacaaagta attccaactg aggaagctca cctgatcctt 1860
agtgtccaag gtttttactg ggggtctgta ggacgagtat ggagtacttg aataattgac 1920
ctgaagtcct cagacctgag gttccctaga gttcaaacag atacagcatg gtccagagtc 1980
ccagatgtac aaaaacaggg attcatcaca aatcccatct ttagcatgaa gggtctggca 2040
tggcccaagg ccccaagtat atcaaggcac ttgggcagaa catgccaagg aatcaaatgt 2100
catctcccag gagttattca agggtgagcc ctttacttgg gatgtacagg ctttgagcag 2160
tgcagggctg ctgagtcaac cttttattgt acaggggatg agggaaaggg agaggatgag 2220
gaagcccccc tggggatttg gtttggtctt gtgatcaggt ggtctatggg gctatcccta 2280
caaagaagaa tccagaaata ggggcacatt gaggaatgat actgagccca aagagcattc 2340
aatcattgtt ttatttgcct tcttttcaca ccattggtga gggagggatt accaccctgg 2400
ggttatgaag atggttgaac accccacaca tagcaccgga gatatgagat caacagtttc 2460
ttagccatag agattcacag cccagagcag gaggacgctg cacaccatgc aggatgacat 2520
gggggatgcg ctcgggattg gtgtgaagaa gcaaggactg ttagaggcag gctttatagt 2580
aacaagacgg tggggcaaac tctgatttcc gtgggggaat gtcatggtct tgctttacta 2640
agttttgaga ctggcaggta gtgaaactca ttaggctgag aaccttgtgg aatgcagctg 2700
acccagctga tagaggaagt agccaggtgg gagcctttcc cagtgggtgt gggacatatc 2760
tggcaagatt ttgtggcact cctggttaca gatactgggg cagcaaataa aactgaatct 2820
tgttttcaga ccttaaaaaa aaaaaaaaaa aaaaa 2855

<210> 141
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK2 isoform 1

<400> 141
Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
1 5 10 15
Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
20 25 30
Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
35 40 45
His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
50 55 60
His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65 70 75 80
Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
85 90 95
Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
100 105 110
Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
115 120 125
Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
130 135 140
Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145 150 155 160
Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
165 170 175
His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
180 185 190
Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr
195 200 205
Cys Gly Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
210 215 220
Gly Ile Thr Ser Trp Gly Pro Glu Pro Cys Ala Leu Pro Glu Lys Pro
225 230 235 240
Ala Val Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
245 250 255
Ile Ala Ala Asn Pro
260

<210> 142
<211> 2892
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK2 transcript variant 2

<400> 142
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ccatcgcctt gtctgtgggg tgcactggtg ccgtgcccct catccagtct cggattgtgg 120

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gggcacactg tgggggtgtc ctggtgcacc cccagtgggt gctcacagct gcccattgcc 240
taaagaagaa tagccaggtc tggctgggtc ggcacaacct gtttgagcct gaagacacag 300
gccagagggt ccctgtcagc cacagcttcc cacacccgct ctacaatatg agccttctga 360
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cagagcctgc caagatcaca gatgttgtga aggtcctggg cctgcccacc caggagccag 480
cactggggac cacctgctac gcctcaggct ggggcagcat cgaaccagag gagttcttgc 540
gccccaggag tcttcagtgt gtgagcctcc atctcctgtc caatgacatg tgtgctagag 600
cttactctga gaaggtgaca gagttcatgt tgtgtgctgg gctctggaca ggtggtaaag 660
acacttgtgg ggtgagtcat ccctactccc aacatctgga ggggaaaggg tgattctggg 720
ggtccacttg tctgtaatgg tgtgcttcaa ggtatcacat catggggccc tgagccatgt 780
gccctgcctg aaaagcctgc tgtgtacacc aaggtggtgc attaccggaa gtggatcaag 840
gacaccatcg cagccaaccc ctgagtgccc ctgtcccacc cctacctcta gtaaatttaa 900
gtccacctca cgttctggca tcacttggcc tttctggatg ctggacacct gaagcttgga 960
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gaggggtggg gcccaccctg gaagagtgga cagtgacaca aggtggacac tctctacaga 1260
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agaaggggag gatcctccta tgttgttgaa ggagggacta gggggagaaa ctgaaagctg 1440
attaattaca ggaggtttgt tcaggtcccc caaaccaccg tcagatttga tgatttccta 1500
gcaggactta cagaaataaa gagctatcat gctgtggttt attatggttt gttacattga 1560
tgggatacat actgaaatca gcaaacaaaa cagatgtata gattagagtg tggagaaaac 1620
agaggaaaac ttgcagttac gaagactggc aacttggctt tactaagttt tcagactggc 1680
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gaactagcca ggtgggggcc tttccctttg gatgggggggc atatctgaca gttattctct 1800
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tggtcttgtg atcaggtggt ctatggggct atccctacaa agaagaatcc agaaataggg 2340
gcacattgag gaatgatact gagcccaaag agcattcaat cattgtttta tttgccttct 2400
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ccacacatag caccggagat atgagatcaa cagtttctta gccatagaga ttcacagccc 2520
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tgaagaagca aggactgtta gaggcaggct ttatagtaac aagacggtgg ggcaaactct 2640
gatttccgtg ggggaatgtc atggtcttgc tttactaagt tttgagactg gcaggtagtg 2700
aaactcatta ggctgagaac cttgtggaat gcagctgacc cagctgatag aggaagtagc 2760
caggtgggag cctttcccag tgggtgtggg acatatctgg caagattttg tggcactcct 2820
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aaaaaaaaaa aa                                                     2892
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<210> 143
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK2 isoform 2

<400> 143

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Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
 1               5                  10                  15
Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20                  25                  30
Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
        35                  40                  45
His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50                  55                  60
His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65                  70                  75                  80
Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
                85                  90                  95
Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
            100                 105                 110
Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
        115                 120                 125
Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
    130                 135                 140
Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160
Glu Pro Glu Glu Phe Leu Arg Pro Arg Ser Leu Gln Cys Val Ser Leu
                165                 170                 175
His Leu Leu Ser Asn Asp Met Cys Ala Arg Ala Tyr Ser Glu Lys Val
            180                 185                 190
Thr Glu Phe Met Leu Cys Ala Gly Leu Trp Thr Gly Gly Lys Asp Thr
        195                 200                 205
Cys Gly Val Ser His Pro Tyr Ser Gln His Leu Glu Gly Lys Gly
    210                 215                 220
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<210> 144
<211> 2879
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK2 transcript variant 3

<400> 144
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gaggctggga gtgtgagaag cattcccaac cctggcaggt ggctgtgtac agtcatggat 180
gggcacactg tgggggtgtc ctggtgcacc cccagtgggt gctcacagct gcccattgcc 240
taaagaagaa tagccaggtc tggctgggtc ggcacaacct gtttgagcct gaagacacag 300
gccagagggt ccctgtcagc cacagcttcc cacacccgct ctacaatatg agccttctga 360
agcatcaaag ccttagacca gatgaagact ccagccatga cctcatgctg ctccgcctgt 420
cagagcctgc caagatcaca gatgttgtga aggtcctggg cctgcccacc caggagccag 480
cactggggac cacctgctac gcctcaggct ggggcagcat cgaaccagag gagtgagtct 540
tcagtgtgtg agcctccatc tcctgtccaa tgacatgtgt gctagagctt actctgagaa 600
ggtgacagag ttcatgttgt gtgctgggct ctggacaggt ggtaaagaca cttgtggggt 660
gagtcatccc tactcccaac atctggaggg gaaagggtga ttctgggggt ccacttgtct 720
gtaatggtgt gcttcaaggt atcacatcat ggggccctga gccatgtgcc ctgcctgaaa 780
agcctgctgt gtacaccaag gtggtgcatt accggaagtg gatcaaggac accatcgcag 840
ccaacccctg agtgcccctg tcccacccct acctctagta aatttaagtc cacctcacgt 900
tctggcatca cttggccttt ctggatgctg gacacctgaa gcttggaact cacctggccg 960
aagctcgagc ctcctgagtc ctactgacct gtgctttctg gtgtggagtc cagggctgct 1020
```

```
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tcctctcctt cggaacactg gctgtctctg aagacttctc gctcagtttc agtgaggaca 1140
cacacaaaga cgtgggtgac catgttgttt gtggggtgca gagatgggag gggtggggcc 1200
caccctggaa gagtggacag tgacacaagg tggacactct ctacagatca ctgaggataa 1260
gctggagcca caatgcatga ggcacacaca cagcaaggat gacgctgtaa acatagccca 1320
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aaataaagag ctatcatgct gtggtttatt atggtttgtt acattgatgg gatacatact 1560
gaaatcagca aacaaaacag atgtatagat tagagtgtgg agaaaacaga ggaaaacttg 1620
cagttacgaa gactggcaac ttggctttac taagttttca gactggcagg aagtcaaacc 1680
tattaggctg aggaccttgt ggagtgtagc tgatccagct gatagaggaa ctagccaggt 1740
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tacggacagc atataattct ccctgcaagg atgtatgata atatgtacaa agtaattcca 1860
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gtatggagta cttgaataat tgacctgaag tcctcagacc tgaggttccc tagagttcaa 1980
acagatacag catggtccag agtcccagat gtacaaaaac agggattcat cacaaatccc 2040
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gatgagggaa agggagagga tgaggaagcc cccctgggga tttggtttgg tcttgtgatc 2280
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tgatactgag cccaaagagc attcaatcat tgttttattt gccttctttt cacaccattg 2400
gtgagggagg gattaccacc ctggggttat gaagatggtt gaacacccca cacatagcac 2460
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gctgcacacc atgcaggatg acatgggggà tgcgctcggg attggtgtga agaagcaagg 2580
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tgagaacctt gtggaatgca gctgacccag ctgatagagg aagtagccag gtgggagcct 2760
ttcccagtgg gtgtgggaca tatctggcaa gattttgtgg cactcctggt tacagatact 2820
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<210> 145
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK2 isoform 3

<400> 145

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Met Trp Asp Leu Val Leu Ser Ile Ala Leu Ser Val Gly Cys Thr Gly
 1               5                  10                  15
Ala Val Pro Leu Ile Gln Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20                  25                  30
Lys His Ser Gln Pro Trp Gln Val Ala Val Tyr Ser His Gly Trp Ala
        35                  40                  45
His Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50                  55                  60
His Cys Leu Lys Lys Asn Ser Gln Val Trp Leu Gly Arg His Asn Leu
65                  70                  75                  80
Phe Glu Pro Glu Asp Thr Gly Gln Arg Val Pro Val Ser His Ser Phe
                85                  90                  95
Pro His Pro Leu Tyr Asn Met Ser Leu Leu Lys His Gln Ser Leu Arg
            100                 105                 110
Pro Asp Glu Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
        115                 120                 125
```

```
Pro Ala Lys Ile Thr Asp Val Val Lys Val Leu Gly Leu Pro Thr Gln
    130                 135                 140
Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160
Glu Pro Glu Glu
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<210> 146
<211> 1464
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 3 transcript variant 1

<400> 146
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gaggctggga gtgcgagaag cattcccaac cctggcaggt gcttgtggcc tctcgtggca 180
gggcagtctg cggcggtgtt ctggtgcacc cccagtgggt cctcacagct gcccactgca 240
tcaggaacaa aagcgtgatc ttgctgggtc ggcacagcct gtttcatcct gaagacacag 300
gccaggtatt tcaggtcagc cacagcttcc cacacccgct ctacgatatg agcctcctga 360
agaatcgatt cctcaggcca ggtgatgact ccagccacga cctcatgctg ctccgcctgt 420
cagagcctgc cgagctcacg gatgctgtga aggtcatgga cctgcccacc caggagccag 480
cactggggac cacctgctac gcctcaggct ggggcagcat tgaaccagag gagttcttga 540
ccccaaagaa acttcagtgt gtggacctcc atgttatttc caatgacgtg tgtgcgcaag 600
ttcaccctca gaaggtgacc aagttcatgc tgtgtgctgg acgctggaca gggggcaaaa 660
gcacctgctc gggtgattct gggggcccac ttgtctgtaa tggtgtgctt caaggtatca 720
cgtcatgggg cagtgaacca tgtgccctgc ccgaaaggcc ttccctgtac accaaggtgg 780
tgcattaccg gaagtggatc aaggacacca tcgtggccaa cccctgagca cccctatcaa 840
ccccctattg tagtaaactt ggaaccttgg aaatgaccag gccaagactc aagcctcccc 900
agttctactg acctttgtcc ttaggtgtga ggtccagggt tgctaggaaa agaaatcagc 960
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tggggtgtct gtgttatttg tggggtacag agatgaaaga ggggtgggat ccacactgag 1140
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acaacgcacc agacactcac agcaaggatg gagctgaaaa cataacccac tctgtcctgg 1260
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ggatggggat gaagtaagga gagggactgg acccccctgga agctgattca ctatgggggg 1380
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gaaataaaga gctgttatac tgtg                                        1464
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<210> 147
<211> 261
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 3 isoform 1

<400> 147
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Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
 1               5                  10                  15
Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20                  25                  30
Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
```

```
        35                  40                  45
Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50                  55                  60
His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
65                  70                  75                  80
Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
                85                  90                  95
Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg
            100                 105                 110
Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
        115                 120                 125
Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln
    130                 135                 140
Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145                 150                 155                 160
Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu
                165                 170                 175
His Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val
            180                 185                 190
Thr Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr
        195                 200                 205
Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
    210                 215                 220
Gly Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro
225                 230                 235                 240
Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
                245                 250                 255
Ile Val Ala Asn Pro
            260
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<210> 148
<211> 1906
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 3 transcript variant 3

<400> 148
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gaggctggga gtgcgagaag cattcccaac cctggcaggt gcttgtggcc tctcgtggca 180
gggcagtctg cggcggtgtt ctggtgcacc cccagtgggt cctcacagct gcccactgca 240
tcaggaacaa aagcgtgatc ttgctgggtc ggcacagcct gtttcatcct gaagacacag 300
gccaggtatt tcaggtcagc cacagcttcc cacacccgct ctacgatatg agcctcctga 360
agaatcgatt cctcaggcca ggtgatgact ccagccacga cctcatgctg ctccgcctgt 420
cagagcctgc cgagctcacg gatgctgtga aggtcatgga cctgcccacc caggagccag 480
cactggggac cacctgctac gcctcaggct ggggcagcat tgaaccagag gagttcttga 540
ccccaaagaa acttcagtgt gtggacctcc atgttatttc caatgacgtg tgtgcgcaag 600
ttcaccctca gaaggtgacc aagttcatgc tgtgtgctgg acgctggaca gggggcaaaa 660
gcacctgctc gtgggtcatt ctgatcaccg aactgaccat gccagccctg ccgatggtcc 720
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ggcctctgtg aggagccacg gggacagcat cctgcagatg gtcctggccc ttgtcccacc 840
gacctgtcta caaggactgt cctcgtggac cctcccctct gcacaggagc tggaccctga 900
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tctgttatct gcctgtccag gtctgaaaga taggattgcc caggcagaaa ctgggactga 1080
cctatctcac tctctccctg cttttaccct tagggtgatt ctgggggccc acttgtctgt 1140
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ccttccctgt acaccaaggt ggtgcattac cggaagtgga tcaaggacac catcgtggcc 1260
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ttctctgagg acacagatag gatggggtgt ctgtgttatt tgtggggtac agagatgaaa 1560
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gcactgagca gaagctggag gcacaacgca ccagacactc acagcaagga tggagctgaa 1680
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gaagctgatt cactatgggg ggaggtgtat tgaagtcctc cagacaaccc tcagatttga 1860
tgatttccta gtagaactca cagaaataaa gagctgttat actgtg 1906

<210> 149
<211> 238
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 3 isoform 3

<400> 149
Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
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Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20   25   30
Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
        35   40   45
Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50   55   60
His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
65   70   75   80
Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
                85   90   95
Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg
            100   105   110
Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
        115   120   125
Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln
    130   135   140
Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
145   150   155   160
Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu
                165   170   175
His Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val
            180   185   190
Thr Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr
        195   200   205
Cys Ser Trp Val Ile Leu Leu Ile Thr Glu Leu Thr Met Pro Ala Leu Pro
    210   215   220
Met Val Leu His Gly Ser Leu Val Pro Trp Arg Gly Gly Val
225   230   235

<210> 150
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 3 transcript variant 4

<400> 150
agccccaagc ttaccacctg cacccggaga gctgtgtcac catgtgggtc ccggttgtct 60
tcctcaccct gtccgtgacg tggattggtg ctgcacccct catcctgtct cggattgtgg 120
gaggctggga gtgcgagaag cattcccaac cctggcaggt gcttgtggcc tctcgtggca 180
gggcagtctg cggcggtgtt ctggtgcacc cccagtgggt cctcacagct gcccactgca 240
tcaggaagcc aggtgatgac tccagccacg acctcatgct gctccgcctg tcagagcctg 300
ccgagctcac ggatgctgtg aaggtcatgg acctgcccac ccaggagcca gcactgggga 360
ccacctgcta cgcctcaggc tggggcagca ttgaaccaga ggagttcttg accccaaaga 420
aacttcagtg tgtggacctc catgttattt ccaatgacgt gtgtgcgcaa gttcaccctc 480
agaaggtgac caagttcatg ctgtgtgctg gacgctggac agggggcaaa agcacctgct 540
cgggtgattc tgggggccca cttgtctgta atggtgtgct tcaaggtatc acgtcatggg 600
gcagtgaacc atgtgccctg cccgaaaggc cttccctgta caccaaggtg gtgcattacc 660
ggaagtggat caaggacacc atcgtggcca acccctgagc acccctatca acccccctatt 720
gtagtaaact tggaaccttg gaaatgacca ggccaagact caagcctccc cagttctact 780
gacctttgtc cttaggtgtg aggtccaggg ttgctaggaa aagaaatcag cagacacagg 840
tgtagaccag agtgtttctt aaatggtgta attttgtcct ctctgtgtcc tggggaatac 900
tggccatgcc tggagacata tcactcaatt tctctgagga cacagatagg atggggtgtc 960
tgtgttattt gtggggtaca gagatgaaag aggggtggga tccacactga gagagtggag 1020
agtgacatgt gctggacact gtccatgaag cactgagcag aagctggagg cacaacgcac 1080
cagacactca cagcaaggat ggagctgaaa acataaccca ctctgtcctg gaggcactgg 1140
gaagcctaga gaaggctgtg agccaaggag ggagggtctt cctttggcat gggatgggga 1200
tgaagtaagg agagggactg gacccctgg aagctgattc actatggggg gaggtgtatt 1260
gaagtcctcc agacaaccct cagatttgat gatttcctag tagaactcac agaaataaag 1320
agctgttata ctgtg 1335

<210> 151
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 3 isoform 4

<400> 151
Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
 1   5   10   15
Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20   25   30
Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
        35   40   45
Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50   55   60
His Cys Ile Arg Lys Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu
65   70   75   80
Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met
                85   90   95
Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser
            100   105   110
Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu

```
        115                 120                 125
Gln Cys Val Asp Leu His Val Ile Ser Asn Asp Val Cys Ala Gln Val
    130                 135                 140
His Pro Gln Lys Val Thr Lys Phe Met Leu Cys Ala Gly Arg Trp Thr
145                 150                 155                 160
Gly Gly Lys Ser Thr Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Cys
                165                 170                 175
Asn Gly Val Leu Gln Gly Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala
            180                 185                 190
Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys
        195                 200                 205
Trp Ile Lys Asp Thr Ile Val Ala Asn Pro
    210                 215
```

<210> 152
<211> 1341
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 3 transcript variant 5

<400> 152
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agccccaagc ttaccacctg cacccggaga gctgtgtcac catgtgggtc ccggttgtct 60
tcctcaccct gtccgtgacg tggattggtg ctgcacccct catcctgtct cggattgtgg 120
gaggctggga gtgcgagaag cattcccaac cctggcaggt gcttgtggcc tctcgtggca 180
gggcagtctg cggcggtgtt ctggtgcacc cccagtgggt cctcacagct gcccactgca 240
tcaggaacaa aagcgtgatc ttgctgggtc ggcacagcct gtttcatcct gaagacacag 300
gccaggtatt tcaggtcagc cacagcttcc cacacccgct ctacgatatg agcctcctga 360
agaatcgatt cctcaggcca ggtgatgact ccagcattga accagaggag ttcttgaccc 420
caaagaaact tcagtgtgtg gacctccatg ttatttccaa tgacgtgtgt gcgcaagttc 480
accctcagaa ggtgaccaag ttcatgctgt gtgctggacg ctggacaggg ggcaaaagca 540
cctgctcggg tgattctggg ggcccacttg tctgtaatgg tgtgcttcaa ggtatcacgt 600
catggggcag tgaaccatgt gccctgcccg aaaggccttc cctgtacacc aaggtggtgc 660
attaccggaa gtggatcaag gacaccatcg tggccaaccc ctgagcaccc ctatcaaccc 720
cctattgtag taaacttgga accttggaaa tgaccaggcc aagactcaag cctccccagt 780
tctactgacc tttgtcctta ggtgtgaggt ccagggttgc taggaaaaga aatcagcaga 840
cacaggtgta gaccagagtg tttcttaaat ggtgtaattt tgtcctctct gtgtcctggg 900
gaatactggc catgcctgga gacatatcac tcaatttctc tgaggacaca gataggatgg 960
ggtgtctgtg ttatttgtgg ggtacagaga tgaaagaggg gtgggatcca cactgagaga 1020
gtggagagtg acatgtgctg gacactgtcc atgaagcact gagcagaagc tggaggcaca 1080
acgcaccaga cactcacagc aaggatggag ctgaaaacat aacccactct gtcctggagg 1140
cactgggaag cctagagaag gctgtgagcc aaggagggag ggtcttcctt tggcatggga 1200
tggggatgaa gtaaggagag ggactggacc ccctggaagc tgattcacta tgggggggagg 1260
tgtattgaag tcctccagac aaccctcaga tttgatgatt tcctagtaga actcacagaa 1320
ataaagagct gttatactgt g                                          1341
```

<210> 153
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 3 isoform 5

<400> 153

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Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
 1               5                  10                  15
Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20                  25                  30
Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
        35                  40                  45
Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50                  55                  60
His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
65                  70                  75                  80
Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
                85                  90                  95
Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg
            100                 105                 110
Pro Gly Asp Asp Ser Ser Ile Glu Pro Glu Glu Phe Leu Thr Pro Lys
        115                 120                 125
Lys Leu Gln Cys Val Asp Leu His Val Ile Ser Asn Asp Val Cys Ala
    130                 135                 140
Gln Val His Pro Gln Lys Val Thr Lys Phe Met Leu Cys Ala Gly Arg
145                 150                 155                 160
Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp Ser Gly Gly Pro Leu
                165                 170                 175
Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser Trp Gly Ser Glu Pro
            180                 185                 190
Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val Val His Tyr
        195                 200                 205
Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro
    210                 215                 220
```

<210> 154
<211> 555
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 3 transcript variant 6

<400> 154
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agccccaagc ttaccacctg cacccggaga gctgtgtcac catgtgggtc ccggttgtct 60
tcctcaccct gtccgtgacg tggattggtg ctgcaccccc catcctgtct cggattgtgg 120
gaggctggga gtgcgagaag cattcccaac cctggcaggt gcttgtggcc tctcgtggca 180
gggcagtctg cggcggtgtt ctggtgcacc cccagtgggt cctcacagct gcccactgca 240
tcaggaagtg agtaggggcc tggggtctgg ggagcaggtg tctgtgtccc agaggaataa 300
cagctgggca ttttccccag gataacctct aaggccagcc ttgggactgg gggagagagg 360
gaaagttctg gttcaggtca catggggagg cagggttggg gctggaccac cctccccatg 420
gctgcctggg tctccatctg tgttcctcta tgtctctttg tgtcgctttc attatgtctc 480
ttggtaactg gcttcggttg tgtctctccg tgtgactatt ttgttctctc tctccctctc 540
ttctctgtct tcagt                                                  555
```

<210> 155
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 3 isoform 6

<400> 155
Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly
 1   5   10   15
Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu
            20   25   30
Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
        35   40   45
Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
    50   55   60
His Cys Ile Arg Lys
65

<210> 156
<211> 807
<212> DNA
<213> Homo sapiens

<220>
<223> Mesotrypsin

<400> 156
acactctacc accatgaatc cattcctgat ccttgccttt gtgggagctg ctgttgctgt 60
ccccttgac gatgatgaca agattgttgg gggctacacc tgtgaggaga attctctccc 120
ctaccaggtg tccctgaatt ctggctccca cttctgcggt ggctccctca tcagcgaaca 180
gtgggtggta tcagcagctc actgctacaa gacccgcatc caggtgagac tgggagagca 240
caacatcaaa gtcctggagg ggaatgagca gttcatcaat gcggccaaga tcatccgcca 300
ccctaaatac aacagggaca ctctggacaa tgacatcatg ctgatcaaac tctcctcacc 360
tgccgtcatc aatgcccgcg tgtccaccat ctctctgccc accgcccctc cagctgctgg 420
cactgagtgc ctcatctccg gctggggcaa cactctgagc tttggtgctg actacccaga 480
cgagctgaag tgcctggatg ctccggtgct gacccaggct gagtgtaaag cctcctaccc 540
tggaaagatt accaacagca tgttctgtgt gggcttcctt gagggaggca aggattcctg 600
ccagcgtgac tctggtggcc ctgtggtctg caacggacag ctccaaggag ttgtctcctg 660
gggccatggc tgtgcctgga agaacaggcc tggagtctac accaaggtct acaactatgt 720
ggactggatt aaggacacca tcgctgccaa cagctaaagc ccccggtccc tctgcagtct 780
ctataccaat aaagtggccc tgctctc   807

<210> 157
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> Mesotrypsin

<400> 157
Met Asn Pro Phe Leu Ile Leu Ala Phe Val Gly Ala Ala Val Ala Val
 1   5   10   15
Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Thr Cys Glu Glu
            20   25   30
Asn Ser Leu Pro Tyr Gln Val Ser Leu Asn Ser Gly Ser His Phe Cys
        35   40   45
Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Ala His Cys
    50   55   60
Tyr Lys Thr Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Lys Val

```
65                  70                  75                  80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
                85                  90                  95
Pro Lys Tyr Asn Arg Asp Thr Leu Asp Asn Asp Ile Met Leu Ile Lys
            100                 105                 110
Leu Ser Ser Pro Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu
        115                 120                 125
Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Cys Leu Ile Ser Gly Trp
    130                 135                 140
Gly Asn Thr Leu Ser Phe Gly Ala Asp Tyr Pro Asp Glu Leu Lys Cys
145                 150                 155                 160
Leu Asp Ala Pro Val Leu Thr Gln Ala Glu Cys Lys Ala Ser Tyr Pro
                165                 170                 175
Gly Lys Ile Thr Asn Ser Met Phe Cys Val Gly Phe Leu Glu Gly Gly
            180                 185                 190
Lys Asp Ser Cys Gln Arg Asp Ser Gly Gly Pro Val Val Cys Asn Gly
        195                 200                 205
Gln Leu Gln Gly Val Val Ser Trp Gly His Gly Cys Ala Trp Lys Asn
    210                 215                 220
Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys
225                 230                 235                 240
Asp Thr Ile Ala Ala Asn Ser
                245
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<210> 158
<211> 1055
<212> DNA
<213> Homo sapiens

<220>
<223> pancreatic endopeptidase E form B (B)

<400> 158
acctgcattt ccaccacctg ttctgggagt ggggcccagt cagccccctt tgcttacctt 60
ctgccctata ttagagcccc aggttctgtg ccctttttcct atcatcgcaa aactcatgat 120
gctccggctg ctcagttccc tcctccttgt ggccgttgcc tcaggctatg gcccaccttc 180
ctctcgccct tccagccgcg ttgtcaatgg tgaggatgcg gtcccctaca gctggccctg 240
gcaggtttcc ctgcagtatg agaaaagcgg aagcttctac cacacctgtg gcggtagcct 300
catcgccccc gactgggttg tgactgccgg ccactgcatc tcgagctccc ggacctacca 360
ggtggtgttg ggcgagtacg accgtgctgt gaaggagggc cccgagcagg tgatccccat 420
caactctggg gacctctttg tgcatccact ctggaaccgc tcgtgtgtgg cctgtggcaa 480
tgacatcgcc ctcatcaagc tctcacgcag cgcccagctg ggagacgccg tccagctcgc 540
ctcactccct ccggctggtg acatccttcc caacgagaca ccctgctaca tcaccggctg 600
gggccgtctc tataccaacg ggccactccc agacaagctg caggaggccc tgctgccggt 660
ggtggactat gaacactgct ccaggtggaa ctggtggggt tcctccgtga agaagaccat 720
ggtgtgtgct ggaggggaca tccgctccgg ctgcaatggt gactctggag gacccctcaa 780
ctgccccaca gaggatggtg gctggcaggt ccatggcgtg accagctttg tttctgcctt 840
tggctgcaac acccgcagga agcccacggt gttcactcga gtctccgcct tcattgactg 900
gattgaggag accatagcaa gccactagaa ccaaggccca gctggcagtg ctgatcgatc 960
ccacatcctg aataaagaat aaagatctct cagaaaattc caaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa   1055

<210> 159
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<223> pancreatic endopeptidase E form B (B)

<400> 159
Met Met Leu Arg Leu Leu Ser Ser Leu Leu Leu Val Ala Val Ala Ser
 1   5   10   15
Gly Tyr Gly Pro Pro Ser Ser Arg Pro Ser Ser Arg Val Val Asn Gly
            20   25   30
Glu Asp Ala Val Pro Tyr Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
        35   40   45
Glu Lys Ser Gly Ser Phe Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
    50   55   60
Pro Asp Trp Val Val Thr Ala Gly His Cys Ile Ser Ser Ser Arg Thr
65   70   75   80
Tyr Gln Val Val Leu Gly Glu Tyr Asp Arg Ala Val Lys Glu Gly Pro
                85   90   95
Glu Gln Val Ile Pro Ile Asn Ser Gly Asp Leu Phe Val His Pro Leu
            100   105   110
Trp Asn Arg Ser Cys Val Ala Cys Gly Asn Asp Ile Ala Leu Ile Lys
        115   120   125
Leu Ser Arg Ser Ala Gln Leu Gly Asp Ala Val Gln Leu Ala Ser Leu
    130   135   140
Pro Pro Ala Gly Asp Ile Leu Pro Asn Glu Thr Pro Cys Tyr Ile Thr
145   150   155   160
Gly Trp Gly Arg Leu Tyr Thr Asn Gly Pro Leu Pro Asp Lys Leu Gln
                165   170   175
Glu Ala Leu Leu Pro Val Val Asp Tyr Glu His Cys Ser Arg Trp Asn
            180   185   190
Trp Trp Gly Ser Ser Val Lys Lys Thr Met Val Cys Ala Gly Gly Asp
        195   200   205
Ile Arg Ser Gly Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Pro
    210   215   220
Thr Glu Asp Gly Gly Trp Gln Val His Gly Val Thr Ser Phe Val Ser
225   230   235   240
Ala Phe Gly Cys Asn Thr Arg Arg Lys Pro Thr Val Phe Thr Arg Val
                245   250   255
Ser Ala Phe Ile Asp Trp Ile Glu Glu Thr Ile Ala Ser His
            260   265   270

<210> 160
<211> 941
<212> DNA
<213> Homo sapiens

<220>
<223> pancreatic elastase II form B (Homos sapiens) (IIB)

<400> 160
cttacagaac tcccacggac acaccatgat taggaccctg ctgctgtcca ctttggtggc 60
tggagccctc agttgtgggg tctccactta cgcgcctgat atgtctagga tgcttggagg 120
tgaagaagcg aggcccaaca gctggccctg gcaggtctcc ctgcagtaca gctccaatgg 180
ccagtggtac cacacctgcg gagggtccct gatagccaac agctgggtcc tgacggctgc 240
ccactgcatc agctcctccg ggatctaccg cgtgatgctg ggccagcata acctctacgt 300
tgcagagtcc ggctcgctgg ccgtcagtgt ctctaagatt gtggtgcaca aggactggaa 360
ctccgaccag gtctccaaag ggaacgacat tgccctgctc aaactggcta accccgtctc 420

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cctcaccgac aagatccagc tggcctgcct ccctcctgcc ggcaccattc tacccaacaa 480
ctacccctgc tacgtcacgg gctggggaag gctgcagacc aacggggctc tccctgatga 540
cctgaagcag ggccggttgc tggttgtgga ctatgccacc tgctccagct ctggctggtg 600
gggcagcacc gtgaagacga atatgatctg tgctgggggt gatggcgtga tatgcacctg 660
caacggagac tccggtgggc cgctgaactg tcaggcatct gacggccggt gggaggtgca 720
tggcatcggc agcctcacgt cggtccttgg ttgcaactac tactacaagc cctccatctt 780
cacgcgggtc tccaactaca acgactggat caattcggtg attgcaaata actaaccaaa 840
agaagtccct gggactgttt cagacttgga aaggtcacag aaggaaaata atattatata 900
aagtgacaac tatgcaaatc acaaaaaaaa aaaaaaaaaa a                     941
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<210> 161
<211> 269
<212> PRT
<213> Homo sapiens

<220>
<223> pancreatic elastase II form B (Homos sapiens) (IIB)

<400> 161

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Met Ile Arg Thr Leu Leu Leu Ser Thr Leu Val Ala Gly Ala Leu Ser
 1               5                  10                  15
Cys Gly Val Ser Thr Tyr Ala Pro Asp Met Ser Arg Met Leu Gly Gly
            20                  25                  30
Glu Glu Ala Arg Pro Asn Ser Trp Pro Trp Gln Val Ser Leu Gln Tyr
        35                  40                  45
Ser Ser Asn Gly Gln Trp Tyr His Thr Cys Gly Gly Ser Leu Ile Ala
    50                  55                  60
Asn Ser Trp Val Leu Thr Ala Ala His Cys Ile Ser Ser Ser Gly Ile
65                  70                  75                  80
Tyr Arg Val Met Leu Gly Gln His Asn Leu Tyr Val Ala Glu Ser Gly
                85                  90                  95
Ser Leu Ala Val Ser Val Ser Lys Ile Val Val His Lys Asp Trp Asn
            100                 105                 110
Ser Asp Gln Val Ser Lys Gly Asn Asp Ile Ala Leu Leu Lys Leu Ala
        115                 120                 125
Asn Pro Val Ser Leu Thr Asp Lys Ile Gln Leu Ala Cys Leu Pro Pro
    130                 135                 140
Ala Gly Thr Ile Leu Pro Asn Asn Tyr Pro Cys Tyr Val Thr Gly Trp
145                 150                 155                 160
Gly Arg Leu Gln Thr Asn Gly Ala Leu Pro Asp Asp Leu Lys Gln Gly
                165                 170                 175
Arg Leu Leu Val Val Asp Tyr Ala Thr Cys Ser Ser Ser Gly Trp Trp
            180                 185                 190
Gly Ser Thr Val Lys Thr Asn Met Ile Cys Ala Gly Gly Asp Gly Val
        195                 200                 205
Ile Cys Thr Cys Asn Gly Asp Ser Gly Gly Pro Leu Asn Cys Gln Ala
    210                 215                 220
Ser Asp Gly Arg Trp Glu Val His Gly Ile Gly Ser Leu Thr Ser Val
225                 230                 235                 240
Leu Gly Cys Asn Tyr Tyr Tyr Lys Pro Ser Ile Phe Thr Arg Val Ser
                245                 250                 255
Asn Tyr Asn Asp Trp Ile Asn Ser Val Ile Ala Asn Asn
            260                 265
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<210> 162
<211> 2048

<212> DNA
<213> Homo sapiens

<220>
<223> coagulation factor XIIa

<400> 162
ctattgatct ggactcctgg ataggcagct ggaccaacgg acggacgcca tgagggctct 60
gctgctcctg gggttcctgc tggtgagctt ggagtcaaca ctttcgattc caccttggga 120
agcccccaag gagcataagt acaaagctga agagcacaca gtcgttctca ctgtcaccgg 180
ggagccctgc cacttccect tccagtacca ccggcagctg taccacaaat gtacccacaa 240
gggccggcca ggccctcagc cctggtgtgc taccaccccc aactttgatc aggaccagcg 300
atggggatac tgtttggagc ccaagaaagt gaaagaccac tgcagcaaac acagcccctg 360
ccagaaagga gggacctgtg tgaacatgcc aagcggcccc cactgtctct gtccacaaca 420
cctcactgga aaccactgcc agaaagagaa gtgctttgag cctcagcttc tccggttttt 480
ccacaagaat gagatatggt atagaactga gcaagcagct gtggccagat gccagtgcaa 540
gggtcctgat gcccactgcc agcggctggc cagccaggcc tgccgcacca acccgtgcct 600
ccatgggggt cgctgcctag aggtggaggg ccaccgcctg tgccactgcc cggtgggcta 660
caccggaccc ttctgcgacg tggacaccaa ggcaagctgc tatgatggcc gcgggctcag 720
ctaccgcggc ctggccagga ccacgctctc gggtgcgccc tgtcagccgt gggcctcgga 780
ggccacctac cggaacgtga ctgccgagca agcgcggaac tggggactgg gcggccacgc 840
cttctgccgg aacccggaca acgacatccg cccgtggtgc ttcgtgctga accgcgaccg 900
gctgagctgg gagtactgcg acctggcaca gtgccagacc ccaacccagg cggcgcctcc 960
gaccccggtg tcccctaggc ttcatgtccc actcatgccc gcgcagccgg caccgccgaa 1020
gcctcagccc acgacccgga ccccgcctca gtcccagacc ccgggagcct tgccggcgaa 1080
gcgggagcag ccgccttccc tgaccaggaa cggcccactg agctgcgggc agcggctccg 1140
caagagtctg tcttcgatga cccgcgtcgt tggcgggctg gtggcgctac gcggggcgca 1200
cccctacatc gccgcgctgt actggggcca cagtttctgc gccggcagcc tcatcgcccc 1260
ctgctgggtg ctgacggccg ctcactgcct gcaggaccgg cccgcacccg aggatctgac 1320
ggtggtgctc ggccaggaac gccgtaacca cagctgtgag ccgtgccaga cgttggccgt 1380
gcgctcctac cgcttgcacg aggccttctc gcccgtcagc taccagcacg acctggctct 1440
gttgcgcctt caggaggatg cggacggcag ctgcgcgctc ctgtcgcctt acgttcagcc 1500
ggtgtgcctg ccaagcggcg ccgcgcgacc ctccgagacc acgctctgcc aggtggccgg 1560
ctggggccac cagttcgagg gggcggagga atatgccagc ttcctgcagg aggcgcaggt 1620
accgttcctc tccctggagc gctgctcagc cccggacgtg cacggatcct ccatcctccc 1680
cggcatgctc tgcgcagggt tcctcgaggg cggcaccgat gcgtgccagg gtgattccgg 1740
aggcccgctg gtgtgtgagg accaagctgc agagcgccgg ctcaccctgc aaggcatcat 1800
cagctgggga tcgggctgtg gtgaccgcaa caagccaggc gtctacaccg atgtggccta 1860
ctacctggcc tggatccggg agcacaccgt ttcctgattg ctcagggact catctttccc 1920
tccttggtga ttccgcagtg agagagtggc tggggcatgg aaggcaagat tgtgtcccat 1980
tcccccagtg cggccagctc cgcgccagga tggcgaggaa ctcaataaag tgctttgaaa 2040
atgctgag 2048

<210> 163
<211> 615
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor XIIa

<400> 163
Met Arg Ala Leu Leu Leu Leu Gly Phe Leu Leu Val Ser Leu Glu Ser
 1   5   10   15
Thr Leu Ser Ile Pro Pro Trp Glu Ala Pro Lys Glu His Lys Tyr Lys
            20   25   30

```
Ala Glu Glu His Thr Val Val Leu Thr Val Thr Gly Glu Pro Cys His
        35                  40                  45
Phe Pro Phe Gln Tyr His Arg Gln Leu Tyr His Lys Cys Thr His Lys
    50                  55                  60
Gly Arg Pro Gly Pro Gln Pro Trp Cys Ala Thr Thr Pro Asn Phe Asp
65                  70                  75                  80
Gln Asp Gln Arg Trp Gly Tyr Cys Leu Glu Pro Lys Lys Val Lys Asp
                85                  90                  95
His Cys Ser Lys His Ser Pro Cys Gln Lys Gly Gly Thr Cys Val Asn
            100                 105                 110
Met Pro Ser Gly Pro His Cys Leu Cys Pro Gln His Leu Thr Gly Asn
        115                 120                 125
His Cys Gln Lys Glu Lys Cys Phe Glu Pro Gln Leu Leu Arg Phe Phe
    130                 135                 140
His Lys Asn Glu Ile Trp Tyr Arg Thr Glu Gln Ala Ala Val Ala Arg
145                 150                 155                 160
Cys Gln Cys Lys Gly Pro Asp Ala His Cys Gln Arg Leu Ala Ser Gln
                165                 170                 175
Ala Cys Arg Thr Asn Pro Cys Leu His Gly Gly Arg Cys Leu Glu Val
            180                 185                 190
Glu Gly His Arg Leu Cys His Cys Pro Val Gly Tyr Thr Gly Pro Phe
        195                 200                 205
Cys Asp Val Asp Thr Lys Ala Ser Cys Tyr Asp Gly Arg Gly Leu Ser
    210                 215                 220
Tyr Arg Gly Leu Ala Arg Thr Thr Leu Ser Gly Ala Pro Cys Gln Pro
225                 230                 235                 240
Trp Ala Ser Glu Ala Thr Tyr Arg Asn Val Thr Ala Glu Gln Ala Arg
                245                 250                 255
Asn Trp Gly Leu Gly Gly His Ala Phe Cys Arg Asn Pro Asp Asn Asp
            260                 265                 270
Ile Arg Pro Trp Cys Phe Val Leu Asn Arg Asp Arg Leu Ser Trp Glu
        275                 280                 285
Tyr Cys Asp Leu Ala Gln Cys Gln Thr Pro Thr Gln Ala Ala Pro Pro
    290                 295                 300
Thr Pro Val Ser Pro Arg Leu His Val Pro Leu Met Pro Ala Gln Pro
305                 310                 315                 320
Ala Pro Pro Lys Pro Gln Pro Thr Thr Arg Thr Pro Pro Gln Ser Gln
                325                 330                 335
Thr Pro Gly Ala Leu Pro Ala Lys Arg Glu Gln Pro Pro Ser Leu Thr
            340                 345                 350
Arg Asn Gly Pro Leu Ser Cys Gly Gln Arg Leu Arg Lys Ser Leu Ser
        355                 360                 365
Ser Met Thr Arg Val Val Gly Gly Leu Val Ala Leu Arg Gly Ala His
    370                 375                 380
Pro Tyr Ile Ala Ala Leu Tyr Trp Gly His Ser Phe Cys Ala Gly Ser
385                 390                 395                 400
Leu Ile Ala Pro Cys Trp Val Leu Thr Ala Ala His Cys Leu Gln Asp
                405                 410                 415
Arg Pro Ala Pro Glu Asp Leu Thr Val Val Leu Gly Gln Glu Arg Arg
            420                 425                 430
Asn His Ser Cys Glu Pro Cys Gln Thr Leu Ala Val Arg Ser Tyr Arg
        435                 440                 445
Leu His Glu Ala Phe Ser Pro Val Ser Tyr Gln His Asp Leu Ala Leu
    450                 455                 460
Leu Arg Leu Gln Glu Asp Ala Asp Gly Ser Cys Ala Leu Leu Ser Pro
465                 470                 475                 480
Tyr Val Gln Pro Val Cys Leu Pro Ser Gly Ala Ala Arg Pro Ser Glu
```

```
                485                 490                 495
Thr Thr Leu Cys Gln Val Ala Gly Trp Gly His Gln Phe Glu Gly Ala
            500                 505                 510
Glu Glu Tyr Ala Ser Phe Leu Gln Glu Ala Gln Val Pro Phe Leu Ser
        515                 520                 525
Leu Glu Arg Cys Ser Ala Pro Asp Val His Gly Ser Ser Ile Leu Pro
    530                 535                 540
Gly Met Leu Cys Ala Gly Phe Leu Glu Gly Gly Thr Asp Ala Cys Gln
545                 550                 555                 560
Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Asp Gln Ala Ala Glu Arg
                565                 570                 575
Arg Leu Thr Leu Gln Gly Ile Ile Ser Trp Gly Ser Gly Cys Gly Asp
            580                 585                 590
Arg Asn Lys Pro Gly Val Tyr Thr Asp Val Ala Tyr Tyr Leu Ala Trp
        595                 600                 605
Ile Arg Glu His Thr Val Ser
    610                 615
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<210> 164
<211> 2245
<212> DNA
<213> Homo sapiens

<220>
<223> plasma kallikrein

<400> 164

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agaacagctt gaagaccgtt catttttaag tgacaagaga ctcacctcca agaagcaatt 60
gtgttttcag aatgatttta ttcaagcaag caacttattt catttccttg tttgctacag 120
tttcctgtgg atgtctgact caactctatg aaaacgcctt cttcagaggt ggggatgtag 180
cttccatgta caccccaaat gcccaatact gccagatgag gtgcacattc cacccaaggt 240
gtttgctatt cagttttctt ccagcaagtt caatcaatga catggagaaa aggtttggtt 300
gcttcttgaa agatagtgtt acaggaaccc tgccaaaagt acatcgaaca ggtgcagttt 360
ctggacattc cttgaagcaa tgtggtcatc aaataagtgc ttgccatcga gacatttata 420
aaggagttga tatgagagga gtcaatttta atgtgtctaa ggttagcagt gttgaagaat 480
gccaaaaaag gtgcaccaat aacattcgct gccagttttt ttcatatgcc acgcaaacat 540
ttcacaaggc agagtaccgg aacaattgcc tattaaagta cagtcccgga ggaacaccta 600
ccgctataaa ggtgctgagt aacgtggaat ctggattctc actgaagccc tgtgcccttt 660
cagaaattgg ttgccacatg aacatcttcc agcatcttgc gttctcagat gtggatgttg 720
ccagggttct cactccagat gcttttgtgt gtcggaccat ctgcacctat caccccaact 780
gcctcttctt tacattctat acaaatgtat ggaaaatcga gtcacaaaga aatgtttgtc 840
ttcttaaaac atctgaaagt ggcacaccaa gttcctctac tcctcaagaa aacaccatat 900
ctggatatag ccttttaacc tgcaaaagaa ctttacctga accctgccat tctaaaattt 960
acccgggagt tgactttgga ggagaagaat tgaatgtgac ttttgttaaa ggagtgaatg 1020
tttgccaaga gacttgcaca aagatgattc gctgtcagtt tttcacttat tctttactcc 1080
cagaagactg taaggaagag aagtgtaagt gtttcttaag attatctatg gatggttctc 1140
caactaggat tgcgtatggg acacaaggga gctctggtta ctctttgaga ttgtgtaaca 1200
ctggggacaa ctctgtctgc acaacaaaaa caagcacacg cattgttgga ggaacaaact 1260
cttcttgggg agagtggccc tggcaggtga gcctgcaggt gaagctgaca gctcagaggc 1320
acctgtgtgg agggtcactc ataggacacc agtgggtcct cactgctgcc cactgctttg 1380
atgggcttcc cctgcaggat gtttggcgca tctatagtgg cattttaaat ctgtcagaca 1440
ttacaaaaga tacacctttc tcacaaataa aagagattat tattcaccaa aactataaag 1500
tctcagaagg gaatcatgat atcgccttga taaaactcca ggctcctttg aattacactg 1560
aattccaaaa accaatatgc ctaccttcca aaggtgacac aagcacaatt tataccaact 1620
gttgggtaac cggatggggc ttctcgaagg agaaaggtga aatccaaaat attctacaaa 1680
aggtaaatat tcctttggta acaaatgaag aatgccagaa aagatatcaa gattataaaa 1740
```

```
taacccaacg gatggtctgt gctggctata aagaaggggg aaaagatgct tgtaagggag 1800
attcaggtgg tcccttagtt tgcaaacaca acggaatgtg gcgtttggtg ggcatcacaa 1860
gctggggtga aggctgtgcc cgcagggagc aacctggtgt ctacaccaaa gtcgctgagt 1920
acatggactg gattttagag aaaacacaga gcagtgatgg aaaagctcag atgcagtcac 1980
cagcatgaga agcagtccag agtctaggca atttttacaa cctgagttca agtcaaattc 2040
tgagcctggg gggtcctcat ctgcaaagca tggagagtgg catcttcttt gcatcctaag 2100
gacgaaagac acagtgcact cagagctgct gaggacaatg tctgctgaag cccgctttca 2160
gcacgccgta accaggggct gacaatgcga ggtcgcaact gagatctcca tgactgtgtg 2220
ttgtgaaata aaatggtgaa agatc                                       2245
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<210> 165
<211> 638
<212> PRT
<213> Homo sapiens

<220>
<223> plasma kallikrein

<400> 165

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Met Ile Leu Phe Lys Gln Ala Thr Tyr Phe Ile Ser Leu Phe Ala Thr
 1               5                  10                  15
Val Ser Cys Gly Cys Leu Thr Gln Leu Tyr Glu Asn Ala Phe Phe Arg
            20                  25                  30
Gly Gly Asp Val Ala Ser Met Tyr Thr Pro Asn Ala Gln Tyr Cys Gln
        35                  40                  45
Met Arg Cys Thr Phe His Pro Arg Cys Leu Leu Phe Ser Phe Leu Pro
    50                  55                  60
Ala Ser Ser Ile Asn Asp Met Glu Lys Arg Phe Gly Cys Phe Leu Lys
65                  70                  75                  80
Asp Ser Val Thr Gly Thr Leu Pro Lys Val His Arg Thr Gly Ala Val
                85                  90                  95
Ser Gly His Ser Leu Lys Gln Cys Gly His Gln Ile Ser Ala Cys His
            100                 105                 110
Arg Asp Ile Tyr Lys Gly Val Asp Met Arg Gly Val Asn Phe Asn Val
        115                 120                 125
Ser Lys Val Ser Ser Val Glu Glu Cys Gln Lys Arg Cys Thr Asn Asn
    130                 135                 140
Ile Arg Cys Gln Phe Phe Ser Tyr Ala Thr Gln Thr Phe His Lys Ala
145                 150                 155                 160
Glu Tyr Arg Asn Asn Cys Leu Leu Lys Tyr Ser Pro Gly Gly Thr Pro
                165                 170                 175
Thr Ala Ile Lys Val Leu Ser Asn Val Glu Ser Gly Phe Ser Leu Lys
            180                 185                 190
Pro Cys Ala Leu Ser Glu Ile Gly Cys His Met Asn Ile Phe Gln His
        195                 200                 205
Leu Ala Phe Ser Asp Val Asp Val Ala Arg Val Leu Thr Pro Asp Ala
    210                 215                 220
Phe Val Cys Arg Thr Ile Cys Thr Tyr His Pro Asn Cys Leu Phe Phe
225                 230                 235                 240
Thr Phe Tyr Thr Asn Val Trp Lys Ile Glu Ser Gln Arg Asn Val Cys
                245                 250                 255
Leu Leu Lys Thr Ser Glu Ser Gly Thr Pro Ser Ser Ser Thr Pro Gln
            260                 265                 270
Glu Asn Thr Ile Ser Gly Tyr Ser Leu Leu Thr Cys Lys Arg Thr Leu
        275                 280                 285
Pro Glu Pro Cys His Ser Lys Ile Tyr Pro Gly Val Asp Phe Gly Gly
    290                 295                 300
```

```
Glu Glu Leu Asn Val Thr Phe Val Lys Gly Val Asn Val Cys Gln Glu
305                 310                 315                 320
Thr Cys Thr Lys Met Ile Arg Cys Gln Phe Phe Thr Tyr Ser Leu Leu
                325                 330                 335
Pro Glu Asp Cys Lys Glu Glu Lys Cys Lys Cys Phe Leu Arg Leu Ser
            340                 345                 350
Met Asp Gly Ser Pro Thr Arg Ile Ala Tyr Gly Thr Gln Gly Ser Ser
        355                 360                 365
Gly Tyr Ser Leu Arg Leu Cys Asn Thr Gly Asp Asn Ser Val Cys Thr
    370                 375                 380
Thr Lys Thr Ser Thr Arg Ile Val Gly Gly Thr Asn Ser Ser Trp Gly
385                 390                 395                 400
Glu Trp Pro Trp Gln Val Ser Leu Gln Val Lys Leu Thr Ala Gln Arg
                405                 410                 415
His Leu Cys Gly Gly Ser Leu Ile Gly His Gln Trp Val Leu Thr Ala
            420                 425                 430
Ala His Cys Phe Asp Gly Leu Pro Leu Gln Asp Val Trp Arg Ile Tyr
        435                 440                 445
Ser Gly Ile Leu Asn Leu Ser Asp Ile Thr Lys Asp Thr Pro Phe Ser
    450                 455                 460
Gln Ile Lys Glu Ile Ile Ile His Gln Asn Tyr Lys Val Ser Glu Gly
465                 470                 475                 480
Asn His Asp Ile Ala Leu Ile Lys Leu Gln Ala Pro Leu Asn Tyr Thr
                485                 490                 495
Glu Phe Gln Lys Pro Ile Cys Leu Pro Ser Lys Gly Asp Thr Ser Thr
            500                 505                 510
Ile Tyr Thr Asn Cys Trp Val Thr Gly Trp Gly Phe Ser Lys Glu Lys
        515                 520                 525
Gly Glu Ile Gln Asn Ile Leu Gln Lys Val Asn Ile Pro Leu Val Thr
    530                 535                 540
Asn Glu Glu Cys Gln Lys Arg Tyr Gln Asp Tyr Lys Ile Thr Gln Arg
545                 550                 555                 560
Met Val Cys Ala Gly Tyr Lys Glu Gly Gly Lys Asp Ala Cys Lys Gly
                565                 570                 575
Asp Ser Gly Gly Pro Leu Val Cys Lys His Asn Gly Met Trp Arg Leu
            580                 585                 590
Val Gly Ile Thr Ser Trp Gly Glu Gly Cys Ala Arg Arg Glu Gln Pro
        595                 600                 605
Gly Val Tyr Thr Lys Val Ala Glu Tyr Met Asp Trp Ile Leu Glu Lys
    610                 615                 620
Thr Gln Ser Ser Asp Gly Lys Ala Gln Met Gln Ser Pro Ala
625                 630                 635
```

<210> 166
<211> 2217
<212> DNA
<213> Homo sapiens

<220>
<223> coagulation factor XIa transcript variant 1

<400> 166
tgctgtactg agagagaatg ttacataaca ttgagaacta gtacaagtaa atattaaagt 60
gaagtgacca tttcctacac aagctcattc agaggaggat gaagaccatt ttggaggaag 120
aaaagcaccc ttattaagaa ttgcagcaag taagccaaca aggtcttttc aggatgattt 180
tcttatatca agtggtacat ttcattttat ttacttcagt ttctggtgaa tgtgtgactc 240

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agttgttgaa ggacacctgc tttgaaggag gggacattac tacggtcttc acaccaagcg 300
ccaagtactg ccaggtagtc tgcacttacc acccaagatg tttactcttc actttcacgg 360
cggaatcacc atctgaggat cccacccgat ggtttacttg tgtcctgaaa gacagtgtta 420
cagaaacact gccaagagtg aataggacag cagcgatttc tgggtattct ttcaagcaat 480
gctcacacca aataagcgct tgcaacaaag acatttatgt ggacctagac atgaagggca 540
taaactataa cagctcagtt gccaagagtg ctcaagaatg ccaagaaaga tgcacggatg 600
acgtccactg ccacttttc acgtacgcca caaggcagtt tcccagcctg gagcatcgta 660
acatttgtct actgaagcac acccaaacag ggacaccaac cagaataacg aagctcgata 720
aagtggtgtc tggattttca ctgaaatcct gtgcactttc taatctggct tgtattaggg 780
acattttccc taatacggtg tttgcagaca gcaacatcga cagtgtcatg gctcccgatg 840
cttttgtctg tggccgaatc tgcactcatc atcccggttg cttgtttttt accttctttt 900
cccaggaatg gcccaaagaa tctcaaagaa atctttgtct ccttaaaaca tctgagagtg 960
gattgcccag tacacgcatt aaaaagagca aagctctttc tggtttcagt ctacaaagct 1020
gcaggcacag catcccagtg ttctgccatt cttcatttta ccatgacact gatttcttgg 1080
gagaagaact ggatattgtt gctgcaaaaa gtcacgaggc ctgccagaaa ctgtgcacca 1140
atgccgtccg ctgccagttt tttacctata ccccagccca agcatcctgc aacgaaggga 1200
agggcaagtg ttacttaaag ctttcttcaa acggatctcc aactaaaata cttcacggga 1260
gaggaggcat ctctggatac acattaaggt tgtgtaaaat ggataatgag tgtaccacca 1320
aaatcaagcc caggatcgtt ggaggaactg cgtctgttcg tggtgagtgg ccgtggcagg 1380
tgaccctgca cacaacctca cccactcaga gacacctgtg tggaggctcc atcattggaa 1440
accagtggat attaacagcc gctcactgtt tctatggggt agagtcacct aagattttgc 1500
gtgtctacag tggcatttta aatcaatctg aaataaaaga ggacacatct ttctttgggg 1560
ttcaagaaat aataatccat gatcagtata aaatggcaga aagcgggtat gatattgcct 1620
tgttgaaact ggaaaccaca gtgaattaca cagattctca acgacccata tgcctgcctt 1680
ccaaaggaga tagaaatgta atatacactg attgctgggt gactggatgg gggtacagaa 1740
aactaagaga caaaatacaa aatactctcc agaaagccaa gataccctta gtgaccaacg 1800
aagagtgcca gaagagatac agaggacata aaataaccca taagatgatc tgtgccggct 1860
acagggaagg agggaaggac gcttgcaagg gagattcggg aggccctctg tcctgcaaac 1920
acaatgaggt ctggcatctg gtaggcatca cgagctgggg cgaaggctgt gctcaaaggg 1980
agcggccagg tgtttacacc aacgtggtcg agtacgtgga ctggattctg gagaaaactc 2040
aagcagtgtg aatgggttcc caggggccat tggagtccct gaaggaccca ggatttgctg 2100
ggagagggtg ttgagttcac tgtgccagca tgcttcctcc acagtaacac gctgaagggg 2160
cttggtgttt gtaagaaaat gctagaagaa aacaaactgt cacaagttgt tatgtcc    2217
```

<210> 167
<211> 625
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor XIa isoform 1

<400> 167

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Met Ile Phe Leu Tyr Gln Val Val His Phe Ile Leu Phe Thr Ser Val
 1               5                  10                  15
Ser Gly Glu Cys Val Thr Gln Leu Leu Lys Asp Thr Cys Phe Glu Gly
            20                  25                  30
Gly Asp Ile Thr Thr Val Phe Thr Pro Ser Ala Lys Tyr Cys Gln Val
        35                  40                  45
Val Cys Thr Tyr His Pro Arg Cys Leu Leu Phe Thr Phe Thr Ala Glu
    50                  55                  60
Ser Pro Ser Glu Asp Pro Thr Arg Trp Phe Thr Cys Val Leu Lys Asp
65                  70                  75                  80
Ser Val Thr Glu Thr Leu Pro Arg Val Asn Arg Thr Ala Ala Ile Ser
                85                  90                  95
Gly Tyr Ser Phe Lys Gln Cys Ser His Gln Ile Ser Ala Cys Asn Lys
            100                 105                 110
```

```
Asp Ile Tyr Val Asp Leu Asp Met Lys Gly Ile Asn Tyr Asn Ser Ser
        115                 120                 125
Val Ala Lys Ser Ala Gln Glu Cys Gln Glu Arg Cys Thr Asp Asp Val
    130                 135                 140
His Cys His Phe Phe Thr Tyr Ala Thr Arg Gln Phe Pro Ser Leu Glu
145                 150                 155                 160
His Arg Asn Ile Cys Leu Leu Lys His Thr Gln Thr Gly Thr Pro Thr
                165                 170                 175
Arg Ile Thr Lys Leu Asp Lys Val Val Ser Gly Phe Ser Leu Lys Ser
            180                 185                 190
Cys Ala Leu Ser Asn Leu Ala Cys Ile Arg Asp Ile Phe Pro Asn Thr
        195                 200                 205
Val Phe Ala Asp Ser Asn Ile Asp Ser Val Met Ala Pro Asp Ala Phe
    210                 215                 220
Val Cys Gly Arg Ile Cys Thr His His Pro Gly Cys Leu Phe Phe Thr
225                 230                 235                 240
Phe Phe Ser Gln Glu Trp Pro Lys Glu Ser Gln Arg Asn Leu Cys Leu
                245                 250                 255
Leu Lys Thr Ser Glu Ser Gly Leu Pro Ser Thr Arg Ile Lys Lys Ser
            260                 265                 270
Lys Ala Leu Ser Gly Phe Ser Leu Gln Ser Cys Arg His Ser Ile Pro
        275                 280                 285
Val Phe Cys His Ser Ser Phe Tyr His Asp Thr Asp Phe Leu Gly Glu
    290                 295                 300
Glu Leu Asp Ile Val Ala Ala Lys Ser His Glu Ala Cys Gln Lys Leu
305                 310                 315                 320
Cys Thr Asn Ala Val Arg Cys Gln Phe Phe Thr Tyr Thr Pro Ala Gln
                325                 330                 335
Ala Ser Cys Asn Glu Gly Lys Gly Lys Cys Tyr Leu Lys Leu Ser Ser
            340                 345                 350
Asn Gly Ser Pro Thr Lys Ile Leu His Gly Arg Gly Gly Ile Ser Gly
        355                 360                 365
Tyr Thr Leu Arg Leu Cys Lys Met Asp Asn Glu Cys Thr Thr Lys Ile
    370                 375                 380
Lys Pro Arg Ile Val Gly Gly Thr Ala Ser Val Arg Gly Glu Trp Pro
385                 390                 395                 400
Trp Gln Val Thr Leu His Thr Thr Ser Pro Thr Gln Arg His Leu Cys
                405                 410                 415
Gly Gly Ser Ile Ile Gly Asn Gln Trp Ile Leu Thr Ala Ala His Cys
            420                 425                 430
Phe Tyr Gly Val Glu Ser Pro Lys Ile Leu Arg Val Tyr Ser Gly Ile
        435                 440                 445
Leu Asn Gln Ser Glu Ile Lys Glu Asp Thr Ser Phe Phe Gly Val Gln
    450                 455                 460
Glu Ile Ile Ile His Asp Gln Tyr Lys Met Ala Glu Ser Gly Tyr Asp
465                 470                 475                 480
Ile Ala Leu Leu Lys Leu Glu Thr Thr Val Asn Tyr Thr Asp Ser Gln
                485                 490                 495
Arg Pro Ile Cys Leu Pro Ser Lys Gly Asp Arg Asn Val Ile Tyr Thr
            500                 505                 510
Asp Cys Trp Val Thr Gly Trp Gly Tyr Arg Lys Leu Arg Asp Lys Ile
        515                 520                 525
Gln Asn Thr Leu Gln Lys Ala Lys Ile Pro Leu Val Thr Asn Glu Glu
    530                 535                 540
Cys Gln Lys Arg Tyr Arg Gly His Lys Ile Thr His Lys Met Ile Cys
545                 550                 555                 560
Ala Gly Tyr Arg Glu Gly Gly Lys Asp Ala Cys Lys Gly Asp Ser Gly
```

```
                565                 570                 575
Gly Pro Leu Ser Cys Lys His Asn Glu Val Trp His Leu Val Gly Ile
            580                 585                 590
Thr Ser Trp Gly Glu Gly Cys Ala Gln Arg Glu Arg Pro Gly Val Tyr
        595                 600                 605
Thr Asn Val Val Glu Tyr Val Asp Trp Ile Leu Glu Lys Thr Gln Ala
    610                 615                 620
Val
625
```

<210> 168
<211> 2055
<212> DNA
<213> Homo sapiens

<220>
<223> coagulation factor XIa transcript variant 2

<400> 168

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tgctgtactg agagagaatg ttacataaca ttgagaacta gtacaagtaa atattaaagt 60
gaagtgacca tttcctacac aagctcattc agaggaggat gaagaccatt ttggaggaag 120
aaaagcaccc ttattaagaa ttgcagcaag taagccaaca aggtcttttc aggatgattt 180
tcttatatca agtggtacat ttcatttat ttacttcagt ttctggtgaa tgtgtgactc 240
agttgttgaa ggacacctgc tttgaaggag gggacattac tacggtcttc acaccaagcg 300
ccaagtactg ccaggtagtc tgcacttacc acccaagatg tttactcttc actttcacgg 360
cggaatcacc atctgaggat cccacccgat ggtttacttg tgtcctgaaa gacagtgtta 420
cagaaacact gccaagagtg aataggacag cagcgatttc tgggtattct ttcaagcaat 480
gctcacacca aataagtaac atttgtctac tgaagcacac ccaaacaggg acaccaacca 540
gaataacgaa gctcgataaa gtggtgtctg gattttcact gaaatcctgt gcactttcta 600
atctggcttg tattagggac attttcccta atacggtgtt tgcagacagc aacatcgaca 660
gtgtcatggc tcccgatgct tttgtctgtg gccgaatctg cactcatcat cccggttgct 720
tgtttttac cttcttttcc caggaatggc ccaaagaatc tcaaagaaat ctttgtctcc 780
ttaaaacatc tgagagtgga ttgcccagta cacgcattaa aaagagcaaa gctctttctg 840
gtttcagtct acaaagctgc aggcacagca tcccagtgtt ctgccattct tcattttacc 900
atgacactga tttcttggga gaagaactgg atattgttgc tgcaaaaagt cacgaggcct 960
gccagaaact gtgcaccaat gccgtccgct gccagttttt tacctatacc ccagcccaag 1020
catcctgcaa cgaagggaag ggcaagtgtt acttaaagct ttcttcaaac ggatctccaa 1080
ctaaaatact tcacgggaga ggaggcatct ctggatacac attaaggttg tgtaaaatgg 1140
ataatgagtg taccaccaaa atcaagccca ggatcgttgg aggaactgcg tctgttcgtg 1200
gtgagtggcc gtggcaggtg accctgcaca caacctcacc cactcagaga cacctgtgtg 1260
gaggctccat cattggaaac cagtggatat taacagccgc tcactgtttc tatggggtag 1320
agtcacctaa gattttgcgt gtctacagtg gcattttaaa tcaatctgaa ataaaagagg 1380
acacatcttt ctttggggtt caagaaataa taatccatga tcagtataaa atggcagaaa 1440
gcgggtatga tattgccttg ttgaaactgg aaaccacagt gaattacaca gattctcaac 1500
gacccatatg cctgccttcc aaaggagata gaaatgtaat atacactgat tgctgggtga 1560
ctggatgggg gtacagaaaa ctaagagaca aaatacaaaa tactctccag aaagccaaga 1620
tacccttagt gaccaacgaa gagtgccaga agagatacag aggacataaa ataacccata 1680
agatgatctg tgccggctac agggaaggag ggaaggacgc ttgcaaggga gattcgggag 1740
gcccctctgtc ctgcaaacac aatgaggtct ggcatctggt aggcatcacg agctggggcg 1800
aaggctgtgc tcaaagggag cggccaggtg tttacaccaa cgtggtcgag tacgtggact 1860
ggattctgga gaaaactcaa gcagtgtgaa tgggttccca ggggccattg gagtccctga 1920
aggacccagg atttgctggg agagggtgtt gagttcactg tgccagcatg cttcctccac 1980
agtaacacgc tgaaggggct tggtgtttgt aagaaaatgc tagaagaaaa caaactgtca 2040
caagttgtta tgtcc                                                  2055
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<210> 169

<211> 571
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor XIa isoform 2

<400> 169
Met Ile Phe Leu Tyr Gln Val Val His Phe Ile Leu Phe Thr Ser Val
 1   5   10   15
Ser Gly Glu Cys Val Thr Gln Leu Leu Lys Asp Thr Cys Phe Glu Gly
            20   25   30
Gly Asp Ile Thr Thr Val Phe Thr Pro Ser Ala Lys Tyr Cys Gln Val
        35   40   45
Val Cys Thr Tyr His Pro Arg Cys Leu Leu Phe Thr Phe Thr Ala Glu
    50   55   60
Ser Pro Ser Glu Asp Pro Thr Arg Trp Phe Thr Cys Val Leu Lys Asp
65   70   75   80
Ser Val Thr Glu Thr Leu Pro Arg Val Asn Arg Thr Ala Ala Ile Ser
                85   90   95
Gly Tyr Ser Phe Lys Gln Cys Ser His Gln Ile Ser Asn Ile Cys Leu
            100   105   110
Leu Lys His Thr Gln Thr Gly Thr Pro Thr Arg Ile Thr Lys Leu Asp
        115   120   125
Lys Val Val Ser Gly Phe Ser Leu Lys Ser Cys Ala Leu Ser Asn Leu
    130   135   140
Ala Cys Ile Arg Asp Ile Phe Pro Asn Thr Val Phe Ala Asp Ser Asn
145   150   155   160
Ile Asp Ser Val Met Ala Pro Asp Ala Phe Val Cys Gly Arg Ile Cys
                165   170   175
Thr His His Pro Gly Cys Leu Phe Phe Thr Phe Phe Ser Gln Glu Trp
            180   185   190
Pro Lys Glu Ser Gln Arg Asn Leu Cys Leu Leu Lys Thr Ser Glu Ser
        195   200   205
Gly Leu Pro Ser Thr Arg Ile Lys Lys Ser Lys Ala Leu Ser Gly Phe
    210   215   220
Ser Leu Gln Ser Cys Arg His Ser Ile Pro Val Phe Cys His Ser Ser
225   230   235   240
Phe Tyr His Asp Thr Asp Phe Leu Gly Glu Glu Leu Asp Ile Val Ala
                245   250   255
Ala Lys Ser His Glu Ala Cys Gln Lys Leu Cys Thr Asn Ala Val Arg
            260   265   270
Cys Gln Phe Phe Thr Tyr Thr Pro Ala Gln Ala Ser Cys Asn Glu Gly
        275   280   285
Lys Gly Lys Cys Tyr Leu Lys Leu Ser Ser Asn Gly Ser Pro Thr Lys
    290   295   300
Ile Leu His Gly Arg Gly Gly Ile Ser Gly Tyr Thr Leu Arg Leu Cys
305   310   315   320
Lys Met Asp Asn Glu Cys Thr Thr Lys Ile Lys Pro Arg Ile Val Gly
                325   330   335
Gly Thr Ala Ser Val Arg Gly Glu Trp Pro Trp Gln Val Thr Leu His
            340   345   350
Thr Thr Ser Pro Thr Gln Arg His Leu Cys Gly Gly Ser Ile Ile Gly
        355   360   365
Asn Gln Trp Ile Leu Thr Ala Ala His Cys Phe Tyr Gly Val Glu Ser
    370   375   380
Pro Lys Ile Leu Arg Val Tyr Ser Gly Ile Leu Asn Gln Ser Glu Ile

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385                 390                 395                 400
Lys Glu Asp Thr Ser Phe Phe Gly Val Gln Glu Ile Ile Ile His Asp
                405                 410                 415
Gln Tyr Lys Met Ala Glu Ser Gly Tyr Asp Ile Ala Leu Leu Lys Leu
            420                 425                 430
Glu Thr Thr Val Asn Tyr Thr Asp Ser Gln Arg Pro Ile Cys Leu Pro
        435                 440                 445
Ser Lys Gly Asp Arg Asn Val Ile Tyr Thr Asp Cys Trp Val Thr Gly
    450                 455                 460
Trp Gly Tyr Arg Lys Leu Arg Asp Lys Ile Gln Asn Thr Leu Gln Lys
465                 470                 475                 480
Ala Lys Ile Pro Leu Val Thr Asn Glu Glu Cys Gln Lys Arg Tyr Arg
                485                 490                 495
Gly His Lys Ile Thr His Lys Met Ile Cys Ala Gly Tyr Arg Glu Gly
            500                 505                 510
Gly Lys Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Ser Cys Lys
        515                 520                 525
His Asn Glu Val Trp His Leu Val Gly Ile Thr Ser Trp Gly Glu Gly
    530                 535                 540
Cys Ala Gln Arg Glu Arg Pro Gly Val Tyr Thr Asn Val Val Glu Tyr
545                 550                 555                 560
Val Asp Trp Ile Leu Glu Lys Thr Gln Ala Val
                565                 570
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<210> 170
<211> 2804
<212> DNA
<213> Homo sapiens

<220>
<223> coagulation factor IXa

<400> 170

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caccaggcct catcaccatc tgccttttag gatatctact cagtgctgaa tgtacagttt 120
ttcttgatca tgaaaacgcc aacaaaattc tgaatcggcc aaagaggtat aattcaggta 180
aattggaaga gtttgttcaa gggaaccttg agagagaatg tatggaagaa aagtgtagtt 240
ttgaagaagc acgagaagtt tttgaaaaca ctgaaagaac aactgaattt tggaagcagt 300
atgttgatgg agatcagtgt gagtccaatc catgtttaaa tggcggcagt tgcaaggatg 360
acattaattc ctatgaatgt tggtgtccct ttggatttga aggaaagaac tgtgaattag 420
atgtaacatg taacattaag aatggcagat gcgagcagtt ttgtaaaaat agtgctgata 480
acaaggtggt ttgctcctgt actgagggat atcgacttgc agaaaaccag aagtcctgtg 540
aaccagcagt gccatttcca tgtggaagag tttctgtttc acaaacttct aagctcaccc 600
gtgctgagac tgtttttcct gatgtggact atgtaaattc tactgaagct gaaaccattt 660
tggataacat cactcaaagc acccaatcat ttaatgactt cactcgggtt gttggtggag 720
aagatgccaa accaggtcaa ttcccttggc aggttgtttt gaatggtaaa gttgatgcat 780
tctgtggagg ctctatcgtt aatgaaaaat ggattgtaac tgctgcccac tgtgttgaaa 840
ctggtgttaa aattacagtt gtcgcaggtg aacataatat tgaggagaca gaacatacag 900
agcaaaagcg aaatgtgatt cgaattattc ctcaccacaa ctacaatgca gctattaata 960
agtacaacca tgacattgcc cttctggaac tggacgaacc cttagtgcta aacagctacg 1020
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gctatgtaag tggctgggga agagtcttcc acaaagggag atcagcttta gttcttcagt 1140
accttagagt tccacttgtt gaccgagcca catgtcttcg atctacaaag ttcaccatct 1200
ataacaacat gttctgtgct ggcttccatg aaggaggtag agattcatgt caaggagata 1260
gtgggggacc ccatgttact gaagtggaag ggaccagttt cttaactgga attattagct 1320
ggggtgaaga gtgtgcaatg aaaggcaaat atggaatata taccaaggta tcccggtatg 1380
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tcaactggat taaggaaaaa acaaagctca cttaatgaaa gatggatttc caaggttaat 1440
tcattggaat tgaaaattaa cagggcctct cactaactaa tcactttccc atcttttgtt 1500
agatttgaat atatacattc tatgatcatt gctttttctc tttacagggg agaatttcat 1560
attttacctg agcaaattga ttagaaaatg gaaccactag aggaatataa tgtgttagga 1620
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ctgtccatca gatactatgg ttctccacta tggcaactaa ctcactcaat tttccctcct 1740
tagcagcatt ccatcttccc gatcttcttt gcttctccaa ccaaaacatc aatgtttatt 1800
agttctgtat acagtacagg atctttggtc tactctatca caaggccagt accacactca 1860
tgaagaaaga acacaggagt agctgagagg ctaaaactca tcaaaaacac tactcctttt 1920
cctctaccct attcctcaat cttttacctt ttccaaatcc caatccccaa atcagttttt 1980
ctctttctta ctccctctct ccctttacc ctccatggtc gttaaaggag agatggggag 2040
catcattctg ttatacttct gtacacagtt atacatgtct atcaaaccca gacttgcttc 2100
catagtggag acttgctttt cagaacatag ggatgaagta aggtgcctga aaagtttggg 2160
ggaaaagttt ctttcagaga gttaagttat tttatatata taatatatat ataaaatata 2220
taatatacaa tataaatata tagtgtgtgt gtgtatgcgt gtgtgtagac acacacgcat 2280
acacacatat aatggaagca ataagccatt ctaagagctt gtatggttat ggaggtctga 2340
ctaggcatga tttcacgaag gcaagattgg catatcattg taactaaaaa agctgacatt 2400
gacccagaca tattgtactc tttctaaaaa taataataat aatgctaaca gaaagaagag 2460
aaccgttcgt ttgcaatcta cagctagtag agactttgag gaagaattca acagtgtgtc 2520
ttcagcagtg ttcagagcca agcaagaagt tgaagttgcc tagaccagag gacataagta 2580
tcatgtctcc tttaactagc ataccccgaa gtggagaagg gtgcagcagg ctcaaaggca 2640
taagtcattc caatcagcca actaagttgt ccttttctgg tttcgtgttc accatggaac 2700
attttgatta tagttaatcc ttctatcttg aatcttctag agagttgctg accaactgac 2760
gtatgtttcc ctttgtgaat taataaactg gtgttctggt tcat                  2804
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<210> 171
<211> 461
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor IXa

<400> 171

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

            20                  25                  30
Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
        35                  40                  45
Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
    50                  55                  60
Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn
65                  70                  75                  80
Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
                85                  90                  95
Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
            100                 105                 110
Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
        115                 120                 125
Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
    130                 135                 140
Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
145                 150                 155                 160
Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
                165                 170                 175
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Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
            180                 185                 190
Glu Thr Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu
        195                 200                 205
Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe
    210                 215                 220
Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
225                 230                 235                 240
Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
                245                 250                 255
Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
            260                 265                 270
Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
        275                 280                 285
His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn
    290                 295                 300
Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu
305                 310                 315                 320
Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile
                325                 330                 335
Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr
            340                 345                 350
Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val
        355                 360                 365
Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg
    370                 375                 380
Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His
385                 390                 395                 400
Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val
                405                 410                 415
Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly
            420                 425                 430
Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser
        435                 440                 445
Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
    450                 455                 460
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<210> 172
<211> 2478
<212> DNA
<213> Homo sapiens

<220>
<223> coagulation factor VIIa transcript variant 1

<400> 172
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caggccctca ggctcctctg ccttctgctt gggcttcagg gctgcctggc tgcaggcggg 120
gtcgctaagg cctcaggagg agaaacacgg gacatgccgt ggaagccggg gcctcacaga 180
gtcttcgtaa cccaggagga agcccacggc gtcctgcacc ggcgccggcg cgccaacgcg 240
ttcctggagg agctgcggcc gggctccctg gagagggagt gcaaggagga gcagtgctcc 300
ttcgaggagg cccgggagat cttcaaggac gcggagagga cgaagctgtt ctggatttct 360
tacagtgatg gggaccagtg tgcctcaagt ccatgccaga atgggggctc ctgcaaggac 420
cagctccagt cctatatctg cttctgcctc cctgccttcg agggccggaa ctgtgagacg 480
cacaaggatg accagctgat ctgtgtgaac gagaacggcg gctgtgagca gtactgcagt 540
gaccacacgg gcaccaagcg ctcctgtcgg tgccacgagg ggtactctct gctggcagac 600

ggggtgtcct gcacacccac agttgaatat ccatgtggaa aaatacctat tctagaaaaa 660
agaaatgcca gcaaacccca aggccgaatt gtgggggggca aggtgtgccc caaaggggag 720
tgtccatggc aggtcctgtt gttggtgaat ggagctcagt tgtgtggggg gaccctgatc 780
aacaccatct gggtggtctc cgcggcccac tgtttcgaca aaatcaagaa ctggaggaac 840
ctgatcgcgg tgctgggcga gcacgacctc agcgagcacg acggggatga gcagagccgg 900
cgggtggcgc aggtcatcat ccccagcacg tacgtcccgg gcaccaccaa ccacgacatc 960
gcgctgctcc gcctgcacca gcccgtggtc ctcactgacc atgtggtgcc cctctgcctg 1020
cccgaacgga cgttctctga gaggacgctg gccttcgtgc gcttctcatt ggtcagcggc 1080
tggggccagc tgctggaccg tggcgccacg gccctggagc tcatggtgct caacgtgccc 1140
cggctgatga cccaggactg cctgcagcag tcacggaagg tgggagactc cccaaatatc 1200
acggagtaca tgttctgtgc cggctactcg gatggcagca aggactcctg caagggggac 1260
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tggggccagg gctgcgcaac cgtgggccac tttggggtgt acaccagggt ctcccagtac 1380
atcgagtggc tgcaaaagct catgcgctca gagccacgcc caggagtcct cctgcgagcc 1440
ccatttccct agcccagcag ccctggcctg tggagagaaa gccaaggctg cgtcgaactg 1500
tcctggcacc aaatcccata tattcttctg cagttaatgg ggtagaggag ggcatgggag 1560
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gactaataga gacacagaga tggaatagaa aagatgagag gcagaggcag acaggcgctg 1740
gacagagggg caggggagtg ccaaggttgt cctggaggca gacagcccag ctgagcctcc 1800
ttacctccct tcagccaagc cccacctgca cgtgatctgc tggccctcag gctgctgctc 1860
tgccttcatt gctggagaca gtagaggcat gaacacacat ggatgcacac acacacacgc 1920
caatgcacac acacagagat atgcacacac acggatgcac acacagatgg tcacacagag 1980
atacgcaaac acaccgatgc acacgcacat agagatatgc acacacagat gcacacacag 2040
atatacacat ggatgcacgc acatgccaat gcacgcacac atcagtgcac acggatgcac 2100
agagatatgc acacaccgat gtgcgcacac acagatatgc acacacatgg atgagcacac 2160
acacaccaag tgcgcacaca caccgatgta cacacacaga tgcacacaca gatgcacaca 2220
caccgatgct gactccatgt gtgctgtcct ctgaaggcgg ttgtttagct ctcacttttc 2280
tggttcttat ccattatcat cttcacttca gacaattcag aagcatcacc atgcatggtg 2340
gcgaatgccc ccaaactctc ccccaaatgt atttctccct tcgctgggtg ccgggctgca 2400
cagactattc cccacctgct tcccagcttc acaataaacg gctgcgtctc ctccgcacac 2460
ctgtggtgcc tgccaccc 2478

<210> 173
<211> 466
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor VIIa isoform 1

<400> 173
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
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Gly Cys Leu Ala Ala Gly Gly Val Ala Lys Ala Ser Gly Gly Glu Thr
20 25 30
Arg Asp Met Pro Trp Lys Pro Gly Pro His Arg Val Phe Val Thr Gln
35 40 45
Glu Glu Ala His Gly Val Leu His Arg Arg Arg Arg Ala Asn Ala Phe
50 55 60
Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu
65 70 75 80
Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
85 90 95
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser
100 105 110
Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr

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        115                 120                 125
Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys Glu Thr His
    130                 135                 140
Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly Cys Glu Gln
145                 150                 155                 160
Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg Cys His Glu
                165                 170                 175
Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro Thr Val Glu
            180                 185                 190
Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
        195                 200                 205
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys
    210                 215                 220
Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly
225                 230                 235                 240
Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His Cys Phe Asp
                245                 250                 255
Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly Glu His Asp
            260                 265                 270
Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val Ala Gln Val
        275                 280                 285
Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp Ile Ala
    290                 295                 300
Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro
305                 310                 315                 320
Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val
                325                 330                 335
Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala
            340                 345                 350
Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu Met Thr Gln
        355                 360                 365
Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro Asn Ile Thr
    370                 375                 380
Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys
385                 390                 395                 400
Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp
                405                 410                 415
Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
            420                 425                 430
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln
        435                 440                 445
Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro
    450                 455                 460
Phe Pro
465
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<210> 174
<211> 2412
<212> DNA
<213> Homo sapiens

<220>
<223> coagulation factor VIIa transcript variant 2

<400> 174
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caggccctca ggctcctctg ccttctgctt gggcttcagg gctgcctggc tgcagtcttc 120
gtaacccagg aggaagccca cggcgtcctg caccggcgcc ggcgcgccaa cgcgttcctg 180
gaggagctgc ggccgggctc cctggagagg gagtgcaagg aggagcagtg ctccttcgag 240
gaggcccggg agatcttcaa ggacgcggag aggacgaagc tgttctggat ttcttacagt 300
gatggggacc agtgtgcctc aagtccatgc cagaatgggg gctcctgcaa ggaccagctc 360
cagtcctata tctgcttctg cctccctgcc ttcgagggcc ggaactgtga gacgcacaag 420
gatgaccagc tgatctgtgt gaacgagaac ggcggctgtg agcagtactg cagtgaccac 480
acgggcacca agcgctcctg tcggtgccac gaggggtact ctctgctggc agacggggtg 540
tcctgcacac ccacagttga atatccatgt ggaaaaatac ctattctaga aaaaagaaat 600
gccagcaaac cccaaggccg aattgtgggg ggcaaggtgt gccccaaagg ggagtgtcca 660
tggcaggtcc tgttgttggt gaatggagct cagttgtgtg gggggaccct gatcaacacc 720
atctgggtgg tctccgcggc ccactgtttc gacaaaatca agaactggag gaacctgatc 780
gcggtgctgg gcgagcacga cctcagcgag cacgacgggg atgagcagag ccggcgggtg 840
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atgacccagg actgcctgca gcagtcacgg aaggtgggag actccccaaa tatcacggag 1140
tacatgttct gtgccggcta ctcggatggc agcaaggact cctgcaaggg ggacagtgga 1200
ggcccacatg ccacccacta ccggggcacg tggtacctga cgggcatcgt cagctggggc 1260
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tggctgcaaa agctcatgcg ctcagagcca cgcccaggag tcctcctgcg agccccattt 1380
ccctagccca gcagccctgg cctgtggaga gaaagccaag gctgcgtcga actgtcctgg 1440
caccaaatcc catatattct tctgcagtta atggggtaga ggagggcatg ggagggaggg 1500
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cattgctgga gacagtagag gcatgaacac acatggatgc acacacacac acgccaatgc 1860
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aaacacaccg atgcacacgc acatagagat atgcacacac agatgcacac acagatatac 1980
acatggatgc acgcacatgc caatgcacgc acacatcagt gcacacggat gcacagagat 2040
atgcacacac cgatgtgcgc acacacagat atgcacacac atggatgagc acacacacac 2100
caagtgcgca cacacaccga tgtacacaca cagatgcaca cacagatgca cacacaccga 2160
tgctgactcc atgtgtgctg tcctctgaag gcggttgttt agctctcact tttctggttc 2220
ttatccatta tcatcttcac ttcagacaat tcagaagcat caccatgcat ggtggcgaat 2280
gcccccaaac tctcccccaa atgtatttct cccttcgctg ggtgccgggc tgcacagact 2340
attccccacc tgcttcccag cttcacaata aacggctgcg tctcctccgc acacctgtgg 2400
tgcctgccac cc 2412

<210> 175
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor VIIa isoform 2

<400> 175
Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
 1   5   10   15
Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
            20   25   30
Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
        35   40   45
Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu

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    50                  55                  60
Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
65                  70                  75                  80
Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
                85                  90                  95
Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
            100                 105                 110
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
        115                 120                 125
Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
    130                 135                 140
Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
145                 150                 155                 160
Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
                165                 170                 175
Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
            180                 185                 190
Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
        195                 200                 205
Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
    210                 215                 220
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
225                 230                 235                 240
Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
                245                 250                 255
Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
            260                 265                 270
Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
        275                 280                 285
Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
    290                 295                 300
Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
305                 310                 315                 320
Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
                325                 330                 335
Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
            340                 345                 350
Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
        355                 360                 365
Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
    370                 375                 380
Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
385                 390                 395                 400
Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
                405                 410                 415
Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
            420                 425                 430
Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
        435                 440
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<210> 176
<211> 1502
<212> DNA
<213> Homo sapiens

<220>

<223> coagulation factor Xa

<400> 176
cagggacaca gtactcggcc acaccatggg gcgcccactg cacctcgtcc tgctcagtgc 60
ctccctggct ggcctcctgc tgctcgggga aagtctgttc atccgcaggg agcaggccaa 120
caacatcctg gcgagggtca cgagggccaa ttcctttctt gaagagatga agaaaggaca 180
cctcgaaaga gagtgcatgg aagagacctg ctcatacgaa gaggcccgcg aggtctttga 240
ggacagcgac aagacgaatg aattctggaa taaatacaaa gatggcgacc agtgtgagac 300
cagtccttgc cagaaccagg gcaaatgtaa agacggcctc ggggaataca cctgcacctg 360
tttagaagga ttcgaaggca aaaactgtga attattcaca cggaagctct gcagcctgga 420
caacggggac tgtgaccagt tctgccacga ggaacagaac tctgtggtgt gctcctgcgc 480
ccgcgggtac accctggctg acaacggcaa ggcctgcatt cccacagggc cctacccctg 540
tgggaaacag accctggaac gcaggaagag gtcagtggcc caggccacca gcagcagcgg 600
ggaggccccc gacagcatca catggaagcc atatgatgca gccgacctgg accccaccga 660
gaaccccttc gacctgcttg acttcaacca gacgcagcct gagaggggcg acaacaacct 720
caccaggatc gtgggaggcc aggaatgcaa ggacggggag tgtccctggc aggccctgct 780
catcaatgag gaaaacgagg gtttctgtgg tggaaccatt ctgagcgagt tctacatcct 840
aacggcagcc cactgtctct accaagccaa gagattcaag gtgagggtag gggaccggaa 900
cacggagcag gaggagggcg gtgaggcggt gcacgaggtg gaggtggtca tcaagcacaa 960
ccggttcaca aaggagacct atgacttcga catcgccgtg ctccggctca agaccccccat 1020
caccttccgc atgaacgtgg cgcctgcctg cctccccgag cgtgactggg ccgagtccac 1080
gctgatgacg cagaagacgg ggattgtgag cggcttcggg cgcacccacg agaagggccg 1140
gcagtccacc aggctcaaga tgctggaggt gccctacgtg gaccgcaaca gctgcaagct 1200
gtccagcagc ttcatcatca cccagaacat gttctgtgcc ggctacgaca ccaagcagga 1260
ggatgcctgc caggggggaca gcgggggccc gcacgtcacc cgcttcaagg acacctactt 1320
cgtgacaggc atcgtcagct ggggagaggg ctgtgcccgt aaggggaagt acgggatcta 1380
caccaaggtc accgccttcc tcaagtggat cgacaggtcc atgaaaacca ggggcttgcc 1440
caaggccaag agccatgccc cggaggtcat aacgtcctct ccattaaagt gagatcccac 1500
tc 1502

<210> 177
<211> 488
<212> PRT
<213> Homo sapiens

<220>
<223> coagulation factor Xa

<400> 177
Met Gly Arg Pro Leu His Leu Val Leu Leu Ser Ala Ser Leu Ala Gly
 1   5   10   15
Leu Leu Leu Leu Gly Glu Ser Leu Phe Ile Arg Arg Glu Gln Ala Asn
            20   25   30
Asn Ile Leu Ala Arg Val Thr Arg Ala Asn Ser Phe Leu Glu Glu Met
        35   40   45
Lys Lys Gly His Leu Glu Arg Glu Cys Met Glu Glu Thr Cys Ser Tyr
    50   55   60
Glu Glu Ala Arg Glu Val Phe Glu Asp Ser Asp Lys Thr Asn Glu Phe
65   70   75   80
Trp Asn Lys Tyr Lys Asp Gly Asp Gln Cys Glu Thr Ser Pro Cys Gln
                85   90   95
Asn Gln Gly Lys Cys Lys Asp Gly Leu Gly Glu Tyr Thr Cys Thr Cys
            100   105   110
Leu Glu Gly Phe Glu Gly Lys Asn Cys Glu Leu Phe Thr Arg Lys Leu
        115   120   125
Cys Ser Leu Asp Asn Gly Asp Cys Asp Gln Phe Cys His Glu Glu Gln
    130   135   140

```
Asn Ser Val Val Cys Ser Cys Ala Arg Gly Tyr Thr Leu Ala Asp Asn
145                 150                 155                 160
Gly Lys Ala Cys Ile Pro Thr Gly Pro Tyr Pro Cys Gly Lys Gln Thr
                165                 170                 175
Leu Glu Arg Arg Lys Arg Ser Val Ala Gln Ala Thr Ser Ser Ser Gly
            180                 185                 190
Glu Ala Pro Asp Ser Ile Thr Trp Lys Pro Tyr Asp Ala Ala Asp Leu
        195                 200                 205

Asp Pro Thr Glu Asn Pro Phe Asp Leu Leu Asp Phe Asn Gln Thr Gln
    210                 215                 220
Pro Glu Arg Gly Asp Asn Asn Leu Thr Arg Ile Val Gly Gly Gln Glu
225                 230                 235                 240
Cys Lys Asp Gly Glu Cys Pro Trp Gln Ala Leu Leu Ile Asn Glu Glu
                245                 250                 255
Asn Glu Gly Phe Cys Gly Gly Thr Ile Leu Ser Glu Phe Tyr Ile Leu
            260                 265                 270
Thr Ala Ala His Cys Leu Tyr Gln Ala Lys Arg Phe Lys Val Arg Val
        275                 280                 285
Gly Asp Arg Asn Thr Glu Gln Glu Glu Gly Gly Glu Ala Val His Glu
    290                 295                 300
Val Glu Val Val Ile Lys His Asn Arg Phe Thr Lys Glu Thr Tyr Asp
305                 310                 315                 320
Phe Asp Ile Ala Val Leu Arg Leu Lys Thr Pro Ile Thr Phe Arg Met
                325                 330                 335
Asn Val Ala Pro Ala Cys Leu Pro Glu Arg Asp Trp Ala Glu Ser Thr
            340                 345                 350
Leu Met Thr Gln Lys Thr Gly Ile Val Ser Gly Phe Gly Arg Thr His
        355                 360                 365
Glu Lys Gly Arg Gln Ser Thr Arg Leu Lys Met Leu Glu Val Pro Tyr
    370                 375                 380
Val Asp Arg Asn Ser Cys Lys Leu Ser Ser Ser Phe Ile Ile Thr Gln
385                 390                 395                 400
Asn Met Phe Cys Ala Gly Tyr Asp Thr Lys Gln Glu Asp Ala Cys Gln
                405                 410                 415
Gly Asp Ser Gly Gly Pro His Val Thr Arg Phe Lys Asp Thr Tyr Phe
            420                 425                 430
Val Thr Gly Ile Val Ser Trp Gly Glu Gly Cys Ala Arg Lys Gly Lys
        435                 440                 445
Tyr Gly Ile Tyr Thr Lys Val Thr Ala Phe Leu Lys Trp Ile Asp Arg
    450                 455                 460
Ser Met Lys Thr Arg Gly Leu Pro Lys Ala Lys Ser His Ala Pro Glu
465                 470                 475                 480
Val Ile Thr Ser Ser Pro Leu Lys
                485
```

<210> 178
<211> 1997
<212> DNA
<213> Homo sapiens

<220>
<223> Thrombin

<400> 178
aattcctcag tgacccagga gctgacacac tatggcgcac gtccgaggct tgcagctgcc 60

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tggctgcctg gccctggctg ccctgtgtag ccttgtgcac agccagcatg tgttcctggc 120
tcctcagcaa gcacggtcgc tgctccagcg ggtccggcga gccaacacct tcttggagga 180
ggtgcgcaag ggcaacctag agcgagagtg cgtggaggag acgtgcagct acgaggaggc 240
cttcgaggct ctggagtcct ccacggctac ggatgtgttc tgggccaagt acacagcttg 300
tgagacagcg aggacgcctc gagataagct tgctgcatgt ctggaaggta actgtgctga 360
gggtctgggt acgaactacc gagggcatgt gaacatcacc cggtcaggca ttgagtgcca 420
gctatggagg agtcgctacc cacataagcc tgaaatcaac tccactaccc atcctggggc 480
cgacctacag gagaatttct gccgcaaccc cgacagcagc accacgggac cctggtgcta 540
cactacagac cccaccgtga ggaggcagga atgcagcatc cctgtctgtg gccaggatca 600
agtcactgta gcgatgactc cacgctccga aggctccagt gtgaatctgt cacctccatt 660
ggagcagtgt gtccctgatc gggggcagca gtaccagggg cgcctggcgg tgaccacaca 720
tgggctcccc tgcctggcct gggccagcgc acaggccaag gccctgagca agcaccagga 780
cttcaactca gctgtgcagc tggtggagaa cttctgccgc aacccagacg gggatgagga 840
gggcgtgtgg tgctatgtgg ccgggaagcc tggcgacttt gggtactgcg acctcaacta 900
ttgtgaggag gccgtggagg aggagacagg agatgggctg gatgaggact cagacagggc 960
catcgaaggg cgtaccgcca ccagtgagta ccagactttc ttcaatccga ggacctttgg 1020
ctcgggagag gcagactgtg ggctgcgacc tctgttcgag aagaagtcgc tggaggacaa 1080
aaccgaaaga gagctcctgg aatcctacat cgacgggcgc attgtggagg gctcggatgc 1140
agagatcggc atgtcacctt ggcaggtgat gcttttccgg aagagtcccc aggagctgct 1200
gtgtggggcc agcctcatca gtgaccgctg ggtcctcacc gccgcccact gcctcctgta 1260
cccgccctgg gacaagaact tcaccgagaa tgaccttctg gtgcgcattg gcaagcactc 1320
ccgcacaagg tacgagcgaa acattgaaaa gatatccatg ttggaaaaga tctacatcca 1380
ccccaggtac aactggcggg agaacctgga ccgggacatt gccctgatga agctgaagaa 1440
gcctgttgcc ttcagtgact acattcaccc tgtgtgtctg cccgacaggg agacggcagc 1500
cagcttgctc caggctggat acaaggggcg ggtgacaggc tggggcaacc tgaaggagac 1560
gtggacagcc aacgttggta aggggcagcc cagtgtcctg caggtggtga acctgcccat 1620
tgtggagcgg ccggtctgca aggactccac ccggatccgc atcactgaca acatgttctg 1680
tgctggttac aagcctgatg aagggaaacg aggggatgcc tgtgaaggtg acagtggggg 1740
acccttttgtc atgaagagcc cctttaacaa ccgctggtat caaatgggca tcgtctcatg 1800
gggtgaaggc tgtgaccggg atgggaaata tggcttctac acacatgtgt tccgcctgaa 1860
gaagtggata cagaaggtca ttgatcagtt tggagagtag gggccactca tattctgggc 1920
tcctggaacc aatcccgtga aagaattatt tttgtgtttc taaaactatg gttcccaata 1980
aaagtgactc tcagcgg                                                1997
```

<210> 179
<211> 622
<212> PRT
<213> Homo sapiens

<220>
<223> Thrombin

<400> 179

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Met Ala His Val Arg Gly Leu Gln Leu Pro Gly Cys Leu Ala Leu Ala
 1               5                  10                  15
Ala Leu Cys Ser Leu Val His Ser Gln His Val Phe Leu Ala Pro Gln
            20                  25                  30
Gln Ala Arg Ser Leu Leu Gln Arg Val Arg Arg Ala Asn Thr Phe Leu
        35                  40                  45
Glu Glu Val Arg Lys Gly Asn Leu Glu Arg Glu Cys Val Glu Glu Thr
    50                  55                  60
Cys Ser Tyr Glu Glu Ala Phe Glu Ala Leu Glu Ser Ser Thr Ala Thr
65                  70                  75                  80
Asp Val Phe Trp Ala Lys Tyr Thr Ala Cys Glu Thr Ala Arg Thr Pro
                85                  90                  95
Arg Asp Lys Leu Ala Ala Cys Leu Glu Gly Asn Cys Ala Glu Gly Leu
            100                 105                 110
```

```
Gly Thr Asn Tyr Arg Gly His Val Asn Ile Thr Arg Ser Gly Ile Glu
        115                 120                 125
Cys Gln Leu Trp Arg Ser Arg Tyr Pro His Lys Pro Glu Ile Asn Ser
    130                 135                 140
Thr Thr His Pro Gly Ala Asp Leu Gln Glu Asn Phe Cys Arg Asn Pro
145                 150                 155                 160
Asp Ser Ser Thr Thr Gly Pro Trp Cys Tyr Thr Thr Asp Pro Thr Val
                165                 170                 175
Arg Arg Gln Glu Cys Ser Ile Pro Val Cys Gly Gln Asp Gln Val Thr
            180                 185                 190
Val Ala Met Thr Pro Arg Ser Glu Gly Ser Ser Val Asn Leu Ser Pro
        195                 200                 205
Pro Leu Glu Gln Cys Val Pro Asp Arg Gly Gln Gln Tyr Gln Gly Arg
    210                 215                 220
Leu Ala Val Thr Thr His Gly Leu Pro Cys Leu Ala Trp Ala Ser Ala
225                 230                 235                 240
Gln Ala Lys Ala Leu Ser Lys His Gln Asp Phe Asn Ser Ala Val Gln
                245                 250                 255
Leu Val Glu Asn Phe Cys Arg Asn Pro Asp Gly Asp Glu Glu Gly Val
            260                 265                 270
Trp Cys Tyr Val Ala Gly Lys Pro Gly Asp Phe Gly Tyr Cys Asp Leu
        275                 280                 285
Asn Tyr Cys Glu Glu Ala Val Glu Glu Glu Thr Gly Asp Gly Leu Asp
    290                 295                 300
Glu Asp Ser Asp Arg Ala Ile Glu Gly Arg Thr Ala Thr Ser Glu Tyr
305                 310                 315                 320
Gln Thr Phe Phe Asn Pro Arg Thr Phe Gly Ser Gly Glu Ala Asp Cys
                325                 330                 335
Gly Leu Arg Pro Leu Phe Glu Lys Lys Ser Leu Glu Asp Lys Thr Glu
            340                 345                 350
Arg Glu Leu Leu Glu Ser Tyr Ile Asp Gly Arg Ile Val Glu Gly Ser
        355                 360                 365
Asp Ala Glu Ile Gly Met Ser Pro Trp Gln Val Met Leu Phe Arg Lys
    370                 375                 380
Ser Pro Gln Glu Leu Leu Cys Gly Ala Ser Leu Ile Ser Asp Arg Trp
385                 390                 395                 400
Val Leu Thr Ala Ala His Cys Leu Leu Tyr Pro Pro Trp Asp Lys Asn
                405                 410                 415
Phe Thr Glu Asn Asp Leu Leu Val Arg Ile Gly Lys His Ser Arg Thr
            420                 425                 430
Arg Tyr Glu Arg Asn Ile Glu Lys Ile Ser Met Leu Glu Lys Ile Tyr
        435                 440                 445
Ile His Pro Arg Tyr Asn Trp Arg Glu Asn Leu Asp Arg Asp Ile Ala
    450                 455                 460
Leu Met Lys Leu Lys Lys Pro Val Ala Phe Ser Asp Tyr Ile His Pro
465                 470                 475                 480
Val Cys Leu Pro Asp Arg Glu Thr Ala Ala Ser Leu Leu Gln Ala Gly
                485                 490                 495
Tyr Lys Gly Arg Val Thr Gly Trp Gly Asn Leu Lys Glu Thr Trp Thr
            500                 505                 510
Ala Asn Val Gly Lys Gly Gln Pro Ser Val Leu Gln Val Val Asn Leu
        515                 520                 525
Pro Ile Val Glu Arg Pro Val Cys Lys Asp Ser Thr Arg Ile Arg Ile
    530                 535                 540
Thr Asp Asn Met Phe Cys Ala Gly Tyr Lys Pro Asp Glu Gly Lys Arg
545                 550                 555                 560
Gly Asp Ala Cys Glu Gly Asp Ser Gly Gly Pro Phe Val Met Lys Ser
```

```
                565                 570                 575
Pro Phe Asn Asn Arg Trp Tyr Gln Met Gly Ile Val Ser Trp Gly Glu
            580                 585                 590
Gly Cys Asp Arg Asp Gly Lys Tyr Gly Phe Tyr Thr His Val Phe Arg
        595                 600                 605
Leu Lys Lys Trp Ile Gln Lys Val Ile Asp Gln Phe Gly Glu
    610                 615                 620
```

<210> 180
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<223> protein C (activated)

<400> 180
ctgcaggggg ggggggggag gggggctgtc atggcggcag gacggcgaac ttgcagtatc 60
tccacgaccc gcccctacag gtgccagtgc ctccagaatg tggcagctca caagcctcct 120
gctgttcgtg gccacctggg gaatttccgg cacaccagct cctcttgact cagtgttctc 180
cagcagcgag cgtgcccacc aggtgctgcg gatccgcaaa cgtgccaact ccttcctgga 240
ggagctccgt cacagcagcc tggagcggga gtgcatagag gagatctgtg acttcgagga 300
ggccaaggaa attttccaaa atgtggatga cacactggcc ttctggtcca agcacgtcga 360
cggtgaccag tgcttggtct tgcccttgga gcacccgtgc gccagcctgt gctgcgggca 420
cggcacgtgc atcgacggca tcggcagctt cagctgcgac tgccgcagcg gctgggaggg 480
ccgcttctgc cagcgcgagg tgagcttcct caattgctcg ctggacaacg gcggctgcac 540
gcattactgc ctagaggagg tgggctggcg gcgctgtagc tgtgcgcctg gctacaagct 600
gggggacgac ctcctgcagt gtcaccccgc agtgaagttc ccttgtggga ggccctggaa 660
gcggatggag aagaagcgca gtcacctgaa acgagacaca gaagaccaag aagaccaagt 720
agatccgcgg ctcattgatg ggaagatgac caggcgggga gacagcccct ggcaggtggt 780
cctgctggac tcaaagaaga agctggcctg cggggcagtg ctcatccacc cctcctgggt 840
gctgacagcg gcccactgca tggatgagtc caagaagctc cttgtcaggc ttggagagta 900
tgacctgcgg cgctgggaga agtgggagct ggacctggac atcaaggagg tcttcgtcca 960
ccccaactac agcaagagca ccaccgacaa tgacatcgca ctgctgcacc tggcccagcc 1020
cgccaccctc tcgcagacca tagtgcccat ctgcctcccg gacagcggcc ttgcagagcg 1080
cgagctcaat caggccggcc aggagaccct cgtgacgggc tggggctacc acagcagccg 1140
agagaaggag gccaagagaa accgcacctt cgtcctcaac ttcatcaaga ttcccgtggt 1200
cccgcacaat gagtgcagcg aggtcatgag caacatggtg tctgagaaca tgctgtgtgc 1260
gggcatcctc ggggaccggc aggatgcctg cgagggcgac agtggggggc ccatggtcgc 1320
ctccttccac ggcacctggt tcctggtggg cctggtgagc tggggtgagg gctgtgggct 1380
ccttcacaac tacggcgttt acaccaaagt cagccgctac ctcgactgga tccatgggca 1440
catcagagac aaggaagccc cccagaagag ctgggcacct tagcgaccct ccctgcaggg 1500
ctgggctttt gcatggcaat ggatgggaca ttaaagggac atgtaacaag cacaccggcc 1560
tgctgttctg tccttccatc cctcttttgg gctcttctgg agggaagtaa catttactga 1620
gcacctgttg tatgtcacat gccttatgaa tagaatctta actcctagag caactctgtg 1680
gggtggggag gagcagatcc aagttttgcg gggtctaaag ctgtgtgtgt tgaggggat 1740
actctgttta tgaaaaagaa taaaaaacac aaccacgaaa aaaaaaaaaa aaaaaaaaaa 1800
aaaaaaaaaa aaaaaaaccc ccccccgccc ccccccccctg cag 1843

<210> 181
<211> 461
<212> PRT
<213> Homo sapiens

<220>
<223> protein C (activated)

<400> 181
Met Trp Gln Leu Thr Ser Leu Leu Leu Phe Val Ala Thr Trp Gly Ile
1 5 10 15
Ser Gly Thr Pro Ala Pro Leu Asp Ser Val Phe Ser Ser Ser Glu Arg
20 25 30
Ala His Gln Val Leu Arg Ile Arg Lys Arg Ala Asn Ser Phe Leu Glu
35 40 45
Glu Leu Arg His Ser Ser Leu Glu Arg Glu Cys Ile Glu Glu Ile Cys
50 55 60
Asp Phe Glu Glu Ala Lys Glu Ile Phe Gln Asn Val Asp Asp Thr Leu
65 70 75 80
Ala Phe Trp Ser Lys His Val Asp Gly Asp Gln Cys Leu Val Leu Pro
85 90 95
Leu Glu His Pro Cys Ala Ser Leu Cys Cys Gly His Gly Thr Cys Ile
100 105 110
Asp Gly Ile Gly Ser Phe Ser Cys Asp Cys Arg Ser Gly Trp Glu Gly
115 120 125
Arg Phe Cys Gln Arg Glu Val Ser Phe Leu Asn Cys Ser Leu Asp Asn
130 135 140
Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg Cys
145 150 155 160
Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys His
165 170 175
Pro Ala Val Lys Phe Pro Cys Gly Arg Pro Trp Lys Arg Met Glu Lys
180 185 190
Lys Arg Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val
195 200 205
Asp Pro Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro
210 215 220
Trp Gln Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala
225 230 235 240
Val Leu Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp
245 250 255
Glu Ser Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg
260 265 270
Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His
275 280 285
Pro Asn Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His
290 295 300
Leu Ala Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu
305 310 315 320
Pro Asp Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu
325 330 335
Thr Leu Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala
340 345 350
Lys Arg Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val
355 360 365
Pro His Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn
370 375 380
Met Leu Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly
385 390 395 400
Asp Ser Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu
405 410 415
Val Gly Leu Val Ser Trp Gly Glu Gly Cys Gly Leu Leu His Asn Tyr
420 425 430

```
Gly Val Tyr Thr Lys Val Ser Arg Tyr Leu Asp Trp Ile His Gly His
        435                 440                 445
Ile Arg Asp Lys Glu Ala Pro Gln Lys Ser Trp Ala Pro
    450                 455                 460
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<210> 182
<211> 1388
<212> DNA
<213> Homo sapiens

<220>
<223> Acrosin

<400> 182

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caggcagtgc aggagtatgg ttgagatgct accaactgcc attctgctgg tcttggcagt 60
gtccgtggtt gctaaagata acgccacgtg tgatggcccc tgtgggttac ggttcaggca 120
aaacccacag ggtggtgtcc gcatcgtcgg cgggaaggct gcacagcatg gggcctggcc 180
ctggatggtc agcctccaga tcttcacgta caacagccac aggtaccaca catgtggagg 240
cagcttgctg aattcacgat gggtgctcac tgctgctcac tgcttcgtcg gcaaaaataa 300
tgtgcatgac tggagactgg ttttcggagc aaaggaaatt acatatggga acaataaacc 360
agtaaaggcg cctgtgcaag agagatatgt ggagaaaatc atcattcatg aaaaatacaa 420
ctctgcgaca gagggaaatg acattgccct cgtggagatc acccctccca tttcgtgtgg 480
gcgcttcatt gggccgggct gcctgcccca cttgaaggca ggcctcccca gaggctccca 540
gagctgctgg gtggccggct ggggatatat agaagagaaa gcccccaggc catcatctat 600
actgatggag gcacgtgtgg atctcatcga cctggacttg tgtaactcga cccagtggta 660
caatgggcgc gttcagccaa ccaatgtgtg cgcggggtat cctgtaggca agatcgacac 720
ctgccaggga gacagcggcg ggcctctcat gtgcaaagac agcaaggaaa gcgcctatgt 780
ggtcgtggga atcacaagct gggggggtagg ctgtgcccgt gccaagcgcc ccggaatcta 840
cacggccacc tggccttatc tgaactggat cgcctccaag attggttcta acgctttgcg 900
tatgattcaa tcggccaccc ctccaccgcc caccactcga ccgcccccga ttcgaccccc 960
cttctcccac cctatctctg ctcaccttcc ttggtatttc caaccgcccc ctcgaccact 1020
tccaccccga ccaccggcag cccagccccg acccccacct tcaccccccgc ccccaccccc 1080
acctccagcc tcacctttac ccccaccccc acccccaccc ccacctacac cctcatctac 1140
cacaaaactt ccccaaggac tttcttttgc caagcgccta cagcagctca tagaggtctt 1200
gaaggggaag acctattccg acggaaagaa ccattatgac atggagacca cagagctccc 1260
agaactgacc tcgacctcct gatctgacct ggttctcaac agacccagtg agcccttcac 1320
tcctgagaaa aaggaaagat gaaataaata aataaacata tatatataga tataaaaaaa 1380
aaaaaaaa                                                        1388
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<210> 183
<211> 421
<212> PRT
<213> Homo sapiens

<220>
<223> Acrosin

<400> 183

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Met Val Glu Met Leu Pro Thr Ala Ile Leu Leu Val Leu Ala Val Ser
 1               5                  10                  15
Val Val Ala Lys Asp Asn Ala Thr Cys Asp Gly Pro Cys Gly Leu Arg
            20                  25                  30
Phe Arg Gln Asn Pro Gln Gly Gly Val Arg Ile Val Gly Gly Lys Ala
        35                  40                  45
Ala Gln His Gly Ala Trp Pro Trp Met Val Ser Leu Gln Ile Phe Thr
    50                  55                  60
```

```
Tyr Asn Ser His Arg Tyr His Thr Cys Gly Gly Ser Leu Leu Asn Ser
65                  70                  75                  80
Arg Trp Val Leu Thr Ala Ala His Cys Phe Val Gly Lys Asn Asn Val
                85                  90                  95
His Asp Trp Arg Leu Val Phe Gly Ala Lys Glu Ile Thr Tyr Gly Asn
            100                 105                 110
Asn Lys Pro Val Lys Ala Pro Val Gln Glu Arg Tyr Val Glu Lys Ile
        115                 120                 125
Ile Ile His Glu Lys Tyr Asn Ser Ala Thr Glu Gly Asn Asp Ile Ala
    130                 135                 140
Leu Val Glu Ile Thr Pro Pro Ile Ser Cys Gly Arg Phe Ile Gly Pro
145                 150                 155                 160
Gly Cys Leu Pro His Leu Lys Ala Gly Leu Pro Arg Gly Ser Gln Ser
                165                 170                 175
Cys Trp Val Ala Gly Trp Gly Tyr Ile Glu Glu Lys Ala Pro Arg Pro
            180                 185                 190
Ser Ser Ile Leu Met Glu Ala Arg Val Asp Leu Ile Asp Leu Asp Leu
        195                 200                 205
Cys Asn Ser Thr Gln Trp Tyr Asn Gly Arg Val Gln Pro Thr Asn Val
    210                 215                 220
Cys Ala Gly Tyr Pro Val Gly Lys Ile Asp Thr Cys Gln Gly Asp Ser
225                 230                 235                 240
Gly Gly Pro Leu Met Cys Lys Asp Ser Lys Glu Ser Ala Tyr Val Val
                245                 250                 255
Val Gly Ile Thr Ser Trp Gly Val Gly Cys Ala Arg Ala Lys Arg Pro
            260                 265                 270
Gly Ile Tyr Thr Ala Thr Trp Pro Tyr Leu Asn Trp Ile Ala Ser Lys
        275                 280                 285
Ile Gly Ser Asn Ala Leu Arg Met Ile Gln Ser Ala Thr Pro Pro Pro
    290                 295                 300
Pro Thr Thr Arg Pro Pro Pro Ile Arg Pro Pro Phe Ser His Pro Ile
305                 310                 315                 320
Ser Ala His Leu Pro Trp Tyr Phe Gln Pro Pro Pro Arg Pro Leu Pro
                325                 330                 335
Pro Arg Pro Pro Ala Ala Gln Pro Arg Pro Pro Pro Ser Pro Pro Pro
            340                 345                 350

Pro Pro Pro Pro Pro Ala Ser Pro Leu Pro Pro Pro Pro Pro Pro Pro
        355                 360                 365
Pro Pro Thr Pro Ser Ser Thr Thr Lys Leu Pro Gln Gly Leu Ser Phe
    370                 375                 380
Ala Lys Arg Leu Gln Gln Leu Ile Glu Val Leu Lys Gly Lys Thr Tyr
385                 390                 395                 400
Ser Asp Gly Lys Asn His Tyr Asp Met Glu Thr Thr Glu Leu Pro Glu
                405                 410                 415
Leu Thr Ser Thr Ser
            420
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<210> 184
<211> 2363
<212> DNA
<213> Homo sapiens

<220>
<223> Hepsin transcript variant 1

<400> 184
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<210> 185
<211> 417
<212> PRT
<213> Homo sapiens

<220>
<223> Hepsin

<400> 185
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Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala Ile
            20   25   30
Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
        35   40   45

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Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
    50                  55                  60
Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
65                  70                  75                  80
Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
                85                  90                  95
Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
            100                 105                 110
Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
        115                 120                 125
Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
    130                 135                 140
Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
145                 150                 155                 160
Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
                165                 170                 175
Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
            180                 185                 190
Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
        195                 200                 205
Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
    210                 215                 220
Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
225                 230                 235                 240
Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
                245                 250                 255
Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
            260                 265                 270
Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
        275                 280                 285
Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
    290                 295                 300
Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
305                 310                 315                 320
Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met
                325                 330                 335
Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
            340                 345                 350
Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
        355                 360                 365
Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
    370                 375                 380
Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
385                 390                 395                 400
Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
                405                 410                 415
Leu
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<210> 186
<211> 1783
<212> DNA
<213> Homo sapiens

<220>
<223> Hepsin transcript variant 2

<400> 186

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tggaccccag ggtcccaccc tggcccagga ggtcagccag ggaatcatta acaagaggca 240
gtgacatggc gcagaaggag ggtggccgga ctgtgccatg ctgctccaga cccaaggtgg 300
cagctctcac tgcggggacc ctgctacttc tgacagccat cggggcggca tcctgggcca 360
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cggacgctcg gctcatggtc tttgacaaga cggaagggac gtggcggctg ctgtgctcct 480
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ctgatgatgg gatgctcttt aaataataaa gatggttttg att 1783

<210> 187
<211> 417
<212> PRT
<213> Homo sapiens

<220>
<223> Hepsin

<400> 187
Met Ala Gln Lys Glu Gly Gly Arg Thr Val Pro Cys Cys Ser Arg Pro
 1   5   10   15
Lys Val Ala Ala Leu Thr Ala Gly Thr Leu Leu Leu Leu Thr Ala Ile
            20   25   30
Gly Ala Ala Ser Trp Ala Ile Val Ala Val Leu Leu Arg Ser Asp Gln
        35   40   45
Glu Pro Leu Tyr Pro Val Gln Val Ser Ser Ala Asp Ala Arg Leu Met
    50   55   60
Val Phe Asp Lys Thr Glu Gly Thr Trp Arg Leu Leu Cys Ser Ser Arg
65   70   75   80
Ser Asn Ala Arg Val Ala Gly Leu Ser Cys Glu Glu Met Gly Phe Leu
                85   90   95
Arg Ala Leu Thr His Ser Glu Leu Asp Val Arg Thr Ala Gly Ala Asn
            100   105   110

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Gly Thr Ser Gly Phe Phe Cys Val Asp Glu Gly Arg Leu Pro His Thr
        115                 120                 125
Gln Arg Leu Leu Glu Val Ile Ser Val Cys Asp Cys Pro Arg Gly Arg
    130                 135                 140
Phe Leu Ala Ala Ile Cys Gln Asp Cys Gly Arg Arg Lys Leu Pro Val
145                 150                 155                 160
Asp Arg Ile Val Gly Gly Arg Asp Thr Ser Leu Gly Arg Trp Pro Trp
                165                 170                 175
Gln Val Ser Leu Arg Tyr Asp Gly Ala His Leu Cys Gly Gly Ser Leu
            180                 185                 190
Leu Ser Gly Asp Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg
        195                 200                 205
Asn Arg Val Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln
    210                 215                 220
Ala Ser Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His
225                 230                 235                 240
Gly Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
                245                 250                 255
Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu Tyr
            260                 265                 270
Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val Asp Gly
        275                 280                 285
Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr Tyr Gly Gln
    290                 295                 300
Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile Ile Ser Asn Asp
305                 310                 315                 320
Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln Ile Lys Pro Lys Met
                325                 330                 335
Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile Asp Ala Cys Gln Gly Asp
            340                 345                 350
Ser Gly Gly Pro Phe Val Cys Glu Asp Ser Ile Ser Arg Thr Pro Arg
        355                 360                 365
Trp Arg Leu Cys Gly Ile Val Ser Trp Gly Thr Gly Cys Ala Leu Ala
    370                 375                 380
Gln Lys Pro Gly Val Tyr Thr Lys Val Ser Asp Phe Arg Glu Trp Ile
385                 390                 395                 400
Phe Gln Ala Ile Lys Thr His Ser Glu Ala Ser Gly Met Val Thr Gln
                405                 410                 415
Leu
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<210> 188
<211> 2038
<212> DNA
<213> Homo sapiens

<220>
<223> hepatocyte growth factor activator

<400> 188
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agtgggggggc tcccgccccc gcccagggca gttccctcga gcagtagccc ccaggcccaa 300
gcactcaccg aggacgggag gccctgcagg ttccccttcc gctacggggg ccgcatgctg 360
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gccctggatc cctgtgcctc cggcccctgc ctcaatggag gctcctgctc caatacccag 540
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gggacaccct ggttcccacc attcctgcc ttgctgacaa taaagatatt tccaagaa   2038
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<210> 189
<211> 655
<212> PRT
<213> Homo sapiens

<220>
<223> hepatocyte growth factor activator

<400> 189

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Met Gly Arg Trp Ala Trp Val Pro Ser Pro Trp Pro Pro Pro Gly Leu
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Gly Pro Phe Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro Arg Gly
            20                  25                  30
Phe Gln Pro Gln Pro Gly Gly Asn Arg Thr Glu Ser Pro Glu Pro Asn
        35                  40                  45
Ala Thr Ala Thr Pro Ala Ile Pro Thr Ile Leu Val Thr Ser Val Thr
    50                  55                  60
Ser Glu Thr Pro Ala Thr Ser Ala Pro Glu Ala Glu Gly Pro Gln Ser
65                  70                  75                  80
Gly Gly Leu Pro Pro Pro Pro Arg Ala Val Pro Ser Ser Ser Ser Pro
                85                  90                  95
Gln Ala Gln Ala Leu Thr Glu Asp Gly Arg Pro Cys Arg Phe Pro Phe
            100                 105                 110
Arg Tyr Gly Gly Arg Met Leu His Ala Cys Thr Ser Glu Gly Ser Ala
        115                 120                 125
His Arg Lys Trp Cys Ala Thr Thr His Asn Tyr Asp Arg Asp Arg Ala
    130                 135                 140
Trp Gly Tyr Cys Val Glu Ala Thr Pro Pro Pro Gly Gly Pro Ala Ala
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145                 150                 155                 160
Leu Asp Pro Cys Ala Ser Gly Pro Cys Leu Asn Gly Gly Ser Cys Ser
                165                 170                 175
Asn Thr Gln Asp Pro Gln Ser Tyr His Cys Ser Cys Pro Arg Ala Phe
            180                 185                 190
Thr Gly Lys Asp Cys Gly Thr Glu Lys Cys Phe Asp Glu Thr Arg Tyr
        195                 200                 205
Glu Tyr Leu Glu Gly Gly Asp Arg Trp Ala Arg Val Arg Gln Gly His
    210                 215                 220
Val Glu Gln Cys Glu Cys Phe Gly Gly Arg Thr Trp Cys Glu Gly Thr
225                 230                 235                 240
Arg His Thr Ala Cys Leu Ser Ser Pro Cys Leu Asn Gly Gly Thr Cys
                245                 250                 255
His Leu Ile Val Ala Thr Gly Thr Thr Val Cys Ala Cys Pro Pro Gly
            260                 265                 270
Phe Ala Gly Arg Leu Cys Asn Ile Glu Pro Asp Glu Arg Cys Phe Leu
        275                 280                 285
Gly Asn Gly Thr Gly Tyr Arg Gly Val Ala Ser Thr Ser Ala Ser Gly
    290                 295                 300
Leu Ser Cys Leu Ala Trp Asn Ser Asp Leu Leu Tyr Gln Glu Leu His
305                 310                 315                 320
Val Asp Ser Val Gly Ala Ala Ala Leu Leu Gly Leu Gly Pro His Ala

                325                 330                 335
Tyr Cys Arg Asn Pro Asp Asn Asp Glu Arg Pro Trp Cys Tyr Val Val
            340                 345                 350
Lys Asp Ser Ala Leu Ser Trp Glu Tyr Cys Arg Leu Glu Ala Cys Glu
        355                 360                 365
Ser Leu Thr Arg Val Gln Leu Ser Pro Asp Leu Leu Ala Thr Leu Pro
    370                 375                 380
Glu Pro Ala Ser Pro Gly Arg Gln Ala Cys Gly Arg Arg His Lys Lys
385                 390                 395                 400
Arg Thr Phe Leu Arg Pro Arg Ile Ile Gly Gly Ser Ser Ser Leu Pro
                405                 410                 415
Gly Ser His Pro Trp Leu Ala Ala Ile Tyr Ile Gly Asp Ser Phe Cys
            420                 425                 430
Ala Gly Ser Leu Val His Thr Cys Trp Val Val Ser Ala Ala His Cys
        435                 440                 445
Phe Ser His Ser Pro Pro Arg Asp Ser Val Ser Val Val Leu Gly Gln
    450                 455                 460
His Phe Phe Asn Arg Thr Thr Asp Val Thr Gln Thr Phe Gly Ile Glu
465                 470                 475                 480
Lys Tyr Ile Pro Tyr Thr Leu Tyr Ser Val Phe Asn Pro Ser Asp His
                485                 490                 495
Asp Leu Val Leu Ile Arg Leu Lys Lys Lys Gly Asp Arg Cys Ala Thr
            500                 505                 510
Arg Ser Gln Phe Val Gln Pro Ile Cys Leu Pro Glu Pro Gly Ser Thr
        515                 520                 525
Phe Pro Ala Gly His Lys Cys Gln Ile Ala Gly Trp Gly His Leu Asp
    530                 535                 540
Glu Asn Val Ser Gly Tyr Ser Ser Ser Leu Arg Glu Ala Leu Val Pro
545                 550                 555                 560
Leu Val Ala Asp His Lys Cys Ser Ser Pro Glu Val Tyr Gly Ala Asp
                565                 570                 575
Ile Ser Pro Asn Met Leu Cys Ala Gly Tyr Phe Asp Cys Lys Ser Asp
            580                 585                 590
Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Ala Cys Glu Lys Asn Gly
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        595                 600                 605
Val Ala Tyr Leu Tyr Gly Ile Ile Ser Trp Gly Asp Gly Cys Gly Arg
    610                 615                 620
Leu His Lys Pro Gly Val Tyr Thr Arg Val Ala Asn Tyr Val Asp Trp
625                 630                 635                 640
Ile Asn Asp Arg Ile Arg Pro Pro Arg Arg Leu Val Ala Pro Ser
                645                 650                 655
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<210> 190
<211> 2360
<212> DNA
<213> Homo sapiens

<220>
<223> u-plasminogen activator (uPA)

<400> 190

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caatgaactt catcaagttc catcgaactg tgactgtcta aatggaggaa catgtgtgtc 240
caacaagtac ttctccaaca ttcactggtg caactgccca aagaaattcg gagggcagca 300
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ggccagcact gacaccatgg gccggccctg cctgccctgg aactctgcca ctgtccttca 420
gcaaacgtac catgcccaca gatctgatgc tcttcagctg ggcctgggga aacataatta 480
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agaagaatta aaatttcagt gtggccaaaa gactctgagg ccccgcttta agattattgg 660
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acgtgacagt gcctgggaat gtattattct gcagcatgac ctgtgaccag cactgtctca 2160
gtttcacttt cacatagatg tccctttctt ggccagttat cccttccttt tagcctagtt 2220
catccaatcc tcactgggtg gggtgaggac cactcctgta cactgaatat ttatatttca 2280
ctatttttat ttatattttt gtaattttaa ataaaagtga tcaataaaat gtgatttttc 2340
```

tgatgaaaaa aaaaaaaaaa 2360

<210> 191
<211> 431
<212> PRT
<213> Homo sapiens

<220>
<223> u-plasminogen activator (uPA)

<400> 191
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20 25 30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35 40 45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50 55 60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65 70 75 80
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85 90 95
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
130 135 140
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
260 265 270
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
275 280 285
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
290 295 300
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
305 310 315 320
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
325 330 335
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
340 345 350
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
355 360 365

```
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
    370                 375                 380
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
385                 390                 395                 400
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
                405                 410                 415
Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
            420                 425                 430
```

<210> 192
<211> 2653
<212> DNA
<213> Homo sapiens

<220>
<223> t-plasminogen activator (tPA) transcript variant 1

<400> 192

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accccacccc ctgcctggaa acttaaggag gccggagctg tggggagctc agagctgaga 120
tcctacagga gtccagggct ggagagaaaa cctctgcgag gaaagggaag gagcaagccg 180
tgaatttaag ggacgctgtg aagcaatcat ggatgcaatg aagagagggc tctgctgtgt 240
gctgctgctg tgtggagcag tcttcgtttc gcccagccag gaaatccatg cccgattcag 300
aagaggagcc agatcttacc aagtgatctg cagagatgaa aaaacgcaga tgatatacca 360
gcaacatcag tcatggctgc gccctgtgct cagaagcaac cgggtggaat attgctggtg 420
caacagtggc agggcacagt gccactcagt gcctgtcaaa agttgcagcg agccaaggtg 480
tttcaacggg ggcacctgcc agcaggccct gtacttctca gatttcgtgt gccagtgccc 540
cgaaggattt gctgggaagt gctgtgaaat agataccagg gccacgtgct acgaggacca 600
gggcatcagc tacaggggca cgtggagcac agcggagagt ggcgccgagt gcaccaactg 660
gaacagcagc gcgttggccc agaagcccta cagcgggcgg aggccagacg ccatcaggct 720
gggcctgggg aaccacaact actgcagaaa cccagatcga gactcaaagc cctggtgcta 780
cgtctttaag gcggggaagt acagctcaga gttctgcagc acccctgcct gctctgaggg 840
aaacagtgac tgctactttg ggaatgggtc agcctaccgt ggcacgcaca gcctcaccga 900
gtcgggtgcc tcctgcctcc cgtggaattc catgatcctg ataggcaagg tttacacagc 960
acagaacccc agtgcccagg cactgggcct gggcaaacat aattactgcc ggaatcctga 1020
tggggatgcc aagccctggt gccacgtgct gaagaaccgc aggctgacgt gggagtactg 1080
tgatgtgccc tcctgctcca cctgcggcct gagacagtac agccagcctc agtttcgcat 1140
caaaggaggg ctcttcgccg acatcgcctc ccacccctgg caggctgcca tctttgccaa 1200
gcacaggagg tcgcccggag agcggttcct gtgcgggggc atactcatca gctcctgctg 1260
gattctctct gccgcccact gcttccagga gaggtttccg ccccaccacc tgacggtgat 1320
cttgggcaga acataccggg tggtccctgg cgaggaggag cagaaatttg aagtcgaaaa 1380
atacattgtc cataaggaat tcgatgatga cacttacgac aatgacattg cgctgctgca 1440
gctgaaatcg gattcgtccc gctgtgccca ggagagcagc gtggtccgca ctgtgtgcct 1500
tcccccggcg gacctgcagc tgccggactg gacggagtgt gagctctccg gctacggcaa 1560
gcatgaggcc ttgtctcctt tctattcgga gcggctgaag gaggctcatg tcagactgta 1620
cccatccagc cgctgcacat cacaacattt acttaacaga acagtcaccg acaacatgct 1680
gtgtgctgga gacactcgga gcggcgggcc ccaggcaaac ttgcacgacg cctgccaggg 1740
cgattcggga ggccccctgg tgtgtctgaa cgatggccgc atgactttgg tgggcatcat 1800
cagctggggc ctgggctgtg gacagaagga tgtcccgggt gtgtacacca aggttaccaa 1860
ctacctagac tggattcgtg acaacatgcg accgtgacca ggaacacccg actcctcaaa 1920
agcaaatgag atcccgcctc ttcttcttca gaagacactg caaaggcgca gtgcttctct 1980
acagacttct ccagacccac cacaccgcag aagcgggacg agaccctaca ggagagggaa 2040
gagtgcattt tcccagatac ttcccatttt ggaagttttc aggacttggt ctgatttcag 2100
gatactctgt cagatgggaa gacatgaatg cacactagcc tctccaggaa tgcctcctcc 2160
ctgggcagaa agtggccatg ccaccctgtt ttcagctaaa gcccaacctc ctgacctgtc 2220
accgtgagca gctttggaaa caggaccaca aaaatgaaag catgtctcaa tagtaaaaga 2280
```

taacaagatc tttcaggaaa gacggattgc attagaaata gacagtatat ttatagtcac 2340
aagagcccag cagggcctca aagttggggc aggctggctg gcccgtcatg ttcctcaaaa 2400
gcacccttga cgtcaagtct ccttcccctt tccccactcc ctggctctca gaaggtattc 2460
cttttgtgta cagtgtgtaa agtgtaaatc ctttttcttt ataaacttta gagtagcatg 2520
agagaattgt atcatttgaa caactaggct tcagcatatt tatagcaatc catgttagtt 2580
tttactttct gttgccacaa ccctgtttta tactgtactt aataaattca gatatatttt 2640
tcacagtttt tcc 2653

<210> 193
<211> 562
<212> PRT
<213> Homo sapiens

<220>
<223> t-plasminogen activator (tPA) isoform 1

<400> 193
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35 40 45
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50 55 60
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
85 90 95
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
100 105 110
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
115 120 125
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
130 135 140
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145 150 155 160
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
165 170 175
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
180 185 190
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
195 200 205
Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
210 215 220
Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225 230 235 240
Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
245 250 255
Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
260 265 270
Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
275 280 285
Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr
290 295 300
Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala
305 310 315 320

```
Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro
                325                 330                 335
Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile
            340                 345                 350
Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
        355                 360                 365
Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
    370                 375                 380
Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
385                 390                 395                 400
Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
                405                 410                 415
Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
            420                 425                 430
Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
        435                 440                 445
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
    450                 455                 460
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
465                 470                 475                 480
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
                485                 490                 495
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
            500                 505                 510
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
        515                 520                 525
Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
    530                 535                 540
Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
545                 550                 555                 560
Arg Pro
```

<210> 194
<211> 2160
<212> DNA
<213> Homo sapiens

<220>
<223> t-plasminogen activator (tPA) transcript variant 2

<400> 194

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atggccctgt ccactgagca tcctcccgcc acacagaaac ccgcccagcc ggggccaccg 60
accccacccc ctgcctggaa acttaaggag gccggagctg tggggagctc agagctgaga 120
tcctacagga gtccagggct ggagagaaaa cctctgcgag gaaagggaag gagcaagccg 180
tgaatttaag ggacgctgtg aagcaatcat ggatgcaatg aagagagggc tctgctgtgt 240
gctgctgctg tgtggagcag tcttcgtttc gcccagccag gaaatccatg cccgattcag 300
aagaggagcc agatcttacc aagtgatctg cagagatgaa aaaacgcaga tgatatacca 360
gcaacatcag tcatggctgc gccctgtgct cagaagcaac cgggtggaat attgctggtg 420
caacagtggc agggcacagt gccactcagt gcctgtcaaa agttgcagcg agccaaggtg 480
tttcaacggg ggcacctgcc agcaggccct gtacttctca gatttcgtgt gccagtgccc 540
cgaaggattt gctgggaagt gctgtgaaat agataccagg gccacgtgct acgaggacca 600
gggcatcagc tacaggggca cgtggagcac agcggagagt ggcgccgagt gcaccaactg 660
gaacagcagc gcgttggccc agaagcccta cagcgggcgg aggccagacg ccatcaggct 720
gggcctgggg aaccacaact actgcagaaa cccagatcga gactcaaagc cctggtgcta 780
cgtctttaag gcggggaagt acagctcaga gttctgcagc acccctgcct gctctgaggg 840
```

```
aaacagtgac tgctactttg ggaatgggtc agcctaccgt ggcacgcaca gcctcaccga 900
gtcgggtgcc tcctgcctcc cgtggaattc catgatcctg ataggcaagg tttacacagc 960
acagaacccc agtgcccagg cactgggcct gggcaaacat aattactgcc ggactggacg 1020
gagtgtgagc tctccggcta cggcaagcat gaggccttgt ctcctttcta ttcggagcgg 1080
ctgaaggagg ctcatgtcag actgtaccca tccagccgct gcacatcaca acatttactt 1140
aacagaacag tcaccgacaa catgctgtgt gctggagaca ctcggagcgg cgggccccag 1200
gcaaacttgc acgacgcctg ccagggcgat tcgggaggcc ccctggtgtg tctgaacgat 1260
ggccgcatga ctttggtggg catcatcagc tggggcctgg gctgtggaca gaaggatgtc 1320
ccgggtgtgt acaccaaggt taccaactac ctagactgga ttcgtgacaa catgcgaccg 1380
tgaccaggaa cacccgactc ctcaaaagca aatgagatcc cgcctcttct tcttcagaag 1440
acactgcaaa ggcgcagtgc ttctctacag acttctccag acccaccaca ccgcagaagc 1500
gggacgagac cctacaggag agggaagagt gcattttccc agatacttcc cattttggaa 1560
gttttcagga cttggtctga tttcaggata ctctgtcaga tgggaagaca tgaatgcaca 1620
ctagcctctc caggaatgcc tcctccctgg gcagaaagtg gccatgccac cctgttttca 1680
gctaaagccc aacctcctga cctgtcaccg tgagcagctt tggaaacagg accacaaaaa 1740
tgaaagcatg tctcaatagt aaaagataac aagatctttc aggaaagacg gattgcatta 1800
gaaatagaca gtatatttat agtcacaaga gcccagcagg gcctcaaagt tggggcaggc 1860
tggctggccc gtcatgttcc tcaaaagcac ccttgacgtc aagtctcctt ccccctttccc 1920
cactccctgg ctctcagaag gtattccttt tgtgtacagt gtgtaaagtg taaatccttt 1980
ttctttataa actttagagt agcatgagag aattgtatca tttgaacaac taggcttcag 2040
catatttata gcaatccatg ttagttttta ctttctgttg ccacaaccct gttttatact 2100
gtacttaata aattcagata tatttttcac agtttttcca aaaaaaaaaa aaaaaaaaaa 2160
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<210> 195
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<223> t-plasminogen activator (tPA) isoform 2

<400> 195

```
Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1               5                  10                  15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
            20                  25                  30
Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
        35                  40                  45
Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
    50                  55                  60
Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65                  70                  75                  80
Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
                85                  90                  95
Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
            100                 105                 110
Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
        115                 120                 125
Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
    130                 135                 140
Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145                 150                 155                 160
Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
                165                 170                 175
Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
            180                 185                 190
```

```
Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
        195                 200                 205
Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
    210                 215                 220
Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225                 230                 235                 240
Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
                245                 250                 255
Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Thr Gly Arg Ser
            260                 265                 270
Val Ser Ser Pro Ala Thr Ala Ser Met Arg Pro Cys Leu Leu Ser Ile
        275                 280                 285
Arg Ser Gly
    290
```

<210> 196
<211> 2534
<212> DNA
<213> Homo sapiens

<220>
<223> t-plasminogen activator (tPA) transcript variant 3

<400> 196

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atggccctgt ccactgagca tcctcccgcc acacagaaac ccgcccagcc ggggccaccg 60
accccacccc ctgcctggaa acttaaggag gccggagctg tggggagctc agagctgaga 120
tcctacagga gtccagggct ggagagaaaa cctctgcgag gaaagggaag gagcaagccg 180
tgaatttaag ggacgctgtg aagcaatcat ggatgcaatg aagagagggc tctgctgtgt 240
gctgctgctg tgtggagcag tcttcgtttc gcccagccag gaaatccatg cccgattcag 300
aagaggagcc agatcttacc aaggttgcag cgagccaagg tgtttcaacg ggggcacctg 360
ccagcaggcc ctgtacttct cagatttcgt gtgccagtgc cccgaaggat ttgctgggaa 420
gtgctgtgaa atagatacca gggccacgtg ctacgaggac cagggcatca gctacagggg 480
cacgtggagc acagcggaga gtggcgccga gtgcaccaac tggaacagca gcgcgttggc 540
ccagaagccc tacagcgggc ggaggccaga cgccatcagg ctgggcctgg ggaaccacaa 600
ctactgcaga aacccagatc gagactcaaa gccctggtgc tacgtcttta aggcggggaa 660
gtacagctca gagttctgca gcacccctgc ctgctctgag ggaaacagtg actgctactt 720
tgggaatggg tcagcctacc gtggcacgca cagcctcacc gagtcgggtg cctcctgcct 780
cccgtggaat tccatgatcc tgataggcaa ggtttacaca gcacagaacc ccagtgccca 840
ggcactgggc ctgggcaaac ataattactg ccggaatcct gatggggatg ccaagccctg 900
gtgccacgtg ctgaagaacc gcaggctgac gtgggagtac tgtgatgtgc cctcctgctc 960
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cgacatcgcc tcccaccccc ggcaggctgc catctttgcc aagcacagga ggtcgcccgg 1080
agagcggttc ctgtgcgggg gcatactcat cagctcctgc tggattctct ctgccgccca 1140
ctgcttccag gagaggtttc cgccccacca cctgacggtg atcttgggca gaacataccg 1200
ggtggtccct ggcgaggagg agcagaaatt tgaagtcgaa aaatacattg tccataagga 1260
attcgatgat gacacttacg acaatgacat tgcgctgctg cagctgaaat cggattcgtc 1320
ccgctgtgcc caggagagca gcgtggtccg cactgtgtgc cttcccccgg cggacctgca 1380
gctgccggac tggacggagt gtgagctctc cggctacggc aagcatgagg ccttgtctcc 1440
tttctattcg gagcggctga aggaggctca tgtcagactg tacccatcca gccgctgcac 1500
atcacaacat ttacttaaca gaacagtcac cgacaacatg ctgtgtgctg gagacactcg 1560
gagcggcggg ccccaggcaa acttgcacga cgcctgccag ggcgattcgg gaggcccccc 1620
ggtgtgtctg aacgatggcc gcatgacttt ggtgggcatc atcagctggg gcctgggctg 1680
tggacagaag gatgtcccgg gtgtgtacac caaggttacc aactacctag actggattcg 1740
tgacaacatg cgaccgtgac caggaacacc cgactcctca aaagcaaatg agatcccgcc 1800
tcttcttctt cagaagacac tgcaaaggcg cagtgcttct ctacagactt ctccagaccc 1860
accacaccgc agaagcggga cgagacccta caggagaggg aagagtgcat tttcccagat 1920
```

```
acttcccatt ttggaagttt tcaggacttg gtctgatttc aggatactct gtcagatggg 1980
aagacatgaa tgcacactag cctctccagg aatgcctcct ccctgggcag aaagtggcca 2040
tgccaccctg ttttcagcta aagcccaacc tcctgacctg tcaccgtgag cagctttgga 2100
aacaggacca caaaaatgaa agcatgtctc aatagtaaaa gataacaaga tctttcagga 2160
aagacggatt gcattagaaa tagacagtat atttatagtc acaagagccc agcagggcct 2220
caaagttggg gcaggctggc tggcccgtca tgttcctcaa aagcaccctt gacgtcaagt 2280
ctccttcccc tttccccact ccctggctct cagaaggtat tccttttgtg tacagtgtgt 2340
aaagtgtaaa tccttttttct ttataaactt tagagtagca tgagagaatt gtatcatttg 2400
aacaactagg cttcagcata tttatagcaa tccatgttag tttttacttt ctgttgccac 2460
aaccctgttt tatactgtac ttaataaatt cagatatatt tttcacagtt tttccaaaaa 2520
aaaaaaaaaa aaaa                                                   2534
```

<210> 197
<211> 516
<212> PRT
<213> Homo sapiens

<220>
<223> t-plasminogen activator (tPA) isoform 3

<400> 197

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1               5                  10                  15
Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
            20                  25                  30
Gly Ala Arg Ser Tyr Gln Gly Cys Ser Glu Pro Arg Cys Phe Asn Gly
        35                  40                  45
Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys
    50                  55                  60
Pro Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr
65                  70                  75                  80
Cys Tyr Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala
                85                  90                  95
Glu Ser Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln
            100                 105                 110
Lys Pro Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly
        115                 120                 125
Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys
    130                 135                 140
Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro
145                 150                 155                 160
Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala
                165                 170                 175
Tyr Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro
            180                 185                 190
Trp Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro
        195                 200                 205
Ser Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro
    210                 215                 220
Asp Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu
225                 230                 235                 240
Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg
                245                 250                 255
Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp
            260                 265                 270
Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg
        275                 280                 285
```

```
Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys
    290                 295                 300
Trp Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His
305                 310                 315                 320
His Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu
                325                 330                 335
Glu Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe
            340                 345                 350
Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser
        355                 360                 365
Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys
    370                 375                 380
Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu
385                 390                 395                 400
Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg
                405                 410                 415
Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser
            420                 425                 430
Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly
        435                 440                 445
Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln
    450                 455                 460
Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr
465                 470                 475                 480
Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val
                485                 490                 495
Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp
            500                 505                 510
Asn Met Arg Pro
        515
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<210> 198
<211> 2732
<212> DNA
<213> Homo sapiens

<220>
<223> Plasmin

<400> 198
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cataaggaag tggttcttct acttctttta tttctgaaat caggtcaagg agagcctctg 120
gatgactatg tgaataccca gggggcttca ctgttcagtg tcactaagaa gcagctggga 180
gcaggaagta tagaagaatg tgcagcaaaa tgtgaggagg acgaagaatt cacctgcagg 240
gcattccaat atcacagtaa agagcaacaa tgtgtgataa tggctgaaaa caggaagtcc 300
tccataatca ttaggatgag agatgtagtt ttatttgaaa agaaagtgta tctctcagag 360
tgcaagactg ggaatggaaa gaactacaga gggacgatgt ccaaaacaaa aaatggcatc 420
acctgtcaaa aatggagttc cacttctccc cacagaccta gattctcacc tgctacacac 480
ccctcagagg gactggagga gaactactgc aggaatccag acaacgatcc gcaggggccc 540
tggtgctata ctactgatcc agaaaagaga tatgactact gcgacattct tgagtgtgaa 600
gaggaatgta tgcattgcag tggagaaaac tatgacggca aaatttccaa gaccatgtct 660
ggactggaat gccaggcctg ggactctcag agcccacacg ctcatggata cattccttcc 720
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ccttggtgtt tcaccaccga ccccaacaag cgctgggaac tttgcgacat cccccgctgc 840
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tatcgcggga atgtggctgt taccgtttcc gggcacacct gtcagcactg gagtgcacag 960
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cggtgggagt actgtaagat accgtcctgt gactcctccc cagtatccac ggaacaattg 1140
gctcccacag caccacctga gctaacccct gtggtccagg actgctacca tggtgatgga 1200
cagagctacc gaggcacatc ctccaccacc accacaggaa agaagtgtca gtcttggtca 1260
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gaagacactg tccccagcta ccagctacgc caaacctcgg catttttgt gttattttct 2640
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acttaacttt gatttgagta aattttggtt tt                              2732
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<210> 199
<211> 810
<212> PRT
<213> Homo sapiens

<220>
<223> Plasmin

<400> 199

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 1               5                  10                  15
Gly Gln Gly Glu Pro Leu Asp Asp Tyr Val Asn Thr Gln Gly Ala Ser
            20                  25                  30
Leu Phe Ser Val Thr Lys Lys Gln Leu Gly Ala Gly Ser Ile Glu Glu
        35                  40                  45
Cys Ala Ala Lys Cys Glu Glu Asp Glu Glu Phe Thr Cys Arg Ala Phe
    50                  55                  60
Gln Tyr His Ser Lys Glu Gln Gln Cys Val Ile Met Ala Glu Asn Arg
65                  70                  75                  80
Lys Ser Ser Ile Ile Ile Arg Met Arg Asp Val Val Leu Phe Glu Lys
                85                  90                  95
Lys Val Tyr Leu Ser Glu Cys Lys Thr Gly Asn Gly Lys Asn Tyr Arg
            100                 105                 110
Gly Thr Met Ser Lys Thr Lys Asn Gly Ile Thr Cys Gln Lys Trp Ser
        115                 120                 125
Ser Thr Ser Pro His Arg Pro Arg Phe Ser Pro Ala Thr His Pro Ser
```

```
    130                 135                 140
Glu Gly Leu Glu Glu Asn Tyr Cys Arg Asn Pro Asp Asn Asp Pro Gln
145                 150                 155                 160
Gly Pro Trp Cys Tyr Thr Thr Asp Pro Glu Lys Arg Tyr Asp Tyr Cys
                165                 170                 175
Asp Ile Leu Glu Cys Glu Glu Glu Cys Met His Cys Ser Gly Glu Asn
            180                 185                 190
Tyr Asp Gly Lys Ile Ser Lys Thr Met Ser Gly Leu Glu Cys Gln Ala
        195                 200                 205
Trp Asp Ser Gln Ser Pro His Ala His Gly Tyr Ile Pro Ser Lys Phe
    210                 215                 220
Pro Asn Lys Asn Leu Lys Lys Asn Tyr Cys Arg Asn Pro Asp Arg Glu
225                 230                 235                 240
Leu Arg Pro Trp Cys Phe Thr Thr Asp Pro Asn Lys Arg Trp Glu Leu
                245                 250                 255
Cys Asp Ile Pro Arg Cys Thr Thr Pro Pro Pro Ser Ser Gly Pro Thr
            260                 265                 270
Tyr Gln Cys Leu Lys Gly Thr Gly Glu Asn Tyr Arg Gly Asn Val Ala
        275                 280                 285
Val Thr Val Ser Gly His Thr Cys Gln His Trp Ser Ala Gln Thr Pro
    290                 295                 300
His Thr His Asn Arg Thr Pro Glu Asn Phe Pro Cys Lys Asn Leu Asp
305                 310                 315                 320
Glu Asn Tyr Cys Arg Asn Pro Asp Gly Lys Arg Ala Pro Trp Cys His
                325                 330                 335
Thr Thr Asn Ser Gln Val Arg Trp Glu Tyr Cys Lys Ile Pro Ser Cys
            340                 345                 350
Asp Ser Ser Pro Val Ser Thr Glu Gln Leu Ala Pro Thr Ala Pro Pro
        355                 360                 365
Glu Leu Thr Pro Val Val Gln Asp Cys Tyr His Gly Asp Gly Gln Ser
    370                 375                 380
Tyr Arg Gly Thr Ser Ser Thr Thr Thr Thr Gly Lys Lys Cys Gln Ser
385                 390                 395                 400
Trp Ser Ser Met Thr Pro His Arg His Gln Lys Thr Pro Glu Asn Tyr
                405                 410                 415
Pro Asn Ala Gly Leu Thr Met Asn Tyr Cys Arg Asn Pro Asp Ala Asp
            420                 425                 430
Lys Gly Pro Trp Cys Phe Thr Thr Asp Pro Ser Val Arg Trp Glu Tyr
        435                 440                 445
Cys Asn Leu Lys Lys Cys Ser Gly Thr Glu Ala Ser Val Val Ala Pro
    450                 455                 460
Pro Pro Val Val Leu Leu Pro Asp Val Glu Thr Pro Ser Glu Glu Asp
465                 470                 475                 480
Cys Met Phe Gly Asn Gly Lys Gly Tyr Arg Gly Lys Arg Ala Thr Thr
                485                 490                 495
Val Thr Gly Thr Pro Cys Gln Asp Trp Ala Ala Gln Glu Pro His Arg
            500                 505                 510
His Ser Ile Phe Thr Pro Glu Thr Asn Pro Arg Ala Gly Leu Glu Lys
        515                 520                 525
Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Gly Gly Pro Trp Cys Tyr
    530                 535                 540
Thr Thr Asn Pro Arg Lys Leu Tyr Asp Tyr Cys Asp Val Pro Gln Cys
545                 550                 555                 560
Ala Ala Pro Ser Phe Asp Cys Gly Lys Pro Gln Val Glu Pro Lys Lys
                565                 570                 575
Cys Pro Gly Arg Val Val Gly Gly Cys Val Ala His Pro His Ser Trp
            580                 585                 590
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Pro Trp Gln Val Ser Leu Arg Thr Arg Phe Gly Met His Phe Cys Gly
        595                 600                 605
Gly Thr Leu Ile Ser Pro Glu Trp Val Leu Thr Ala Ala His Cys Leu
    610                 615                 620
Glu Lys Ser Pro Arg Pro Ser Ser Tyr Lys Val Ile Leu Gly Ala His
625                 630                 635                 640
Gln Glu Val Asn Leu Glu Pro His Val Gln Glu Ile Glu Val Ser Arg
                645                 650                 655
Leu Phe Leu Glu Pro Thr Arg Lys Asp Ile Ala Leu Leu Lys Leu Ser
            660                 665                 670
Ser Pro Ala Val Ile Thr Asp Lys Val Ile Pro Ala Cys Leu Pro Ser
        675                 680                 685
Pro Asn Tyr Val Val Ala Asp Arg Thr Glu Cys Phe Ile Thr Gly Trp
    690                 695                 700
Gly Glu Thr Gln Gly Thr Phe Gly Ala Gly Leu Leu Lys Glu Ala Gln
705                 710                 715                 720
Leu Pro Val Ile Glu Asn Lys Val Cys Asn Arg Tyr Glu Phe Leu Asn
                725                 730                 735
Gly Arg Val Gln Ser Thr Glu Leu Cys Ala Gly His Leu Ala Gly Gly
            740                 745                 750
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Phe Glu
        755                 760                 765
Lys Asp Lys Tyr Ile Leu Gln Gly Val Thr Ser Trp Gly Leu Gly Cys
    770                 775                 780
Ala Arg Pro Asn Lys Pro Gly Val Tyr Val Arg Val Ser Arg Phe Val
785                 790                 795                 800
Thr Trp Ile Glu Gly Val Met Arg Asn Asn
                805                 810
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<210> 200
<211> 1527
<212> DNA
<213> Homo sapiens

<220>
<223> Neurosin transcript variant A

<400> 200
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gcccggggca ggggcggggg ccagtgtggt gacacacgct gtagctgtct ccccggctgg 120
ctggctcgct ctctcctggg gacacagagg tcggcaggca gcacacagag ggacctacgg 180
gcagctgttc cttccccga ctcaagaatc cccggaggcc cggaggcctg cagcaggagc 240
ggccatgaag aagctgatgg tggtgctgag tctgattgct gcagcctggg cagaggagca 300
gaataagttg gtgcatggcg gaccctgcga caagacatct caccctacc aagctgccct 360
ctacacctcg ggccacttgc tctgtggtgg ggtccttatc catccactgt gggtcctcac 420
agctgcccac tgcaaaaaac cgaatcttca ggtcttcctg gggaagcata accttcggca 480
aagggagagt tcccaggagc agagttctgt tgtccgggct gtgatccacc ctgactatga 540
tgccgccagc catgaccagg acatcatgct gttgcgcctg gcacgcccag ccaaactctc 600
tgaactcatc cagccccttc ccctggagag ggactgctca gccaacacca ccagctgcca 660
catcctgggc tggggcaaga cagcagatgg tgatttccct gacaccatcc agtgtgcata 720
catccacctg gtgtcccgtg aggagtgtga gcatgcctac cctggccaga tcacccagaa 780
catgttgtgt gctggggatg agaagtacgg gaaggattcc tgccagggtg attctggggg 840
tccgctggta tgtggagacc acctccgagg ccttgtgtca tggggtaaca tcccctgtgg 900
atcaaaggag aagccaggag tctacaccaa cgtctgcaga tacacgaact ggatccaaaa 960
aaccattcag gccaagtgac cctgacatgt gacatctacc tcccgaccta ccaccccact 1020
ggctggttcc agaacgtctc tcacctagac cttgcctccc ctcctctcct gcccagctct 1080

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gaccctgatg cttaataaac gcagcgacgt gagggtcctg attctccctg gttttacccc 1140
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acccccacca ctaagagaat acaggaaaat cccttctagg catctcctct ccccaaccct 1260
tccacacgtt tgatttcttc ctgcagaggc ccagccacgt gtctggaatc ccagctccgc 1320
tgcttactgt cggtgtcccc ttgggatgta cctttcttca ctgcagattt ctcacctgta 1380
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attttattat gaaaaaaaaa aaaaaaa                                     1527
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<210> 201
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<223> Neurosin isoform A

<400> 201

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Met Lys Lys Leu Met Val Val Leu Ser Leu Ile Ala Ala Ala Trp Ala
 1               5                  10                  15
Glu Glu Gln Asn Lys Leu Val His Gly Gly Pro Cys Asp Lys Thr Ser
            20                  25                  30
His Pro Tyr Gln Ala Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly
        35                  40                  45
Gly Val Leu Ile His Pro Leu Trp Val Leu Thr Ala Ala His Cys Lys
    50                  55                  60
Lys Pro Asn Leu Gln Val Phe Leu Gly Lys His Asn Leu Arg Gln Arg
65                  70                  75                  80
Glu Ser Ser Gln Glu Gln Ser Ser Val Val Arg Ala Val Ile His Pro
                85                  90                  95
Asp Tyr Asp Ala Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu
            100                 105                 110
Ala Arg Pro Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu
        115                 120                 125
Arg Asp Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly
    130                 135                 140
Lys Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile
145                 150                 155                 160
His Leu Val Ser Arg Glu Glu Cys Glu His Ala Tyr Pro Gly Gln Ile
                165                 170                 175
Thr Gln Asn Met Leu Cys Ala Gly Asp Glu Lys Tyr Gly Lys Asp Ser
            180                 185                 190
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Asp His Leu Arg
        195                 200                 205
Gly Leu Val Ser Trp Gly Asn Ile Pro Cys Gly Ser Lys Glu Lys Pro
    210                 215                 220
Gly Val Tyr Thr Asn Val Cys Arg Tyr Thr Asn Trp Ile Gln Lys Thr
225                 230                 235                 240
Ile Gln Ala Lys
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<210> 202
<211> 1527
<212> DNA
<213> Homo sapiens

<220>
<223> Neurosin transcript variant B

<400> 202
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ggctctgcca ctgcatctga gtgtcttctc tcctcacggc tccccgcatt tctaactctt 180
tctgcctcct cgtctcaaag ctgttccttc ccccgactca agaatccccg gaggcccgga 240
ggcctgcagc aggagcggcc atgaagaagc tgatggtggt gctgagtctg attgctgcag 300
cctgggcaga ggagcagaat aagttggtgc atggcggacc ctgcgacaag acatctcacc 360
cctaccaagc tgccctctac acctcgggcc acttgctctg tggtggggtc cttatccatc 420
cactgtgggt cctcacagct gcccactgca aaaaaccgaa tcttcaggtc ttcctgggga 480

agcataacct tcggcaaagg gagagttccc aggagcagag ttctgttgtc cgggctgtga 540
tccaccctga ctatgatgcc gccagccatg accaggacat catgctgttg cgcctggcac 600
gcccagccaa actctctgaa ctcatccagc cccttccccc ggagagggac tgctcagcca 660
acaccaccag ctgccacatc ctgggctggg gcaagacagc agatggtgat ttccctgaca 720
ccatccagtg tgcatacatc cacctggtgt cccgtgagga gtgtgagcat gcctaccctg 780
gccagatcac ccagaacatg ttgtgtgctg gggatgagaa gtacgggaag gattcctgcc 840
agggtgattc tgggggtccg ctggtatgtg gagaccacct ccgaggcctt gtgtcatggg 900
gtaacatccc ctgtggatca aaggagaagc caggagtcta caccaacgtc tgcagataca 960
cgaactggat ccaaaaaacc attcaggcca agtgaccctg acatgtgaca tctacctccc 1020
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ggaatcccag ctccgctgct tactgtcggt gtccccttgg gatgtacctt tcttcactgc 1380
agatttctca cctgtaagat gaagataagg atgatacagt ctccataagg cagtggctgt 1440
tggaaagatt taaggtttca cacctatgac atacatggaa tagcacctgg gccaccatgc 1500
actcaataaa gaatgaattt tattatg 1527

<210> 203
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<223> Neurosin isoform A preprotein

<400> 203
Met Lys Lys Leu Met Val Val Leu Ser Leu Ile Ala Ala Ala Trp Ala
 1   5   10   15
Glu Glu Gln Asn Lys Leu Val His Gly Gly Pro Cys Asp Lys Thr Ser
            20   25   30
His Pro Tyr Gln Ala Ala Leu Tyr Thr Ser Gly His Leu Leu Cys Gly
        35   40   45
Gly Val Leu Ile His Pro Leu Trp Val Leu Thr Ala Ala His Cys Lys
    50   55   60
Lys Pro Asn Leu Gln Val Phe Leu Gly Lys His Asn Leu Arg Gln Arg
65   70   75   80
Glu Ser Ser Gln Glu Gln Ser Ser Val Val Arg Ala Val Ile His Pro
                85   90   95
Asp Tyr Asp Ala Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu
            100   105   110
Ala Arg Pro Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu
        115   120   125

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Arg Asp Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly
    130                 135                 140
Lys Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile
145                 150                 155                 160
His Leu Val Ser Arg Glu Glu Cys Glu His Ala Tyr Pro Gly Gln Ile
                165                 170                 175
Thr Gln Asn Met Leu Cys Ala Gly Asp Glu Lys Tyr Gly Lys Asp Ser
            180                 185                 190
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Asp His Leu Arg
        195                 200                 205
Gly Leu Val Ser Trp Gly Asn Ile Pro Cys Gly Ser Lys Glu Lys Pro
    210                 215                 220
Gly Val Tyr Thr Asn Val Cys Arg Tyr Thr Asn Trp Ile Gln Lys Thr
225                 230                 235                 240
Ile Gln Ala Lys
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<210> 204
<211> 1495
<212> DNA
<213> Homo sapiens

<220>
<223> Neurosin transcript variant C

<400> 204
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ggctctgcca ctgcatctga gtgtcttctc tcctcacggc tccccgcatt tctaactctt 180
tctgcctcct cgtctcaaag ctgttccttc ccccgactca agaatccccg gaggcccgga 240
ggcctgcagc agcctgggca gaggagcaga ataagttggt gcatggcgga ccctgcgaca 300
agacatctca cccctaccaa gctgccctct acacctcggg ccacttgctc tgtggtgggg 360
tccttatcca tccactgtgg gtcctcacag ctgcccactg caaaaaaccg aatcttcagg 420
tcttcctggg gaagcataac cttcggcaaa gggagagttc ccaggagcag agttctgttg 480
tccgggctgt gatccaccct gactatgatg ccgccagcca tgaccaggac atcatgctgt 540
tgcgcctggc acgcccagcc aaactctctg aactcatcca gcccccttccc ctggagaggg 600
actgctcagc caacaccacc agctgccaca tcctgggctg gggcaagaca gcagatggtg 660
atttccctga caccatccag tgtgcataca tccacctggt gtcccgtgag gagtgtgagc 720
atgcctaccc tggccagatc acccagaaca tgttgtgtgc tggggatgag aagtacggga 780
aggattcctg ccagggtgat tctgggggtc cgctggtatg tggagaccac ctccgaggcc 840
ttgtgtcatg gggtaacatc ccctgtggat caaaggagaa gccaggagtc tacaccaacg 900
tctgcagata cacgaactgg atccaaaaaa ccattcaggc caagtgaccc tgacatgtga 960
catctacctc ccgacctacc accccactgg ctggttccag aacgtctctc acctagacct 1020
tgcctccccc cctctcctgc ccagctctga ccctgatgct taataaacgc agcgacgtga 1080
gggtcctgat tctccctggt tttaccccag ctccatcctt gcatcactgg ggaggacgtg 1140
atgagtgagg acttgggtcc tcggtcttac ccccaccact aagagaatac aggaaaatcc 1200
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ggcagtggct gttggaaaga tttaaggttt cacacctatg acatacatgg aatagcacct 1440
gggccaccat gcactcaata aagaatgaat tttattatga aaaaaaaaaa aaaaa 1495

<210> 205
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<223> Neurosin isoform B

<400> 205
Met Leu Leu Arg Leu Ala Arg Pro Ala Lys Leu Ser Glu Leu Ile Gln
 1   5   10   15
Pro Leu Pro Leu Glu Arg Asp Cys Ser Ala Asn Thr Thr Ser Cys His
            20   25   30
Ile Leu Gly Trp Gly Lys Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile
        35   40   45
Gln Cys Ala Tyr Ile His Leu Val Ser Arg Glu Glu Cys Glu His Ala
    50   55   60
Tyr Pro Gly Gln Ile Thr Gln Asn Met Leu Cys Ala Gly Asp Glu Lys
65   70   75   80
Tyr Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
                85   90   95
Gly Asp His Leu Arg Gly Leu Val Ser Trp Gly Asn Ile Pro Cys Gly
            100   105   110
Ser Lys Glu Lys Pro Gly Val Tyr Thr Asn Val Cys Arg Tyr Thr Asn
        115   120   125
Trp Ile Gln Lys Thr Ile Gln Ala Lys
    130   135

<210> 206
<211> 1386
<212> DNA
<213> Homo sapiens

<220>
<223> Neurosin transcript variant D

<400> 206
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ggggtgtgtg tctggcagtc cctgcagccc tgggctctgc ggcccctgcg tcctccgctt 120
ggctctgcca ctgcatctga gtgtcttctc tcctcacggc tccccgcatt tctaactctt 180
tctgcctcct cgtctcaaag ctgttccttc ccccgactca agaatccccg gaggcccgga 240
ggcctgcagc aggagcggcc atgaagaagc tgatggtggt gctgagtctg attgctgcag 300
gaatcttcag gtcttcctgg ggaagcataa ccttcggcaa agggagagtt cccaggagca 360
gagttctgtt gtccgggctg tgatccaccc tgactatgat gccgccagcc atgaccagga 420
catcatgctg ttgcgcctgg cacgcccagc caaactctct gaactcatcc agccccttcc 480
cctggagagg gactgctcag ccaacaccac cagctgccac atcctgggct ggggcaagac 540
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ggagtgtgag catgcctacc ctggccagat cacccagaac atgttgtgtg ctggggatga 660
gaagtacggg aaggattcct gccagggtga ttctgggggt ccgctggtat gtggagacca 720
cctccgaggc cttgtgtcat ggggtaacat cccctgtgga tcaaaggaga agccaggagt 780
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aaaaaa 1386

<210> 207
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<223> Neurosin isoform C

<400> 207
Met Lys Lys Leu Met Val Val Leu Ser Leu Ile Ala Ala Gly Ile Phe
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Arg Ser Ser Trp Gly Ser Ile Thr Phe Gly Lys Gly Arg Val Pro Arg
20 25 30
Ser Arg Val Leu Leu Ser Gly Leu
35 40

<210> 208
<211> 3351
<212> DNA
<213> Homo sapiens

<220>
<223> Neurotrypsin

<400> 208
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tcaatgattc cctccaccac agccaccgcc attcgccccc tgcgggtccg cactacccct 180
attaccttcc cacccagcag cggcccccga cgacgcgtcc gccgccgcct ctcccgcgct 240
tcccgcgccc cccgcgggcg ctccctgccc agcgcccgca cgccctccag gccgggcaca 300
cgccccggcc gcacccctgg ggctgccccg ccggcgagcc atgggtcagc gtgacggact 360
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cgagctgggc tcagctgcga ggacagcgcc acaacttttg tcggagcccc gacggcgcgg 480
gcagaccctg gtgtttctac ggagacgccc gtggcaaggt ggactggggc tactgcgact 540
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tatatgcaag tggagtttgg ggcactgtct gtagcagcca ctgggatgat tctgatgcat 660
cagtcatttg tcaccagctg cagctgggag gaaaaggaat agcaaaacaa accccgtttt 720
ctggactggg ccttattccc atttattgga gcaatgtccg ttgccgagga gatgaagaaa 780
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gctaccctgg cggcgaggga cacaggctct ctctgggttt tcctgtcaga ctgatggatg 1560
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gtgatgatgg atggactgat aaggatgcag ctgtgatctg tcgtcagctt ggctacaagg 1680
gtcctgccag agcaagaacc atggcttact ttggagaagg aaaaggaccc atccatgtgg 1740

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aggcctcagg taacagtaat aaagagtccc tctcatctgt ttgtggcttg agattactgc 1920
accgtcggca gaagcggatc attggtggga aaaattcttt aaggggtggt tggccttggc 1980
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gttacataac aggatggggt gacacaggac gagcctattc aagaacacta caacaagcag 2400
ccattccctt acttcctaaa aggttttgtg aagaacgtta taagggtcgg tttacaggga 2460
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aagaattcca ctataaactt ttaggcctga ataggagtag taaagcctca aggacatctg 3240
cctgtcacaa tatattctca aagtgatctg atatttggaa acaagtatcc ttgttgagta 3300
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<210> 209
<211> 875
<212> PRT
<213> Homo sapiens

<220>
<223> Neurotrypsin

<400> 209

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Met Thr Leu Ala Arg Phe Val Leu Ala Leu Met Leu Gly Ala Leu Pro
 1               5                  10                  15
Glu Val Val Gly Phe Asp Ser Val Leu Asn Asp Ser Leu His His Ser
            20                  25                  30
His Arg His Ser Pro Pro Ala Gly Pro His Tyr Pro Tyr Tyr Leu Pro
        35                  40                  45
Thr Gln Gln Arg Pro Pro Thr Thr Arg Pro Pro Pro Pro Leu Pro Arg
    50                  55                  60
Phe Pro Arg Pro Pro Arg Ala Leu Pro Ala Gln Arg Pro His Ala Leu
65                  70                  75                  80
Gln Ala Gly His Thr Pro Arg Pro His Pro Trp Gly Cys Pro Ala Gly
                85                  90                  95
Glu Pro Trp Val Ser Val Thr Asp Phe Gly Ala Pro Cys Leu Arg Trp
            100                 105                 110
Ala Glu Val Pro Pro Phe Leu Glu Arg Ser Pro Pro Ala Ser Trp Ala
        115                 120                 125
Gln Leu Arg Gly Gln Arg His Asn Phe Cys Arg Ser Pro Asp Gly Ala
    130                 135                 140
Gly Arg Pro Trp Cys Phe Tyr Gly Asp Ala Arg Gly Lys Val Asp Trp
145                 150                 155                 160
```

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Gly Tyr Cys Asp Cys Arg His Gly Ser Val Arg Leu Arg Gly Gly Lys
                165                 170                 175
Asn Glu Phe Glu Gly Thr Val Glu Val Tyr Ala Ser Gly Val Trp Gly
            180                 185                 190
Thr Val Cys Ser Ser His Trp Asp Asp Ser Asp Ala Ser Val Ile Cys
        195                 200                 205
His Gln Leu Gln Leu Gly Gly Lys Gly Ile Ala Lys Gln Thr Pro Phe
    210                 215                 220
Ser Gly Leu Gly Leu Ile Pro Ile Tyr Trp Ser Asn Val Arg Cys Arg
225                 230                 235                 240
Gly Asp Glu Glu Asn Ile Leu Leu Cys Glu Lys Asp Ile Trp Gln Gly
                245                 250                 255
Gly Val Cys Pro Gln Lys Met Ala Ala Ala Val Thr Cys Ser Phe Ser
            260                 265                 270
His Gly Pro Thr Phe Pro Ile Ile Arg Leu Ala Gly Gly Ser Ser Val
        275                 280                 285
His Glu Gly Arg Val Glu Leu Tyr His Ala Gly Gln Trp Gly Thr Val
    290                 295                 300
Cys Asp Asp Gln Trp Asp Asp Ala Asp Ala Glu Val Ile Cys Arg Gln
305                 310                 315                 320
Leu Gly Leu Ser Gly Ile Ala Lys Ala Trp His Gln Ala Tyr Phe Gly
                325                 330                 335
Glu Gly Ser Gly Pro Val Met Leu Asp Glu Val Arg Cys Thr Gly Asn
            340                 345                 350
Glu Leu Ser Ile Glu Gln Cys Pro Lys Ser Ser Trp Gly Glu His Asn
        355                 360                 365
Cys Gly His Lys Glu Asp Ala Gly Val Ser Cys Thr Pro Leu Thr Asp
    370                 375                 380
Gly Val Ile Arg Leu Ala Gly Gly Lys Gly Ser His Glu Gly Arg Leu
385                 390                 395                 400
Glu Val Tyr Tyr Arg Gly Gln Trp Gly Thr Val Cys Asp Asp Gly Trp
                405                 410                 415
Thr Glu Leu Asn Thr Tyr Val Val Cys Arg Gln Leu Gly Phe Lys Tyr
            420                 425                 430
Gly Lys Gln Ala Ser Ala Asn His Phe Glu Glu Ser Thr Gly Pro Ile
        435                 440                 445
Trp Leu Asp Asp Val Ser Cys Ser Gly Lys Glu Thr Arg Phe Leu Gln
    450                 455                 460
Cys Ser Arg Arg Gln Trp Gly Arg His Asp Cys Ser His Arg Glu Asp
465                 470                 475                 480
Val Ser Ile Ala Cys Tyr Pro Gly Gly Glu Gly His Arg Leu Ser Leu
                485                 490                 495
Gly Phe Pro Val Arg Leu Met Asp Gly Glu Asn Lys Lys Glu Gly Arg
            500                 505                 510
Val Glu Val Phe Ile Asn Gly Gln Trp Gly Thr Ile Cys Asp Asp Gly
        515                 520                 525
Trp Thr Asp Lys Asp Ala Ala Val Ile Cys Arg Gln Leu Gly Tyr Lys
    530                 535                 540
Gly Pro Ala Arg Ala Arg Thr Met Ala Tyr Phe Gly Glu Gly Lys Gly
545                 550                 555                 560
Pro Ile His Val Asp Asn Val Lys Cys Thr Gly Asn Glu Arg Ser Leu
                565                 570                 575
Ala Asp Cys Ile Lys Gln Asp Ile Gly Arg His Asn Cys Arg His Ser
            580                 585                 590
Glu Asp Ala Gly Val Ile Cys Asp Tyr Phe Gly Lys Lys Ala Ser Gly
        595                 600                 605
Asn Ser Asn Lys Glu Ser Leu Ser Ser Val Cys Gly Leu Arg Leu Leu
```

```
    610                 615                 620
His Arg Arg Gln Lys Arg Ile Ile Gly Gly Lys Asn Ser Leu Arg Gly
625                 630                 635                 640
Gly Trp Pro Trp Gln Val Ser Leu Arg Leu Lys Ser Ser His Gly Asp
                645                 650                 655
Gly Arg Leu Leu Cys Gly Ala Thr Leu Leu Ser Ser Cys Trp Val Leu
            660                 665                 670
Thr Ala Ala His Cys Phe Lys Arg Tyr Gly Asn Ser Thr Arg Ser Tyr
        675                 680                 685
Ala Val Arg Val Gly Asp Tyr His Thr Leu Val Pro Glu Glu Phe Glu
    690                 695                 700
Glu Glu Ile Gly Val Gln Gln Ile Val Ile His Arg Glu Tyr Arg Pro
705                 710                 715                 720
Asp Arg Ser Asp Tyr Asp Ile Ala Leu Val Arg Leu Gln Gly Pro Glu
                725                 730                 735
Glu Gln Cys Ala Arg Phe Ser Ser His Val Leu Pro Ala Cys Leu Pro
            740                 745                 750
Leu Trp Arg Glu Arg Pro Gln Lys Thr Ala Ser Asn Cys Tyr Ile Thr
        755                 760                 765
Gly Trp Gly Asp Thr Gly Arg Ala Tyr Ser Arg Thr Leu Gln Gln Ala
    770                 775                 780
Ala Ile Pro Leu Leu Pro Lys Arg Phe Cys Glu Glu Arg Tyr Lys Gly
785                 790                 795                 800
Arg Phe Thr Gly Arg Met Leu Cys Ala Gly Asn Leu His Glu His Lys
                805                 810                 815
Arg Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Cys Glu
            820                 825                 830
Arg Pro Gly Glu Ser Trp Val Val Tyr Gly Val Thr Ser Trp Gly Tyr
        835                 840                 845
Gly Cys Gly Val Lys Asp Ser Pro Gly Val Tyr Thr Lys Val Ser Ala
    850                 855                 860
Phe Val Pro Trp Ile Lys Ser Val Thr Lys Leu
865                 870                 875
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<210> 210
<211> 1165
<212> DNA
<213> Homo sapiens

<220>
<223> tryptase beta 2 (I)

<400> 210

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ggggtcagga ggccccccagg agcaagtggc cctggcaggt gagcctgaga gtccgcgacc 180
gatactggat gcacttctgc gggggctccc tcatccaccc ccagtgggtg ctgaccgcag 240
cgcactgcgt gggaccggac gtcaaggatc tggccgccct cagggtgcaa ctgcgggagc 300
agcacctcta ctaccaggac cagctgctgc cggtcagcag gatcatcgtg cacccacagt 360
tctacaccgc ccagatcgga gcggacatcg ccctgctgga gctggaggag ccggtgaacg 420
tctccagcca cgtccacacg gtcaccctgc cccctgcctc agagaccttc ccccgggga 480
tgccgtgctg ggtcactggc tggggcgatg tggacaatga tgagcgcctc ccaccgccat 540
ttcctctgaa gcaggtgaag gtccccataa tggaaaacca catttgtgac gcaaaatacc 600
accttggcgc ctacacggga gacgacgtcc gcatcgtccg tgacgacatg ctgtgtgccg 660
ggaacacccg gagggactca tgccagggcg actccggagg gcccctggtg tgcaaggtga 720
atggcacctg gctgcaggcg ggcgtggtca gctggggcga gggctgtgcc cagcccaacc 780
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ggcctggcat ctacacccgt gtcacctact acttggactg gatccaccac tatgtcccca 840
aaaagccgtg agtcaggcct ggggtgtcca cctgggtcac tggagagcca gcccctcctg 900
tccaaaacac cactgcttcc tacccaggtg gcgactgccc cccacacctt ccctgccccg 960
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tgaggaccct tccccatcct gagccccctt ccctgtccta agcctgacgc ctgcaccggg 1080
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acctcattaa agtgcatgga aatca                                      1165

<210> 211
<211> 275
<212> PRT
<213> Homo sapiens

<220>
<223> tryptase beta 2 (I)

<400> 211
Met Leu Asn Leu Leu Leu Leu Ala Leu Pro Val Leu Ala Ser Arg Ala
 1               5                  10                  15
Tyr Ala Ala Pro Ala Pro Gly Gln Ala Leu Gln Arg Val Gly Ile Val
            20                  25                  30
Gly Gly Gln Glu Ala Pro Arg Ser Lys Trp Pro Trp Gln Val Ser Leu
        35                  40                  45
Arg Val Arg Asp Arg Tyr Trp Met His Phe Cys Gly Gly Ser Leu Ile
    50                  55                  60
His Pro Gln Trp Val Leu Thr Ala Ala His Cys Val Gly Pro Asp Val
65                  70                  75                  80
Lys Asp Leu Ala Ala Leu Arg Val Gln Leu Arg Glu Gln His Leu Tyr
                85                  90                  95
Tyr Gln Asp Gln Leu Leu Pro Val Ser Arg Ile Ile Val His Pro Gln
            100                 105                 110
Phe Tyr Thr Ala Gln Ile Gly Ala Asp Ile Ala Leu Leu Glu Leu Glu
        115                 120                 125
Glu Pro Val Asn Val Ser Ser His Val His Thr Val Thr Leu Pro Pro
    130                 135                 140
Ala Ser Glu Thr Phe Pro Pro Gly Met Pro Cys Trp Val Thr Gly Trp
145                 150                 155                 160
Gly Asp Val Asp Asn Asp Glu Arg Leu Pro Pro Pro Phe Pro Leu Lys
                165                 170                 175
Gln Val Lys Val Pro Ile Met Glu Asn His Ile Cys Asp Ala Lys Tyr
            180                 185                 190
His Leu Gly Ala Tyr Thr Gly Asp Asp Val Arg Ile Val Arg Asp Asp
        195                 200                 205
Met Leu Cys Ala Gly Asn Thr Arg Arg Asp Ser Cys Gln Gly Asp Ser
    210                 215                 220
Gly Gly Pro Leu Val Cys Lys Val Asn Gly Thr Trp Leu Gln Ala Gly
225                 230                 235                 240
Val Val Ser Trp Gly Glu Gly Cys Ala Gln Pro Asn Arg Pro Gly Ile
                245                 250                 255
Tyr Thr Arg Val Thr Tyr Tyr Leu Asp Trp Ile His His Tyr Val Pro
            260                 265                 270
Lys Lys Pro
        275


<210> 212
<211> 1013
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<212> DNA
<213> Homo sapiens

<220>
<223> Neuropsin transcript variant 1

<400> 212
gttcccagaa gctccccagg ctctagtgca ggaggagaag gaggaggagc aggaggtgga 60
gattcccagt taaaaggctc cagaatcgtg taccaggcag agaactgaag tactggggcc 120
tcctccactg ggtccgaatc agtaggtgac cccgcccctg gattctggaa gacctcacca 180
tgggacgccc ccgacctcgt gcggccaaga cgtggatgtt cctgctcttg ctgggggggag 240
cctgggcagg acactccagg gcacaggagg acaaggtgct ggggggtcat gagtgccaac 300
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tacgcctggg agaccacagc ctacagaata aagatggccc agagcaagaa atacctgtgg 480
ttcagtccat cccacacccc tgctacaaca gcagcgatgt ggaggaccac aaccatgatc 540
tgatgcttct tcaactgcgt gaccaggcat ccctggggtc caaagtgaag cccatcagcc 600
tggcagatca ttgcacccag cctggccaga agtgcaccgt ctcaggctgg ggcactgtca 660
ccagtccccg agagaatttt cctgacactc tcaactgtgc agaagtaaaa atctttcccc 720
agaagaagtg tgaggatgct tacccggggc agatcacaga tggcatggtc tgtgcaggca 780
gcagcaaagg ggctgacacg tgccagggcg attctggagg ccccctggtg tgtgatggtg 840
cactccaggg catcacatcc tggggctcag accccctgtgg gaggtccgac aaacctggcg 900
tctataccaa catctgccgc tacctggact ggatcaagaa gatcataggc agcaagggct 960
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<210> 213
<211> 260
<212> PRT
<213> Homo sapiens

<220>
<223> Neuropsin isoform 1

<400> 213
Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu Leu
 1   5   10   15
Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu Asp Lys
            20   25   30
Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro Trp Gln Ala
        35   40   45
Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly Val Leu Val Gly
    50   55   60
Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Lys Tyr Thr
65   70   75   80
Val Arg Leu Gly Asp His Ser Leu Gln Asn Lys Asp Gly Pro Glu Gln
                85   90   95
Glu Ile Pro Val Val Gln Ser Ile Pro His Pro Cys Tyr Asn Ser Ser
            100   105   110
Asp Val Glu Asp His Asn His Asp Leu Met Leu Leu Gln Leu Arg Asp
        115   120   125
Gln Ala Ser Leu Gly Ser Lys Val Lys Pro Ile Ser Leu Ala Asp His
    130   135   140
Cys Thr Gln Pro Gly Gln Lys Cys Thr Val Ser Gly Trp Gly Thr Val
145   150   155   160
Thr Ser Pro Arg Glu Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val
                165   170   175
Lys Ile Phe Pro Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile

```
            180                 185                 190
Thr Asp Gly Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys
        195                 200                 205
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly
    210                 215                 220
Ile Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
225                 230                 235                 240
Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile Ile
                245                 250                 255
Gly Ser Lys Gly
            260
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<210> 214
<211> 1148
<212> DNA
<213> Homo sapiens

<220>
<223> Neuropsin transcript variant 2

<400> 214
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gattcccagt taaaaggctc cagaatcgtg taccaggcag agaactgaag tactggggcc 120
tcctccactg ggtccgaatc agtaggtgac cccgcccctg gattctggaa gacctcacca 180
tgggacgccc ccgacctcgt gcggccaaga cgtggatgtt cctgctcttg ctgggggggag 240
cctgggcagc gtgtggaagc ctggacctcc tcactaagtt gtatgcggag aacttgccgt 300
gtgtccattt gaacccacag tggccttccc agccctcgca ctgccccaga gggtggcgat 360
ccaaccctct ccctcctgct gcaggacact ccagggcaca ggaggacaag gtgctggggg 420
gtcatgagtg ccaaccccat tcgcagcctt ggcaggcggc cttgttccag ggccagcaac 480
tactctgtgg cggtgtcctt gtaggtggca actgggtcct tacagctgcc cactgtaaaa 540
aaccgaaata cacagtacgc ctgggagacc acagcctaca gaataaagat ggcccagagc 600
aagaaatacc tgtggttcag tccatcccac acccctgcta caacagcagc gatgtggagg 660
accacaacca tgatctgatg cttcttcaac tgcgtgacca ggcatccctg gggtccaaag 720
tgaagcccat cagcctggca gatcattgca cccagcctgg ccagaagtgc accgtctcag 780
gctggggcac tgtcaccagt ccccgagaga attttcctga cactctcaac tgtgcagaag 840
taaaaatctt tccccagaag aagtgtgagg atgcttaccc ggggcagatc acagatggca 900
tggtctgtgc aggcagcagc aaaggggctg acacgtgcca gggcgattct ggaggccccc 960
tggtgtgtga tggtgcactc cagggcatca catcctgggg ctcagacccc tgtgggaggt 1020
ccgacaaacc tggcgtctat accaacatct gccgctacct ggactggatc aagaagatca 1080
taggcagcaa gggctgattc taggataagc actagatctc ccttaataaa ctcacaactc 1140
tctggttc   1148

<210> 215
<211> 305
<212> PRT
<213> Homo sapiens

<220>
<223> Neuropsin isoform 2

<400> 215
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Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu Leu
 1               5                  10                  15
Leu Leu Gly Gly Ala Trp Ala Ala Cys Gly Ser Leu Asp Leu Leu Thr
            20                  25                  30
Lys Leu Tyr Ala Glu Asn Leu Pro Cys Val His Leu Asn Pro Gln Trp
```

```
        35                  40                  45
Pro Ser Gln Pro Ser His Cys Pro Arg Gly Trp Arg Ser Asn Pro Leu
    50                  55                  60
Pro Pro Ala Ala Gly His Ser Arg Ala Gln Glu Asp Lys Val Leu Gly
65                  70                  75                  80
Gly His Glu Cys Gln Pro His Ser Gln Pro Trp Gln Ala Ala Leu Phe
                85                  90                  95
Gln Gly Gln Gln Leu Leu Cys Gly Gly Val Leu Val Gly Gly Asn Trp
            100                 105                 110
Val Leu Thr Ala Ala His Cys Lys Lys Pro Lys Tyr Thr Val Arg Leu
        115                 120                 125
Gly Asp His Ser Leu Gln Asn Lys Asp Gly Pro Glu Gln Glu Ile Pro
    130                 135                 140
Val Val Gln Ser Ile Pro His Pro Cys Tyr Asn Ser Ser Asp Val Glu
145                 150                 155                 160
Asp His Asn His Asp Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser
                165                 170                 175
Leu Gly Ser Lys Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln
            180                 185                 190
Pro Gly Gln Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro
        195                 200                 205
Arg Glu Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe
    210                 215                 220
Pro Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
225                 230                 235                 240
Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly Asp
                245                 250                 255
Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile Thr Ser
            260                 265                 270
Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly Val Tyr Thr
        275                 280                 285
Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile Ile Gly Ser Lys
    290                 295                 300
Gly
305
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<210> 216
<211> 590
<212> DNA
<213> Homo sapiens

<220>
<223> Neuropsin transcript variant 3

<400> 216
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tcctccactg ggtccgaatc agtaggtgac cccgcccctg gattctggaa gacctcacca 180
tgggacgccc ccgacctcgt gcggccaaga cgtggatgtt cctgctcttg ctgggggggag 240
cctgggcaga gaattttcct gacactctca actgtgcaga agtaaaaatc tttccccaga 300
agaagtgtga ggatgcttac ccggggcaga tcacagatgg catggtctgt gcaggcagca 360
gcaaaggggc tgacacgtgc cagggcgatt ctggaggccc cctggtgtgt gatggtgcac 420
tccagggcat cacatcctgg ggctcagacc cctgtgggag gtccgacaaa cctggcgtct 480
ataccaacat ctgccgctac ctggactgga tcaagaagat cataggcagc aagggctgat 540
tctaggataa gcactagatc tcccttaata aactcacaac tctctggttc             590
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<210> 217
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<223> Neuropsin isoform 3

<400> 217
Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu Leu
 1   5   10   15
Leu Leu Gly Gly Ala Trp Ala Glu Asn Phe Pro Asp Thr Leu Asn Cys
            20   25   30
Ala Glu Val Lys Ile Phe Pro Gln Lys Lys Cys Glu Asp Ala Tyr Pro
        35   40   45
Gly Gln Ile Thr Asp Gly Met Val Cys Ala Gly Ser Ser Lys Gly Ala
    50   55   60
Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala
65   70   75   80
Leu Gln Gly Ile Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp
                85   90   95
Lys Pro Gly Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys
            100   105   110
Lys Ile Ile Gly Ser Lys Gly
        115

<210> 218
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<223> Neuropsin transcript variant 4

<400> 218
gttcccagaa gctccccagg ctctagtgca ggaggagaag gaggaggagc aggaggtgga 60
gattcccagt taaaaggctc cagaatcgtg taccaggcag agaactgaag tactggggcc 120
tcctccactg ggtccgaatc agtaggtgac cccgcccctg gattctggaa gacctcacca 180
tgggacgccc ccgacctcgt gcggccaaga cgtggatgtt cctgctcttg ctgggggggag 240
cctgggcagg gcgattctgg aggcccccctg gtgtgtgatg gtgcactcca gggcatcaca 300
tcctggggct cagacccctg tgggaggtcc gacaaacctg gcgtctatac caacatctgc 360
cgctacctgg actggatcaa gaagatcata ggcagcaagg gctgattcta ggataagcac 420
tagatctccc ttaataaact cacaactctc tggttc   456

<210> 219
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<223> Neuropsin isoform 4

<400> 219
Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu Leu
 1   5   10   15
Leu Leu Gly Gly Ala Trp Ala Gly Arg Phe Trp Arg Pro Pro Gly Val

20 25 30

<210> 220
<211> 1580
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK10 transcript variant 1

<400> 220
catcctgcca cccctagcct tgctggggac gtgaaccctc tccccgcgcc tgggaagcct 60
tcttggcacc gggacccgga gaatccccac ggaagccagt tccaaaaggg atgaaaaggg 120
ggcgtttcgg gcactgggag aagcctgtat tccagggccc ctcccagagc aggaatctgg 180
gacccaggag tgccagcctc acccacgcag atcctggcca tgagagctcc gcacctccac 240
ctctccgccg cctctggcgc ccgggctctg gcgaagctgc tgccgctgct gatggcgcaa 300
ctctgggccg cagaggcggc gctgctcccc caaaacgaca cgcgcttgga ccccgaagcc 360
tatggctccc cgtgcgcgcg cggctcgcag ccctggcagg tctcgctctt caacggcctc 420
tcgttccact gcgcgggtgt cctggtggac cagagttggg tgctgacggc cgcgcactgc 480
ggaaacaagc cactgtgggc tcgagtaggg gatgaccacc tgctgcttct tcagggagag 540
cagctccgcc ggaccactcg ctctgttgtc catcccaagt accaccaggg ctcaggcccc 600
atcctgccaa ggcgaacgga tgagcacgat ctcatgttgc tgaagctggc caggcccgta 660
gtgctggggc cccgcgtccg ggccctgcag cttccctacc gctgtgctca gcccggagac 720
cagtgccagg ttgctggctg gggcaccacg gccgcccgga gagtgaagta caacaagggc 780
ctgacctgct ccagcatcac tatcctgagc cctaaagagt gtgaggtctt ctaccctggc 840
gtggtcacca acaacatgat atgtgctgga ctggaccggg gccaggaccc ttgccagagt 900
gactctggag gccccctggt ctgtgacgag accctccaag gcatcctctc gtggggtgtt 960
taccccctgtg gctctgccca gcatccagct gtctacaccc agatctgcaa atacatgtcc 1020
tggatcaata aagtcatacg ctccaactga tccagatgct acgctccagc tgatccagat 1080
gttatgctcc tgctgatcca gatgcccaga ggctccatcg tccatcctct tcctccccag 1140
tcggctgaac tctccccttg tctgcactgt tcaaacctct gccgccctcc acacctctaa 1200
acatctcccc tctcacctca ttcccccacc tatccccatt ctctgcctgt actgaagctg 1260
aaatgcagga agtggtggca aaggtttatt ccagagaagc caggaagccg gtcatcaccc 1320
agcctctgag agcagttact ggggtcaccc aacctgactt cctctgccac tccctgctgt 1380
gtgactttgg gcaagccaag tgccctctct gaacctcagt ttcctcatct gcaaaatggg 1440
aacaatgacg tgcctacctc ttagacatgt tgtgaggaga ctatgatata acatgtgtat 1500
gtaaatcttc atggtgattg tcatgtaagg cttaacacag tgggtggtga gttctgacta 1560
aaggttacct gttgtcgtga 1580

<210> 221
<211> 276
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK10

<400> 221

Met Arg Ala Pro His Leu His Leu Ser Ala Ala Ser Gly Ala Arg Ala
1 5 10 15
Leu Ala Lys Leu Leu Pro Leu Leu Met Ala Gln Leu Trp Ala Ala Glu
20 25 30
Ala Ala Leu Leu Pro Gln Asn Asp Thr Arg Leu Asp Pro Glu Ala Tyr
35 40 45
Gly Ser Pro Cys Ala Arg Gly Ser Gln Pro Trp Gln Val Ser Leu Phe

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    50                  55                  60
Asn Gly Leu Ser Phe His Cys Ala Gly Val Leu Val Asp Gln Ser Trp
65                  70                  75                  80
Val Leu Thr Ala Ala His Cys Gly Asn Lys Pro Leu Trp Ala Arg Val
                85                  90                  95
Gly Asp Asp His Leu Leu Leu Leu Gln Gly Glu Gln Leu Arg Arg Thr
            100                 105                 110
Thr Arg Ser Val Val His Pro Lys Tyr His Gln Gly Ser Gly Pro Ile
        115                 120                 125
Leu Pro Arg Arg Thr Asp Glu His Asp Leu Met Leu Leu Lys Leu Ala
    130                 135                 140
Arg Pro Val Val Leu Gly Pro Arg Val Arg Ala Leu Gln Leu Pro Tyr
145                 150                 155                 160
Arg Cys Ala Gln Pro Gly Asp Gln Cys Gln Val Ala Gly Trp Gly Thr
                165                 170                 175
Thr Ala Ala Arg Arg Val Lys Tyr Asn Lys Gly Leu Thr Cys Ser Ser
            180                 185                 190
Ile Thr Ile Leu Ser Pro Lys Glu Cys Glu Val Phe Tyr Pro Gly Val
        195                 200                 205
Val Thr Asn Asn Met Ile Cys Ala Gly Leu Asp Arg Gly Gln Asp Pro
    210                 215                 220
Cys Gln Ser Asp Ser Gly Gly Pro Leu Val Cys Asp Glu Thr Leu Gln
225                 230                 235                 240
Gly Ile Leu Ser Trp Gly Val Tyr Pro Cys Gly Ser Ala Gln His Pro
                245                 250                 255
Ala Val Tyr Thr Gln Ile Cys Lys Tyr Met Ser Trp Ile Asn Lys Val
            260                 265                 270
Ile Arg Ser Asn
        275
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<210> 222
<211> 1443
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK10 transcript variant 2

<400> 222
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cgcccgggct ctggcgaagc tgctgccgct gctgatggcg caactctggg ccgcagaggc 180
ggcgctgctc ccccaaaacg acacgcgctt ggaccccgaa gcctatggct ccccgtgcgc 240
gcgcggctcg cagccctggc aggtctcgct cttcaacggc ctctcgttcc actgcgcggg 300
tgtcctggtg gaccagagtt gggtgctgac ggccgcgcac tgcggaaaca agccactgtg 360
ggctcgagta ggggatgacc acctgctgct tcttcaggga gagcagctcc gccggaccac 420
tcgctctgtt gtccatccca agtaccacca gggctcaggc cccatcctgc caaggcgaac 480
ggatgagcac gatctcatgt tgctgaagct ggccaggccc gtagtgctgg ggccccgcgt 540
ccgggccctg cagcttccct accgctgtgc tcagcccgga gaccagtgcc aggttgctgg 600
ctggggcacc acggccgccc ggagagtgaa gtacaacaag ggcctgacct gctccagcat 660
cactatcctg agccctaaag agtgtgaggt cttctaccct ggcgtggtca ccaacaacat 720
gatatgtgct ggactggacc ggggccagga cccttgccag agtgactctg gaggcccccc 780
ggtctgtgac gagaccctcc aaggcatcct ctcgtggggt gtttacccct gtggctctgc 840
ccagcatcca gctgtctaca cccagatctg caaatacatg tcctggatca ataaagtcat 900
acgctccaac tgatccagat gctacgctcc agctgatcca gatgttatgc tcctgctgat 960
ccagatgccc agaggctcca tcgtccatcc tcttcctccc cagtcggctg aactctcccc 1020

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tcattccccc acctatcccc attctctgcc tgtactgaag ctgaaatgca ggaagtggtg 1140
gcaaaggttt attccagaga agccaggaag ccggtcatca cccagcctct gagagcagtt 1200
actggggtca cccaacctga cttcctctgc cactccctgc tgtgtgactt tgggcaagcc 1260
aagtgccctc tctgaacctc agtttcctca tctgcaaaat gggaacaatg acgtgcctac 1320
ctcttagaca tgttgtgagg agactatgat ataacatgtg tatgtaaatc ttcatggtga 1380
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tga                                                               1443

<210> 223
<211> 276
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK10

<400> 223
Met Arg Ala Pro His Leu His Leu Ser Ala Ala Ser Gly Ala Arg Ala
 1               5                  10                  15
Leu Ala Lys Leu Leu Pro Leu Leu Met Ala Gln Leu Trp Ala Ala Glu
            20                  25                  30
Ala Ala Leu Leu Pro Gln Asn Asp Thr Arg Leu Asp Pro Glu Ala Tyr
        35                  40                  45
Gly Ser Pro Cys Ala Arg Gly Ser Gln Pro Trp Gln Val Ser Leu Phe
    50                  55                  60
Asn Gly Leu Ser Phe His Cys Ala Gly Val Leu Val Asp Gln Ser Trp
65                  70                  75                  80
Val Leu Thr Ala Ala His Cys Gly Asn Lys Pro Leu Trp Ala Arg Val
                85                  90                  95
Gly Asp Asp His Leu Leu Leu Leu Gln Gly Glu Gln Leu Arg Arg Thr

            100                 105                 110
Thr Arg Ser Val Val His Pro Lys Tyr His Gln Gly Ser Gly Pro Ile
        115                 120                 125
Leu Pro Arg Arg Thr Asp Glu His Asp Leu Met Leu Leu Lys Leu Ala
    130                 135                 140
Arg Pro Val Val Leu Gly Pro Arg Val Arg Ala Leu Gln Leu Pro Tyr
145                 150                 155                 160
Arg Cys Ala Gln Pro Gly Asp Gln Cys Gln Val Ala Gly Trp Gly Thr
                165                 170                 175
Thr Ala Ala Arg Arg Val Lys Tyr Asn Lys Gly Leu Thr Cys Ser Ser
            180                 185                 190
Ile Thr Ile Leu Ser Pro Lys Glu Cys Glu Val Phe Tyr Pro Gly Val
        195                 200                 205
Val Thr Asn Asn Met Ile Cys Ala Gly Leu Asp Arg Gly Gln Asp Pro
    210                 215                 220
Cys Gln Ser Asp Ser Gly Gly Pro Leu Val Cys Asp Glu Thr Leu Gln
225                 230                 235                 240
Gly Ile Leu Ser Trp Gly Val Tyr Pro Cys Gly Ser Ala Gln His Pro
                245                 250                 255
Ala Val Tyr Thr Gln Ile Cys Lys Tyr Met Ser Trp Ile Asn Lys Val
            260                 265                 270
Ile Arg Ser Asn
        275
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<210> 224
<211> 3226
<212> DNA
<213> Homo sapiens

<220>
<223> Epitheliasin

<400> 224
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gagcgcggca ggtcatattg aacattccag atacctatca ttactcgatg ctgttgataa 120
cagcaagatg gctttgaact cagggtcacc accagctatt ggaccttact atgaaaacca 180
tggataccaa ccggaaaacc cctatcccgc acagcccact gtggtcccca ctgtctacga 240
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gcaggcttcc aaccccgtcg tctgcacgca gcccaaatcc ccatccggga cagtgtgcac 360
ctcaaagact aagaaagcac tgtgcatcac cttgaccctg gggaccttcc tcgtgggagc 420
tgcgctggcc gctggcctac tctggaagtt catgggcagc aagtgctcca actctgggat 480
agagtgcgac tcctcaggta cctgcatcaa cccctctaac tggtgtgatg gcgtgtcaca 540
ctgccccggc ggggaggacg agaatcggtg tgttcgcctc tacggaccaa acttcatcct 600
tcagatgtac tcatctcaga ggaagtcctg gcaccctgtg tgccaagacg actggaacga 660
gaactacggg cgggcggcct gcagggacat gggctataag aataatttt actctagcca 720
aggaatagtg gatgacagcg gatccaccag ctttatgaaa ctgaacacaa gtgccggcaa 780
tgtcgatatc tataaaaaac tgtaccacag tgatgcctgt tcttcaaaag cagtggtttc 840
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cggtgagagc gcgctcccgg gggcctggcc ctggcaggtc agcctgcacg tccagaacgt 960
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ggaaaaacct cttaacaatc catggcattg gacggcattt gcggggattt tgagacaatc 1080
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cgacctagtg aaaccagtgt gtctgcccaa cccaggcatg atgctgcagc cagaacagct 1260
ctgctggatt tccgggtggg gggccaccga ggagaaaggg aagacctcag aagtgctgaa 1320
cgctgccaag gtgcttctca ttgagacaca gagatgcaac agcagatatg tctatgacaa 1380
cctgatcaca ccagccatga tctgtgccgg cttcctgcag gggaacgtcg attcttgcca 1440
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tacaagctgg ggttctggct gtgccaaagc ttacagacca ggagtgtacg ggaatgtgat 1560
ggtattcacg gactggattt atcgacaaat gagggcagac ggctaatcca catggtcttc 1620
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gcccttggtg cgagggaagc aattgaaaag gaacttgccc tgagcactcc tggtgcaggt 2280
ctccacctgc acattgggtg gggctcctgg gagggagact cagccttcct cctcatcctc 2340
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atgctgtggg tttccaacca ggggaagggt ccctttgca ttgccaagtg ccataaccat 2820
gagcactact ctaccatggt tctgcctcct ggccaagcag gctggtttgc aagaatgaaa 2880

tgaatgattc tacagctagg acttaacctt gaaatggaaa gtcttgcaat cccatttgca 2940
ggatccgtct gtgcacatgc ctctgtagag agcagcattc ccagggacct tggaaacagt 3000
tggcactgta aggtgcttgc tccccaagac acatcctaaa aggtgttgta atggtgaaaa 3060
cgtcttcctt ctttattgcc ccttcttatt tatgtgaaca actgtttgtc ttttttgta 3120
tctttttaa actgtaaagt tcaattgtga aaatgaatat catgcaaata aattatgcga 3180
ttttttttc aaagcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3226

<210> 225
<211> 492
<212> PRT
<213> Homo sapiens

<220>
<223> Epitheliasin

<400> 225
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1 5 10 15
Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
20 25 30
Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
100 105 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
115 120 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
130 135 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145 150 155 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
165 170 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
180 185 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
195 200 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210 215 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225 230 235 240
Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
245 250 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
260 265 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
275 280 285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
290 295 300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305 310 315 320
Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn

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                325                 330                 335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
            340                 345                 350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
        355                 360                 365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
    370                 375                 380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385                 390                 395                 400
Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
                405                 410                 415
Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
            420                 425                 430
Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
        435                 440                 445
Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
    450                 455                 460
Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465                 470                 475                 480
Thr Asp Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
                485                 490
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<210> 226
<211> 1280
<212> DNA
<213> Homo sapiens

<220>
<223> Prostase

<400> 226

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tcgcagccct ggcaggcggc actggtcatg gaaaacgaat tgttctgctc gggcgtcctg 180
gtgcatccgc agtgggtgct gtcagccgca cactgtttcc agaactccta caccatcggg 240
ctgggcctgc acagtcttga ggccgaccaa gagccaggga gccagatggt ggaggccagc 300
ctctccgtac ggcacccaga gtacaacaga cccttgctcg ctaacgacct catgctcatc 360
aagttggacg aatccgtgtc cgagtctgac accatccgga gcatcagcat tgcttcgcag 420
tgccctaccg cggggaactc ttgcctcgtt tctggctggg gtctgctggc gaacggcaga 480
atgcctaccg tgctgcagtg cgtgaacgtg tcggtggtgt ctgaggaggt ctgcagtaag 540
ctctatgacc cgctgtacca ccccagcatg ttctgcgccg gcggagggca agaccagaag 600
gactcctgca acggtgactc tgggggggcc ctgatctgca acgggtactt gcagggcctt 660
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tgcaaattca ctgagtggat agagaaaacc gtccaggcca gttaactctg gggactggga 780
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gcccctcctc cctcaggccc aggagtccag gcccccagcc cctcctccct caaaccaagg 900
gtacagatcc ccagcccctc ctccctcaga cccaggagtc cagacccccc agcccctcct 960
ccctcagacc caggagtcca gcccctcctc cctcagaccc aggagtccag acccccccagc 1020
ccctcctccc tcagacccag gggtccaggc ccccaacccc tcctccctca gactcagagg 1080
tccaagcccc caacccctcc ttccccagac ccagaggtcc aggtcccagc ccctcctccc 1140
tcagacccag cggtccaatg ccacctagac tctccctgta cacagtgccc ccttgtggca 1200
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ataaagtcta agagaagcgc                                              1280
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<210> 227
<211> 254

<212> PRT
<213> Homo sapiens

<220>
<223> Prostase

<400> 227

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Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
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Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
            20                  25                  30
Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
        35                  40                  45
Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
    50                  55                  60
Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
65                  70                  75                  80
Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met
                85                  90                  95
Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu
            100                 105                 110
Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu
        115                 120                 125
Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala
    130                 135                 140
Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg
145                 150                 155                 160
Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu
                165                 170                 175
Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys
            180                 185                 190
Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly
        195                 200                 205
Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly
    210                 215                 220
Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu
225                 230                 235                 240
Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
                245                 250
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<210> 228
<211> 1391
<212> DNA
<213> Homo sapiens

<220>
<223> Brain serine proteinase 2

<400> 228

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acacaccctg acccgcatcg ccctgggtct ctcgagcctg ctgcctgctc ccccgcccca 60
ccagccatgg tggtttctgg agcgccccca gccctgggtg ggggctgtct cggcaccttc 120
acctccctgc tgctgctggc gtcgacagcc atcctcaatg cggccaggat acctgttccc 180
ccagcctgtg ggaagcccca gcagctgaac cgggttgtgg gcggcgagga cagcactgac 240
agcgagtggc cctggatcgt gagcatccag aagaatggga cccaccactg cgcaggttct 300
ctgctcacca gccgctgggt gatcactgct gcccactgtt tcaaggacaa cctgaacaaa 360
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ccatacctgt tctctgtgct gctgggggcc tggcagctgg ggaaccctgg ctctcggtcc 420
cagaaggtgg gtgttgcctg ggtggagccc caccctgtgt attcctggaa ggaaggtgcc 480
tgtgcagaca ttgccctggt gcgtctcgag cgctccatac agttctcaga gcgggtcctg 540
cccatctgcc tacctgatgc ctctatccac ctccctccaa acacccactg ctggatctca 600
ggctgggggа gcatccaaga tggagttccc ttgccccacc ctcagaccct gcagaagctg 660
aaggttccta tcatcgactc ggaagtctgc agccatctgt actggcgggg agcaggacag 720
ggacccatca ctgaggacat gctgtgtgcc ggctacttgg agggggagcg ggatgcttgt 780
ctgggcgact ccgggggccc cctcatgtgc caggtggacg gcgcctggct gctggccggc 840
atcatcagct ggggcgaggg ctgtgccgag cgcaacaggc ccggggtcta catcagcctc 900
tctgcgcacc gctcctgggt ggagaagatc gtgcaagggg tgcagctccg cgggcgcgct 960

caggggggtg gggccctcag ggcaccgagc cagggctctg gggccgccgc gcgctcctag 1020
ggcgcagcgg gacgcggggc tcggatctga aaggcggcca gatccacatc tggatctgga 1080
tctgcggcgg cctcgggcgg tttccccccgc cgtaaatagg ctcatctacc tctacctctg 1140
ggggcccgga cggctgctgc ggaaaggaaa ccccctcccc gacccgcccg acggcctcag 1200
gccccgcctc caaggcatca ggccccgccc aacggcctca tgtccccgcc cccacgactt 1260
ccggccccgc cccgggcccc agcgcttttg tgtatataaa tgttaatgat ttttataggt 1320
atttgtaacc ctgcccacat atcttattta ttcctccaat ttcaataaat tatttattct 1380
ccagtgaaaa a 1391

<210> 229
<211> 317
<212> PRT
<213> Homo sapiens

<220>
<223> Brain serine proteinase 2

<400> 229
Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu Gly
 1   5   10   15
Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu Asn Ala
            20   25   30
Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln Gln Leu Asn
        35   40   45
Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu Trp Pro Trp Ile
    50   55   60
Val Ser Ile Gln Lys Asn Gly Thr His His Cys Ala Gly Ser Leu Leu
65   70   75   80
Thr Ser Arg Trp Val Ile Thr Ala Ala His Cys Phe Lys Asp Asn Leu
                85   90   95
Asn Lys Pro Tyr Leu Phe Ser Val Leu Leu Gly Ala Trp Gln Leu Gly
            100   105   110
Asn Pro Gly Ser Arg Ser Gln Lys Val Gly Val Ala Trp Val Glu Pro
        115   120   125
His Pro Val Tyr Ser Trp Lys Glu Gly Ala Cys Ala Asp Ile Ala Leu
    130   135   140
Val Arg Leu Glu Arg Ser Ile Gln Phe Ser Glu Arg Val Leu Pro Ile
145   150   155   160
Cys Leu Pro Asp Ala Ser Ile His Leu Pro Pro Asn Thr His Cys Trp
                165   170   175
Ile Ser Gly Trp Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro
            180   185   190
Gln Thr Leu Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys
        195   200   205
Ser His Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp
    210   215   220

```
Met Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
225                 230                 235                 240
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu Leu
                245                 250                 255
Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn Arg Pro
            260                 265                 270
Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val Glu Lys Ile
        275                 280                 285
Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly Gly Gly Ala Leu
    290                 295                 300
Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala Arg Ser
305                 310                 315
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<210> 230
<211> 1184
<212> DNA
<213> Homo sapiens

<220>
<223> Chymopasin

<400> 230
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gggctgcggc attcctgcca tcaaaccggc actgagcttc agccagagga ttgtcaacgg 120
ggagaatgca gtgttgggct cctggccctg gcaggtgtcc ctgcaggaca gcagcggctt 180
ccacttctgc ggtggttctc tcatcagcca gtcctgggtg gtcactgctg cccactgcaa 240
tgtcagccct ggccgccatt ttgttgtcct gggcgagtat gaccgatcat caaacgcaga 300
gcccttgcag gttctgtccg tctctcgggc cattacacac cctagctgga actctaccac 360
catgaacaat gacgtgacgc tgctgaagct cgcctcgcca gcccagtaca caacacgcat 420
ctcgccagtt tgcctggcat cctcaaacga ggctctgact gaaggcctca cgtgtgtcac 480
caccggctgg ggtcgcctca gtggcgtggg caatgtgaca ccagcacatc tgcagcaggt 540
ggctttgccc ctggtcactg tgaatcagtg ccggcagtac tggggctcaa gtatcactga 600
ctccatgatc tgtgcaggtg gcgcaggtgc ctcctcgtgc cagggtgact ccggaggccc 660
tcttgtctgc cagaagggaa acacatgggt gcttattggt attgtctcct ggggcaccaa 720
aaactgcaat gtgcgcgcac ctgctgtgta tactcgagtt agcaagttca gcacctggat 780
caaccaggtc atagcctaca actgagctca ccacaggccc tccccagctc aacccattaa 840
agacccaggc cctgtcccat catgcattca tgtctgtctt cctggctcag gagaaagaag 900
aggctgttga gggtccgact ccctacttgg acttctggca cagaaggggc tgagtgactc 960
cttgagtagc agtggctctt cctagagtag ccatgccgag gccggggccc ccacccctcc 1020
tccagggcaa ccccttggtc ctacagcaag aagccagaac tgttggaatg aatggcagcc 1080
ctccctggag aggcagcctg tttactgaat acagaggata cgtttacaaa ctgaatacgc 1140
ataataaata actgcacatt ctccatccaa aaaaaaaaaa aaaa   1184

<210> 231
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<223> Chymopasin

<400> 231
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Met Leu Leu Leu Ser Leu Thr Leu Ser Leu Val Leu Leu Gly Ser Ser
 1               5                  10                  15
Trp Gly Cys Gly Ile Pro Ala Ile Lys Pro Ala Leu Ser Phe Ser Gln
            20                  25                  30
```

```
Arg Ile Val Asn Gly Glu Asn Ala Val Leu Gly Ser Trp Pro Trp Gln
        35                  40                  45
Val Ser Leu Gln Asp Ser Ser Gly Phe His Phe Cys Gly Gly Ser Leu
    50                  55                  60
Ile Ser Gln Ser Trp Val Val Thr Ala Ala His Cys Asn Val Ser Pro
65                  70                  75                  80
Gly Arg His Phe Val Val Leu Gly Glu Tyr Asp Arg Ser Ser Asn Ala
                85                  90                  95
Glu Pro Leu Gln Val Leu Ser Val Ser Arg Ala Ile Thr His Pro Ser
            100                 105                 110
Trp Asn Ser Thr Thr Met Asn Asn Asp Val Thr Leu Leu Lys Leu Ala
        115                 120                 125
Ser Pro Ala Gln Tyr Thr Thr Arg Ile Ser Pro Val Cys Leu Ala Ser
    130                 135                 140
Ser Asn Glu Ala Leu Thr Glu Gly Leu Thr Cys Val Thr Thr Gly Trp
145                 150                 155                 160
Gly Arg Leu Ser Gly Val Gly Asn Val Thr Pro Ala His Leu Gln Gln
                165                 170                 175
Val Ala Leu Pro Leu Val Thr Val Asn Gln Cys Arg Gln Tyr Trp Gly
            180                 185                 190
Ser Ser Ile Thr Asp Ser Met Ile Cys Ala Gly Gly Ala Gly Ala Ser
        195                 200                 205
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Gly Asn
    210                 215                 220
Thr Trp Val Leu Ile Gly Ile Val Ser Trp Gly Thr Lys Asn Cys Asn
225                 230                 235                 240
Val Arg Ala Pro Ala Val Tyr Thr Arg Val Ser Lys Phe Ser Thr Trp
                245                 250                 255
Ile Asn Gln Val Ile Ala Tyr Asn
            260
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<210> 232
<211> 1207
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 11 transcript variant 1

<400> 232
ggagtgcagg cttggaaagc aggagagctc agcctacgtc tttaatcctc ctgcccaccc 60
cttggattct gtctccactg ggactcaaga gaggaacctg gggcccgctc ctccccccctc 120
caggccatga ggattctgca gttaatcctg cttgctctgg caacagggct tgtaggggga 180
gagaccagga tcatcaaggg gttcgagtgc aagcctcact cccagccctg gcaggcagcc 240
ctgttcgaga agacgcggct actctgtggg gcgacgctca tcgcccccag atggctcctg 300
acagcagccc actgcctcaa gccccgctac atagttcacc tggggcagca caacctccag 360
aaggaggagg gctgtgagca gacccggaca gccactgagt ccttccccca ccccggcttc 420
aacaacagcc tccccaacaa agaccaccgc aatgacatca tgctggtgaa gatggcatcg 480
ccagtctcca tcacctgggc tgtgcgaccc ctcaccctct cctcacgctg tgtcactgct 540
ggcaccagct gcctcatttc cggctggggc agcacgtcca gcccccagtt acgcctgcct 600
cacaccttgc gatgcgccaa catcaccatc attgagcacc agaagtgtga gaacgcctac 660
cccggcaaca tcacagacac catggtgtgt gccagcgtgc aggaaggggg caaggactcc 720
tgccagggtg actccggggg ccctctggtc tgtaaccagt ctcttcaagg cattatctcc 780
tggggccagg atccgtgtgc gatcacccga aagcctggtg tctacacgaa agtctgcaaa 840
tatgtggact ggatccagga gacgatgaag aacaattaga ctggacccac ccaccacagc 900
ccatcaccct ccatttccac ttggtgtttg gttcctgttc actctgttaa taagaaaccc 960

taagccaaga ccctctacga acattctttg ggcctcctgg actacaggag atgctgtcac 1020
ttaataatca acctggggtt cgaaatcagt gagacctgga ttcaaattct gccttgaaat 1080
attgtgactc tgggaatgac aacacctggt ttgttctctg ttgtatcccc agccccaaag 1140
acagctcctg gccatatatc aaggtttcaa taaatatttg ctaaatgagt gaaaaaaaaa 1200
aaaaaaa 1207

<210> 233
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 11 isoform 1

<400> 233
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
1 5 10 15
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
20 25 30
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
35 40 45
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
50 55 60
Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
65 70 75 80
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
85 90 95
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
100 105 110
Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
115 120 125
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
130 135 140
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
145 150 155 160
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
165 170 175
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
180 185 190
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
195 200 205
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
210 215 220
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
225 230 235 240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
245 250

<210> 234
<211> 1289
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein 11 transcript variant 2

<400> 234
ctgccttgct ccacacctgg tcaggggaga gaggggagga aagccaaggg aagggaccta 60
actgaaaaca aacaagctgg gagaagcagg aatctgcgct cgggttccgc agatgcagag 120
gttgaggtgg ctgcgggact ggaagtcatc gggcagaggt ctcacagcag ccaaggaacc 180
tggggcccgc tcctcccccc tccaggccat gaggattctg cagttaatcc tgcttgctct 240
ggcaacaggg cttgtagggg gagagaccag gatcatcaag gggttcgagt gcaagcctca 300
ctcccagccc tggcaggcag ccctgttcga gaagacgcgg ctactctgtg gggcgacgct 360
catcgccccc agatggctcc tgacagcagc ccactgcctc aagccccgct acatagttca 420
cctggggcag cacaacctcc agaaggagga gggctgtgag cagacccgga cagccactga 480
gtccttcccc caccccggct tcaacaacag cctccccaac aaagaccacc gcaatgacat 540
catgctggtg aagatggcat cgccagtctc catcacctgg gctgtgcgac ccctcaccct 600
ctcctcacgc tgtgtcactg ctggcaccag ctgcctcatt tccggctggg gcagcacgtc 660
cagccccag ttacgcctgc ctcacacctt gcgatgcgcc aacatcacca tcattgagca 720
ccagaagtgt gagaacgcct accccggcaa catcacagac accatggtgt gtgccagcgt 780
gcaggaaggg ggcaaggact cctgccaggg tgactccggg ggccctctgg tctgtaacca 840
gtctcttcaa ggcattatct cctggggcca ggatccgtgt gcgatcaccc gaaagcctgg 900
tgtctacacg aaagtctgca aatatgtgga ctggatccag gagacgatga agaacaatta 960
gactggaccc acccaccaca gcccatcacc ctccatttcc acttggtgtt tggttcctgt 1020
tcactctgtt aataagaaac cctaagccaa gaccctctac gaacattctt tgggcctcct 1080
ggactacagg agatgctgtc acttaataat caacctgggg ttcgaaatca gtgagacctg 1140
gattcaaatt ctgccttgaa atattgtgac tctgggaatg acaacacctg gtttgttctc 1200
tgttgtatcc ccagccccaa agacagctcc tggccatata tcaaggtttc aataaatatt 1260
tgctaaatga gtgaaaaaaa aaaaaaaaa 1289

<210> 235
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein 11 isoform 2

<400> 235
Met Gln Arg Leu Arg Trp Leu Arg Asp Trp Lys Ser Ser Gly Arg Gly
 1   5   10   15
Leu Thr Ala Ala Lys Glu Pro Gly Ala Arg Ser Ser Pro Leu Gln Ala
            20   25   30
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu Val
        35   40   45
Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro His Ser
    50   55   60
Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu Leu Cys Gly
65   70   75   80
Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala Ala His Cys Leu
                85   90   95
Lys Pro Arg Tyr Ile Val His Leu Gly Gln His Asn Leu Gln Lys Glu
            100   105   110
Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr Glu Ser Phe Pro His Pro
        115   120   125
Gly Phe Asn Asn Ser Leu Pro Asn Lys Asp His Arg Asn Asp Ile Met
    130   135   140
Leu Val Lys Met Ala Ser Pro Val Ser Ile Thr Trp Ala Val Arg Pro
145   150   155   160
Leu Thr Leu Ser Ser Arg Cys Val Thr Ala Gly Thr Ser Cys Leu Ile
                165   170   175
Ser Gly Trp Gly Ser Thr Ser Ser Pro Gln Leu Arg Leu Pro His Thr
            180   185   190

```
Leu Arg Cys Ala Asn Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn
        195                 200                 205
Ala Tyr Pro Gly Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln
    210                 215                 220
Glu Gly Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
225                 230                 235                 240
Cys Asn Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys
                245                 250                 255
Ala Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
            260                 265                 270
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
        275                 280
```

<210> 236
<211> 802
<212> DNA
<213> Homo sapiens

<220>
<223> anionic trypsin (II)

<400> 236
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accaccatga atctacttct gatccttacc tttgttgcag ctgctgttgc tgccccctttt 60
gatgatgatg acaagatcgt tgggggctac atctgtgagg agaattctgt cccctaccag 120
gtgtccttga attctggcta ccacttctgc ggtggctccc tcatcagcga acagtgggtg 180
gtgtcagcag gtcactgcta caagtcccgc atccaggtga gactgggaga gcacaacatc 240
gaagtcctgg aggggaatga acagttcatc aatgcagcca agatcatccg ccaccccaaa 300
tacaacagcc ggactctgga caatgacatc ctgctgatca agctctcctc acctgccgtc 360
atcaattccc gcgtgtccgc catctctctg cccactgccc ctccagctgc tggcaccgag 420
tccctcatct ccggctgggg caacactctg agttctggtg ccgactaccc agacgagctg 480
cagtgcctgg atgctcctgt gctgagccag gctgagtgtg aagcctccta ccctggaaag 540
attaccaaca acatgttctg tgtgggcttc ctcgagggag gcaaggattc ctgccagggt 600
gattctggtg gccctgtggt ctccaatgga gagctccaag gaattgtctc ctggggctat 660
ggctgtgccc agaagaacag gcctggagtc tacaccaagg tctacaacta tgtggactgg 720
attaaggaca ccatagctgc caacagctaa agcccctggt ccctctgcag tctctatacc 780
aataaagtga ccctgctctc ac                                          802
```

<210> 237
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> anionic trypsin (II)

<400> 237
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Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala Ala
 1               5                  10                  15
Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Ile Cys Glu Glu
            20                  25                  30
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Tyr His Phe Cys
        35                  40                  45
Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Gly His Cys
    50                  55                  60
Tyr Lys Ser Arg Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
65                  70                  75                  80
```

```
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
                85                  90                  95
Pro Lys Tyr Asn Ser Arg Thr Leu Asp Asn Asp Ile Leu Leu Ile Lys
            100                 105                 110
Leu Ser Ser Pro Ala Val Ile Asn Ser Arg Val Ser Ala Ile Ser Leu
        115                 120                 125
Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Ser Leu Ile Ser Gly Trp
    130                 135                 140
Gly Asn Thr Leu Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
145                 150                 155                 160
Leu Asp Ala Pro Val Leu Ser Gln Ala Glu Cys Glu Ala Ser Tyr Pro
                165                 170                 175
Gly Lys Ile Thr Asn Asn Met Phe Cys Val Gly Phe Leu Glu Gly Gly
            180                 185                 190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Ser Asn Gly
        195                 200                 205
Glu Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Asn
    210                 215                 220
Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys
225                 230                 235                 240
Asp Thr Ile Ala Ala Asn Ser
                245
```

<210> 238
<211> 1475
<212> DNA
<213> Homo sapiens

<220>
<223> LOC144757 peptidase

<400> 238
acctgccgcc atcttgctca ccagcctcca aaatgcggct ggggctcctg agcgtggcgc 60
tgttgtttgt ggggagctct cacttatact cagaccacta ctcgccctct ggaaggcaca 120
ggctcggccc ctcgccggaa ccggcggcta gttcccagca ggctgaggcc gtccgcaaga 180
ggctccggcg gcggagggag ggaggggcgc atgcaaagga ttgtggaaca gcaccgctta 240
aggatgtgtt gcaagggtct cggattatag ggggcaccga agcacaagct ggcgcatggc 300
cgtgggtggt gagcctgcag attaaatatg gccgtgttct tgttcatgta tgtgggggaa 360
ccctagtgag agagaggtgg gtcctcacag ctgcccactg cactaaagac gctagcgatc 420
ctttaatgtg gacagctgtg attggaacta ataatataca tggacgctat cctcatacca 480
agaagataaa aattaaagca atcattattc atccaaactt cattttggaa tcttatgtaa 540
atgatattgc acttttttcac ttaaaaaaag cagtgaggta taatgactat attcagccta 600
tttgcctacc ttttgatgtt ttccaaatcc tggacggaaa cacaaagtgt tttataagtg 660
gctggggaag aacaaaagaa gaaggtaacg ctacaaatat tttacaagat gcagaagtgc 720
attatatttc tcgagagatg tgtaattctg agaggagtta tgggggaata attcctaaca 780
cttcattttg tgcaggtgat gaagatggag cttttgatac ttgcaggggt gacagtgggg 840
gaccattaat gtgctactta ccagaatata aaagattttt tgtaatggga attaccagtt 900
acggacatgg ctgtggtcga agaggttttc ctggtgtcta tattgggcca tccttctacc 960
aaaagtggct gacagagcat ttcttccatg caagcactca aggcatactt actataaata 1020
ttttacgtgg ccagatcctc atagctttat gttttgtcat cttactagca acaacataaa 1080
gaaattctga aggctttcat atctttattt tgcattgtgt ccctttctat gttctatata 1140
atgaacatca tttattcttc tagcaattaa ttgcctacat tagagatttc atgtgaacat 1200
tttatgggct ataagtattg tgacagatat acaattgtaa ttttggcact gaatcacatg 1260
tctccttgaa atatcttgat tattttataa tcataattct gtatctggaa tactcataga 1320
gtttgtacaa aatattcagt taaacatata tgtgtataaa tgccaaataa tagtttataa 1380
ttaaaatgaa agctgtcatt tggttaaatt aataaaaatt ctttcttaga ttttattcta 1440

aaaaaaaaaa aaaaaaaaga aaaaaaaaaa aaaaa 1475

<210> 239
<211> 348
<212> PRT
<213> Homo sapiens

<220>
<223> LOC144757 peptidase

<400> 239
Met Arg Leu Gly Leu Leu Ser Val Ala Leu Leu Phe Val Gly Ser Ser
1 5 10 15
His Leu Tyr Ser Asp His Tyr Ser Pro Ser Gly Arg His Arg Leu Gly
20 25 30
Pro Ser Pro Glu Pro Ala Ala Ser Ser Gln Gln Ala Glu Ala Val Arg
35 40 45
Lys Arg Leu Arg Arg Arg Arg Glu Gly Gly Ala His Ala Lys Asp Cys
50 55 60
Gly Thr Ala Pro Leu Lys Asp Val Leu Gln Gly Ser Arg Ile Ile Gly
65 70 75 80
Gly Thr Glu Ala Gln Ala Gly Ala Trp Pro Trp Val Val Ser Leu Gln
85 90 95
Ile Lys Tyr Gly Arg Val Leu Val His Val Cys Gly Gly Thr Leu Val
100 105 110
Arg Glu Arg Trp Val Leu Thr Ala Ala His Cys Thr Lys Asp Ala Ser
115 120 125
Asp Pro Leu Met Trp Thr Ala Val Ile Gly Thr Asn Asn Ile His Gly
130 135 140
Arg Tyr Pro His Thr Lys Lys Ile Lys Ile Lys Ala Ile Ile Ile His
145 150 155 160
Pro Asn Phe Ile Leu Glu Ser Tyr Val Asn Asp Ile Ala Leu Phe His
165 170 175
Leu Lys Lys Ala Val Arg Tyr Asn Asp Tyr Ile Gln Pro Ile Cys Leu
180 185 190
Pro Phe Asp Val Phe Gln Ile Leu Asp Gly Asn Thr Lys Cys Phe Ile
195 200 205
Ser Gly Trp Gly Arg Thr Lys Glu Glu Gly Asn Ala Thr Asn Ile Leu
210 215 220
Gln Asp Ala Glu Val His Tyr Ile Ser Arg Glu Met Cys Asn Ser Glu
225 230 235 240
Arg Ser Tyr Gly Gly Ile Ile Pro Asn Thr Ser Phe Cys Ala Gly Asp
245 250 255
Glu Asp Gly Ala Phe Asp Thr Cys Arg Gly Asp Ser Gly Gly Pro Leu
260 265 270
Met Cys Tyr Leu Pro Glu Tyr Lys Arg Phe Phe Val Met Gly Ile Thr
275 280 285
Ser Tyr Gly His Gly Cys Gly Arg Arg Gly Phe Pro Gly Val Tyr Ile
290 295 300
Gly Pro Ser Phe Tyr Gln Lys Trp Leu Thr Glu His Phe Phe His Ala
305 310 315 320

Ser Thr Gln Gly Ile Leu Thr Ile Asn Ile Leu Arg Gly Gln Ile Leu
325 330 335
Ile Ala Leu Cys Phe Val Ile Leu Leu Ala Thr Thr
340 345

<210> 240
<211> 1164
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA169 peptidase

<400> 240
atgattgccg ttctcattgt gttgtccctg acagtggtgg cagtgaccat aggtctcctg 60
gttcacttcc tagtatttga ccaaaaaaag gagtactatc atggctcctt taaaatttta 120
gatccacaaa tcaataacaa tttcggacaa agcaacacat atcaacttaa ggacttacga 180
gagacgaccg aaaatttggt ggatgagata tttatagatt cagcctggaa gaaaaattat 240
atcaagaacc aagtagtcag actgactcca gaggaagatg gtgtgaaagt agatgtcatt 300
atggtgttcc agttcccctc tactgaacaa agggcagtaa gagagaagaa aatccaaagc 360
atcttaaatc agaagataag gaatttaaga gccttgccaa taaatgcctc atcagttcaa 420
gttaatggtt gtggtaaacg agttgttcca ttaaacgtca acagaatagc atctggagtc 480
attgcaccca aggcggcctg gccttggcaa gcttcccttc agtatgataa catccatcag 540
tgtggggcca ccttgattag taacacatgg cttgtcactg cagcacactg cttccagaag 600
tataaaaatc cacatcaatg gactgttagt tttggaacaa aaatcaaccc tcccttaatg 660
aaaagaaatg tcagaagatt tattatccat gagaagtacc gctctgcagc aagagagtac 720
gacattgctg ttgtgcaggt ctcttccaga gtcacctttt cggatgacat acgccagatt 780
tgtttgccag aagcctctgc atccttccaa ccaaatttga ctgtccacat cacaggattt 840
ggagcacttt actatggtgg ggaatcccaa aatgatctcc gagaagccag agtgaaaatc 900
ataagtgatg atgtctgcaa gcaaccacag gtgtatggca atgatataaa acctggaatg 960
ttctgtgccg gatatatgga aggaatttat gatgcctgca ggggtgattc tgggggacct 1020
ttagtcacaa gggatctgaa agatacgtgg tatctcattg gaattgtaag ctggggagat 1080
aactgtggtc aaaaggacaa gcctggagtc tacacacaag tgacttatta ccgaaactgg 1140
attgcttcaa aaacaggcat ctaa 1164

<210> 241
<211> 387
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA169 peptidase

<400> 241
Met Ile Ala Val Leu Ile Val Leu Ser Leu Thr Val Val Ala Val Thr
 1   5   10   15
Ile Gly Leu Leu Val His Phe Leu Val Phe Asp Gln Lys Lys Glu Tyr
            20   25   30
Tyr His Gly Ser Phe Lys Ile Leu Asp Pro Gln Ile Asn Asn Asn Phe
        35   40   45
Gly Gln Ser Asn Thr Tyr Gln Leu Lys Asp Leu Arg Glu Thr Thr Glu
    50   55   60
Asn Leu Val Asp Glu Ile Phe Ile Asp Ser Ala Trp Lys Lys Asn Tyr
65   70   75   80
Ile Lys Asn Gln Val Val Arg Leu Thr Pro Glu Glu Asp Gly Val Lys
                85   90   95
Val Asp Val Ile Met Val Phe Gln Phe Pro Ser Thr Glu Gln Arg Ala
            100   105   110
Val Arg Glu Lys Lys Ile Gln Ser Ile Leu Asn Gln Lys Ile Arg Asn
        115   120   125
Leu Arg Ala Leu Pro Ile Asn Ala Ser Ser Val Gln Val Asn Gly Cys

```
    130                 135                 140
Gly Lys Arg Val Val Pro Leu Asn Val Asn Arg Ile Ala Ser Gly Val
145                 150                 155                 160
Ile Ala Pro Lys Ala Ala Trp Pro Trp Gln Ala Ser Leu Gln Tyr Asp
                165                 170                 175
Asn Ile His Gln Cys Gly Ala Thr Leu Ile Ser Asn Thr Trp Leu Val
            180                 185                 190
Thr Ala Ala His Cys Phe Gln Lys Tyr Lys Asn Pro His Gln Trp Thr
        195                 200                 205
Val Ser Phe Gly Thr Lys Ile Asn Pro Pro Leu Met Lys Arg Asn Val
    210                 215                 220
Arg Arg Phe Ile Ile His Glu Lys Tyr Arg Ser Ala Ala Arg Glu Tyr
225                 230                 235                 240
Asp Ile Ala Val Val Gln Val Ser Ser Arg Val Thr Phe Ser Asp Asp
                245                 250                 255
Ile Arg Gln Ile Cys Leu Pro Glu Ala Ser Ala Ser Phe Gln Pro Asn
            260                 265                 270
Leu Thr Val His Ile Thr Gly Phe Gly Ala Leu Tyr Tyr Gly Gly Glu
        275                 280                 285
Ser Gln Asn Asp Leu Arg Glu Ala Arg Val Lys Ile Ile Ser Asp Asp
    290                 295                 300
Val Cys Lys Gln Pro Gln Val Tyr Gly Asn Asp Ile Lys Pro Gly Met
305                 310                 315                 320
Phe Cys Ala Gly Tyr Met Glu Gly Ile Tyr Asp Ala Cys Arg Gly Asp
                325                 330                 335
Ser Gly Gly Pro Leu Val Thr Arg Asp Leu Lys Asp Thr Trp Tyr Leu
            340                 345                 350
Ile Gly Ile Val Ser Trp Gly Asp Asn Cys Gly Gln Lys Asp Lys Pro
        355                 360                 365
Gly Val Tyr Thr Gln Val Thr Tyr Tyr Arg Asn Trp Ile Ala Ser Lys
    370                 375                 380
Thr Gly Ile
385
```

<210> 242
<211> 431
<212> PRT
<213> Rattus norvegicus

<220>
<223> Mername-AA171 peptidase

```
<400> 242
Met Ala Arg Gly Gln Pro Arg Arg Ser Glu Glu Pro Trp Thr Ala Leu
 1                5                  10                  15
Arg Asn Arg Thr Glu Cys Lys Thr Lys Ile Lys Leu Thr Lys Cys Gly
            20                  25                  30
Lys Ile Thr Leu Gly Ile Leu Thr Ala Val Ile Ala Ala Val Val Ile
        35                  40                  45
Gly Leu Ile Ala Tyr Phe Ala Ala Cys Gly Lys Thr Pro Phe Tyr Tyr
    50                  55                  60
His Val Ser Phe Lys Val Asn Asn Ile Asp Tyr Asp Ser Lys Phe Ala
65                  70                  75                  80
Lys Pro Tyr Ser Gln Glu Tyr Met Asp Leu Asn Lys Arg Ile Val Ser
                85                  90                  95
Leu Met Asn Glu Thr Phe His Glu Ser Lys Leu Arg Lys Gln Tyr Val
```

```
                100                 105                 110
Lys Ala His Thr Val Gln Val Ser Lys Ala Lys Gly Lys Val Val Ile
        115                 120                 125
His Gly Val Leu Lys Phe Lys Ser Cys Tyr Lys Asn Asn Val Glu Lys
    130                 135                 140
Phe Trp Asp Ser Val Glu Thr Ile Leu Tyr Gln Lys Leu Lys Ser Gln
145                 150                 155                 160
Thr Arg Leu Leu Ile Asp Ser Ser Ser Phe Lys Phe Ser Asp Ile Ala
                165                 170                 175
Met Pro Ile Ala Glu Asp Leu Leu Asn Thr Cys Cys Gly Arg Arg Thr
            180                 185                 190
Ile Thr Pro Gly Gly His Lys Val Ala Gly Gly Gln Asp Ala Glu Glu
        195                 200                 205
Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Gln Asn Asn Val His Arg
    210                 215                 220
Cys Gly Ala Thr Leu Ile Ser Asn Ser Trp Leu Ile Thr Ala Ala His
225                 230                 235                 240
Cys Phe Val Arg Ser Ala Asn Pro Lys Asp Trp Lys Val Ser Phe Gly
                245                 250                 255
Phe Leu Leu Ser Lys Pro Gln Ala Gln Arg Ala Val Lys Ser Ile Val
            260                 265                 270
Ile His Glu Asn Tyr Ser Tyr Pro Ala His Asn Asn Asp Ile Ala Val
        275                 280                 285
Val Arg Leu Ser Ser Pro Val Leu Tyr Glu Asn Asn Ile Arg Arg Ala
    290                 295                 300
Cys Leu Pro Glu Ala Thr Gln Lys Phe Pro Pro Asn Ser Asp Val Val
305                 310                 315                 320
Val Thr Gly Trp Gly Thr Leu Lys Ser Asp Gly Asp Ser Pro Asn Ile
                325                 330                 335
Leu Gln Lys Gly Arg Val Lys Ile Ile Asp Asn Lys Thr Cys Asn Ser
            340                 345                 350
Gly Lys Ala Tyr Gly Gly Val Ile Thr Pro Gly Met Leu Cys Ala Gly
        355                 360                 365
Phe Leu Glu Gly Arg Val Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro
    370                 375                 380
Leu Val Ser Glu Asp Ser Lys Gly Ile Trp Phe Leu Ala Gly Ile Val
385                 390                 395                 400
Ser Trp Gly Asp Glu Cys Ala Leu Pro Asn Lys Pro Gly Val Tyr Thr
                405                 410                 415
Arg Val Thr His Tyr Arg Asp Trp Ile Ser Ser Lys Thr Gly Leu
            420                 425                 430
```

<210> 243
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA174 peptidase

<400> 243

```
Met Asn Pro Leu Leu Ile Leu Ala Phe Val Gly Ala Ala Val Ala Val
 1               5                  10                  15
Pro Phe Asp Asp Asp Asp Lys Ile Val Gly Gly Tyr Thr Cys Glu Glu
            20                  25                  30
Asn Ser Val Pro Tyr Gln Val Ser Leu Asn Ser Gly Ser His Phe Cys
```

```
        35                  40                  45
Gly Gly Ser Leu Ile Ser Glu Gln Trp Val Val Ser Ala Gly His Cys
    50                  55                  60
Tyr Lys Pro His Ile Gln Val Arg Leu Gly Glu His Asn Ile Glu Val
65                  70                  75                  80
Leu Glu Gly Asn Glu Gln Phe Ile Asn Ala Ala Lys Ile Ile Arg His
                85                  90                  95
Pro Lys Tyr Asn Arg Ile Thr Leu Asn Asn Asp Ile Met Leu Ile Lys
            100                 105                 110
Leu Ser Thr Pro Ala Val Ile Asn Ala His Val Ser Thr Ile Ser Leu
        115                 120                 125
Pro Thr Ala Pro Pro Ala Ala Gly Thr Glu Cys Leu Ile Ser Gly Trp
    130                 135                 140
Gly Asn Thr Leu Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys
145                 150                 155                 160
Leu Asp Ala Pro Val Leu Thr Gln Ala Lys Cys Lys Ala Ser Tyr Pro
                165                 170                 175
Leu Lys Ile Thr Ser Lys Met Phe Cys Val Gly Phe Leu Glu Gly Gly
            180                 185                 190
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Val Val Cys Asn Gly
        195                 200                 205
Gln Leu Gln Gly Ile Val Ser Trp Gly Tyr Gly Cys Ala Gln Lys Arg
    210                 215                 220
Arg Pro Gly Val Tyr Thr Lys Val Tyr Asn Tyr Val Asp Trp Ile Lys
225                 230                 235                 240
Asp Thr Ile Ala Ala Asn Ser
                245
```

<210> 244
<211> 1099
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA175 peptidase

<400> 244
gcacagccca gggccatgct cctgttctca gtgttgctgc tcctgtccct ggtcacggga 60
actcagctcg gtccacggac tcctctccca gaggctggag tggctatcct aggcagggct 120
aggggagccc accgccctca gccccgtcat ccccccagcc cagtcagtga atgtggtgac 180
agatctattt tcgagggaag aactcggtat tccagaatca caggggggat ggaggcggag 240
gtgggtgagt ttccgtggca ggtgagtatt caggcaagaa gtgaaccttt ctgtggcggc 300
tccatcctca acaagtggtg gattctcact gcggctcact gcttatattc cgaggagctg 360
tttccagaag aactgagtgt cgtgctgggg accaacgact taactagccc atccatggaa 420
ataaaggagg tcgccagcat cattcttcac aaagacttta agagagccaa catggacaat 480
gacattgcct tgctgctgct ggcttcgccc atcaagctcg atgacctgaa ggtgcccatc 540
tgcctcccca cgcagcccgg ccctgccaca tggcgcgaat gctgggtggc aggttggggc 600
cagaccaatg ctgctgacaa aaactctgtg aaaacggatc tgatgaaagt gccaatggtc 660
atcatggact gggaggagtg ttcaaagatg tttccaaaac ttaccaaaaa tatgctgtgt 720
gccggataca agaatgagag ctatgatgcc tgcaagggtg acagtggggg gcctctggtc 780
tgcaccccag agcctggtga gaagtggtac caggtgggca tcatcagctg gggaaagagc 840
tgtggagaga agaacacccc agggatatac acctcgttgg tgaactacaa cctctggatc 900
gagaaagtga cccagctaga gggcaggccc ttcaatgcag agaaaaggag gacttctgtc 960
aaacagaaac ctatgggctc cccagtctcg ggagtcccag agccaggcag ccccagatcc 1020
tggctcctgc tctgtccccc gtcccatgtg ttgttcagag ctattttgta ctgataataa 1080
aatagaggct attctttca 1099

<210> 245
<211> 352
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA175 peptidase

<400> 245
Met Leu Leu Phe Ser Val Leu Leu Leu Leu Ser Leu Val Thr Gly Thr
 1   5   10   15
Gln Leu Gly Pro Arg Thr Pro Leu Pro Glu Ala Gly Val Ala Ile Leu
            20   25   30
Gly Arg Ala Arg Gly Ala His Arg Pro Gln Pro Arg His Pro Pro Ser
        35   40   45
Pro Val Ser Glu Cys Gly Asp Arg Ser Ile Phe Glu Gly Arg Thr Arg
    50   55   60
Tyr Ser Arg Ile Thr Gly Gly Met Glu Ala Glu Val Gly Glu Phe Pro
65   70   75   80
Trp Gln Val Ser Ile Gln Ala Arg Ser Glu Pro Phe Cys Gly Gly Ser
                85   90   95
Ile Leu Asn Lys Trp Trp Ile Leu Thr Ala Ala His Cys Leu Tyr Ser
            100   105   110
Glu Glu Leu Phe Pro Glu Glu Leu Ser Val Val Leu Gly Thr Asn Asp
        115   120   125
Leu Thr Ser Pro Ser Met Glu Ile Lys Glu Val Ala Ser Ile Ile Leu
    130   135   140
His Lys Asp Phe Lys Arg Ala Asn Met Asp Asn Asp Ile Ala Leu Leu
145   150   155   160
Leu Leu Ala Ser Pro Ile Lys Leu Asp Asp Leu Lys Val Pro Ile Cys
                165   170   175
Leu Pro Thr Gln Pro Gly Pro Ala Thr Trp Arg Glu Cys Trp Val Ala
            180   185   190
Gly Trp Gly Gln Thr Asn Ala Ala Asp Lys Asn Ser Val Lys Thr Asp
        195   200   205
Leu Met Lys Val Pro Met Val Ile Met Asp Trp Glu Glu Cys Ser Lys
    210   215   220
Met Phe Pro Lys Leu Thr Lys Asn Met Leu Cys Ala Gly Tyr Lys Asn
225   230   235   240
Glu Ser Tyr Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys
                245   250   255
Thr Pro Glu Pro Gly Glu Lys Trp Tyr Gln Val Gly Ile Ile Ser Trp
            260   265   270
Gly Lys Ser Cys Gly Glu Lys Asn Thr Pro Gly Ile Tyr Thr Ser Leu
        275   280   285
Val Asn Tyr Asn Leu Trp Ile Glu Lys Val Thr Gln Leu Glu Gly Arg
    290   295   300
Pro Phe Asn Ala Glu Lys Arg Arg Thr Ser Val Lys Gln Lys Pro Met
305   310   315   320
Gly Ser Pro Val Ser Gly Val Pro Glu Pro Gly Ser Pro Arg Ser Trp
                325   330   335
Leu Leu Leu Cys Pro Leu Ser His Val Leu Phe Arg Ala Ile Leu Tyr
            340   345   350

<210> 246

<211> 1927
<212> DNA
<213> Homo sapiens

<220>
<223> stratum corneum chymotryptic enzyme transcript variant 1

<400> 246
tgccagccca agtcggaact tggatcacat cagatcctct cgagctccag caggagaggc 60
ccttcctcgc ctggcagccc ctgagcggct cagcagggca ccatggcaag atcccttctc 120
ctgcccctgc agatcttact gctatcctta gccttggaaa ctgcaggaga agaagcccag 180
ggtgacaaga ttattgatgg cgccccatgt gcaagaggct cccacccatg gcaggtggcc 240
ctgctcagtg gcaatcagct ccactgcgga ggcgtcctgg tcaatgagcg ctgggtgctc 300
actgccgccc actgcaagat gaatgagtac accgtgcacc tgggcagtga tacgctgggc 360
gacaggagag ctcagaggat caaggcctcg aagtcattcc gccaccccgg ctactccaca 420
cagacccatg ttaatgacct catgctcgtg aagctcaata gccaggccag gctgtcatcc 480
atggtgaaga aagtcaggct gccctcccgc tgcgaacccc ctggaaccac ctgtactgtc 540
tccggctggg gcactaccac gagcccagat gtgacctttc cctctgacct catgtgcgtg 600
gatgtcaagc tcatctcccc ccaggactgc acgaaggttt acaaggactt actggaaaat 660
tccatgctgt gcgctggcat ccccgactcc aagaaaaacg cctgcaatgg tgactcaggg 720
ggaccgttgg tgtgcagagg taccctgcaa ggtctggtgt cctggggaac tttcccttgc 780
ggccaaccca atgacccagg agtctacact caagtgtgca agttcaccaa gtggataaat 840
gacaccatga aaaagcatcg ctaacgccac actgagttaa ttaactgtgt gcttccaaca 900
gaaaatgcac aggagtgagg acgccgatga cctatgaagt caaatttgac tttacctttc 960
ctcaaagata tatttaaacc aacctcatgc cctgttgata aaccaatcaa attggtaaag 1020
acctaaaacc aaaacaaata aagaaacaca aaaccctcag tgctggagaa gagtcagtga 1080
gaccagcact ctcaaacact ggaactggac gttcgtacag tctttacgga agacacttgg 1140
tcaacgtaca ccgagaccct tattcaccac ctttgaccca gtaactctaa tcttaggaag 1200
aacctactga aacaaaaaaa atccaaaatg tagaacaaga cttgaattta ccatgatatt 1260
atttatcaca gaaatgaagt gaaaccatca aacatgttcc aaaagtacca gatggcttaa 1320
ataatagtct ggcttggcac aacgatgttt tttttctttg agacagagtc tctgttgctt 1380
gggctgcaat gcagtgatgc aatcttggct cactgcaacc tccgcctcct gggttcaagt 1440
gattctcgtg cttcagcctc ccaagtacct gggactacag gtgtgcacca ccacaccagg 1500
ctaatttttt gtgtattttt actagagaca gggtttcacc atgttggcca gcgtggtctt 1560
gaacgcctga cctcagatga tccacccacc ttggcctccc aaagtgctgg gattacaggc 1620
atgagccacc acggccagcc cacaatgata ttacaaacct attaaaaatg atacttagac 1680
agaattgtca gtattattca agaacattta ggctatagga tgttaaatga caaaaggaag 1740
gacaaaaata tatatgtatg tgaccctacc cataaaaaat gaaatattca cagaatcaga 1800
tctgaaaaca catgtcccag actgcatact ggggtcgtca tgaggtgtct ccttccttct 1860
gtgtactttt ccttgaatgt gcacttttat aacatgaaaa ataaaggtgg ggaaaaaagt 1920
ctgaaga 1927

<210> 247
<211> 253
<212> PRT
<213> Homo sapiens

<220>
<223> stratum corneum chymotryptic enzyme transcript variant 1

<400> 247
Met Ala Arg Ser Leu Leu Leu Pro Leu Gln Ile Leu Leu Leu Ser Leu
 1   5   10   15
Ala Leu Glu Thr Ala Gly Glu Glu Ala Gln Gly Asp Lys Ile Ile Asp
            20   25   30
Gly Ala Pro Cys Ala Arg Gly Ser His Pro Trp Gln Val Ala Leu Leu
        35   40   45

```
Ser Gly Asn Gln Leu His Cys Gly Gly Val Leu Val Asn Glu Arg Trp
    50                  55                  60
Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val His Leu
65                  70                  75                  80
Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile Lys Ala Ser
                85                  90                  95
Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr His Val Asn Asp
            100                 105                 110
Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg Leu Ser Ser Met Val
        115                 120                 125
Lys Lys Val Arg Leu Pro Ser Arg Cys Glu Pro Pro Gly Thr Thr Cys
    130                 135                 140
Thr Val Ser Gly Trp Gly Thr Thr Thr Ser Pro Asp Val Thr Phe Pro
145                 150                 155                 160
Ser Asp Leu Met Cys Val Asp Val Lys Leu Ile Ser Pro Gln Asp Cys
                165                 170                 175
Thr Lys Val Tyr Lys Asp Leu Leu Glu Asn Ser Met Leu Cys Ala Gly
            180                 185                 190
Ile Pro Asp Ser Lys Lys Asn Ala Cys Asn Gly Asp Ser Gly Gly Pro
        195                 200                 205
Leu Val Cys Arg Gly Thr Leu Gln Gly Leu Val Ser Trp Gly Thr Phe
    210                 215                 220
Pro Cys Gly Gln Pro Asn Asp Pro Gly Val Tyr Thr Gln Val Cys Lys
225                 230                 235                 240
Phe Thr Lys Trp Ile Asn Asp Thr Met Lys Lys His Arg
                245                 250
```

<210> 248
<211> 1927
<212> DNA
<213> Homo sapiens

<220>
<223> stratum corneum chymotryptic enzyme transcript variant 2

<400> 248
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ggagagggtg atgctggctc caagcctgac tctgctctcg agagctccag caggagaggc 60
ccttcctcgc ctggcagccc ctgagcggct cagcagggca ccatggcaag atcccttctc 120
ctgcccctgc agatcttact gctatcctta gccttggaaa ctgcaggaga agaagcccag 180
ggtgacaaga ttattgatgg cgccccatgt gcaagaggct cccacccatg gcaggtggcc 240
ctgctcagtg gcaatcagct ccactgcgga ggcgtcctgg tcaatgagcg ctgggtgctc 300
actgccgccc actgcaagat gaatgagtac accgtgcacc tgggcagtga tacgctgggc 360
gacaggagag ctcagaggat caaggcctcg aagtcattcc gccaccccgg ctactccaca 420
cagacccatg ttaatgacct catgctcgtg aagctcaata gccaggccag gctgtcatcc 480
atggtgaaga aagtcaggct gccctcccgc tgcgaacccc ctggaaccac ctgtactgtc 540
tccggctggg gcactaccac gagcccagat gtgacctttc cctctgacct catgtgcgtg 600
gatgtcaagc tcatctcccc ccaggactgc acgaaggttt acaaggactt actggaaaat 660
tccatgctgt gcgctggcat ccccgactcc aagaaaaacg cctgcaatgg tgactcaggg 720
ggaccgttgg tgtgcagagg taccctgcaa ggtctggtgt cctggggaac tttcccttgc 780
ggccaaccca atgacccagg agtctacact caagtgtgca agttcaccaa gtggataaat 840
gacaccatga aaaagcatcg ctaacgccac actgagttaa ttaactgtgt gcttccaaca 900
gaaaatgcac aggagtgagg acgccgatga cctatgaagt caaatttgac tttacctttc 960
ctcaaagata tatttaaacc aacctcatgc cctgttgata aaccaatcaa attggtaaag 1020
acctaaaacc aaaacaaata aagaaacaca aaaccctcag tgctggagaa gagtcagtga 1080
gaccagcact ctcaaacact ggaactggac gttcgtacag tctttacgga agacacttgg 1140
tcaacgtaca ccgagaccct tattcaccac ctttgaccca gtaactctaa tcttaggaag 1200
```

```
aacctactga aacaaaaaaa atccaaaatg tagaacaaga cttgaattta ccatgatatt 1260
atttatcaca gaaatgaagt gaaaccatca aacatgttcc aaaagtacca gatggcttaa 1320
ataatagtct ggcttggcac aacgatgttt ttttttctttg agacagagtc tctgttgctt 1380
gggctgcaat gcagtgatgc aatcttggct cactgcaacc tccgcctcct gggttcaagt 1440
gattctcgtg cttcagcctc ccaagtacct gggactacag gtgtgcacca ccacaccagg 1500
ctaatttttt gtgtattttt actagagaca gggtttcacc atgttggcca gcgtggtctt 1560
gaacgcctga cctcagatga tccacccacc ttggcctccc aaagtgctgg gattacaggc 1620
atgagccacc acggccagcc cacaatgata ttacaaacct attaaaaatg atacttagac 1680
agaattgtca gtattattca agaacattta ggctatagga tgttaaatga caaaaggaag 1740
gacaaaaata tatatgtatg tgaccctacc cataaaaaat gaaatattca cagaatcaga 1800
tctgaaaaca catgtcccag actgcatact ggggtcgtca tgaggtgtct ccttccttct 1860
gtgtactttt ccttgaatgt gcacttttat aacatgaaaa ataaaggtgg ggaaaaaagt 1920
ctgaaga                                                          1927
```

<210> 249
<211> 253
<212> PRT
<213> Homo sapiens

<220>
<223> stratum corneum chymotryptic enzyme

<400> 249

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Met Ala Arg Ser Leu Leu Leu Pro Leu Gln Ile Leu Leu Leu Ser Leu
 1               5                  10                  15
Ala Leu Glu Thr Ala Gly Glu Glu Ala Gln Gly Asp Lys Ile Ile Asp
            20                  25                  30
Gly Ala Pro Cys Ala Arg Gly Ser His Pro Trp Gln Val Ala Leu Leu
        35                  40                  45
Ser Gly Asn Gln Leu His Cys Gly Gly Val Leu Val Asn Glu Arg Trp
    50                  55                  60
Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val His Leu
65                  70                  75                  80
Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile Lys Ala Ser
                85                  90                  95
Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr His Val Asn Asp
            100                 105                 110
Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg Leu Ser Ser Met Val
        115                 120                 125
Lys Lys Val Arg Leu Pro Ser Arg Cys Glu Pro Pro Gly Thr Thr Cys
    130                 135                 140
Thr Val Ser Gly Trp Gly Thr Thr Thr Ser Pro Asp Val Thr Phe Pro
145                 150                 155                 160
Ser Asp Leu Met Cys Val Asp Val Lys Leu Ile Ser Pro Gln Asp Cys
                165                 170                 175
Thr Lys Val Tyr Lys Asp Leu Leu Glu Asn Ser Met Leu Cys Ala Gly
            180                 185                 190
Ile Pro Asp Ser Lys Lys Asn Ala Cys Asn Gly Asp Ser Gly Gly Pro
        195                 200                 205
Leu Val Cys Arg Gly Thr Leu Gln Gly Leu Val Ser Trp Gly Thr Phe
    210                 215                 220
Pro Cys Gly Gln Pro Asn Asp Pro Gly Val Tyr Thr Gln Val Cys Lys
225                 230                 235                 240
Phe Thr Lys Trp Ile Asn Asp Thr Met Lys Lys His Arg
                245                 250
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<210> 250
<211> 2800
<212> DNA
<213> Homo sapiens

<220>
<223> trypsin-like enzyme, respiratory

<400> 250
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tatgtttcat tgtcgtcgca ggggtagtga tcctggcagt caccatagct ctacttgttt 180
acttttagc ttttgatcaa aaatcttact tttataggag cagttttcaa ctcctaaatg 240
ttgaatataa tagtcagtta aattcaccag ctacacagga atacaggact ttgagtggaa 300
gaattgaatc tctgattact aaaacattca aagaatcaaa tttaagaaat cagttcatca 360
gagctcatgt tgccaaactg aggcaagatg gtagtggtgt gagagcggat gttgtcatga 420
aatttcaatt cactagaaat aacaatggag catcaatgaa aagcagaatt gagtctgttt 480
tacgacaaat gctgaataac tctggaaacc tggaaataaa cccttcaact gagataacat 540
cacttactga ccaggctgca gcaaattggc ttattaatga atgtggggcc ggtccagacc 600
taataacatt gtctgagcag agaatccttg gaggcactga ggctgaggag ggaagctggc 660
cgtggcaagt cagtctgcgg ctcaataatg cccaccactg tggaggcagc ctgatcaata 720
acatgtggat cctgacagca gctcactgct tcagaagcaa ctctaatcct cgtgactgga 780
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tgagacccaa agaattatag atatttttca tgatgaccca tgaaaaatat cactcatcta 2040
cataaaggag agactatatc tattttatag agaagctaag aaatatacct acacaaactt 2100
gtcaggtgct ttacaactac atagtacttt ttaacaacaa aataataatt ttaagaatga 2160
aaaatttaat catcgggaag aacgtcccac tacagacttc ctatcactgg cagttatatt 2220
tttgagcgta aaagggtcgt caaacgctaa atctaagtaa cgaattgaaa gtttaaagag 2280
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<210> 251
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<223> trypsin-like enzyme, respiratory

<400> 251
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20 25 30
Thr Ile Ala Leu Leu Val Tyr Phe Leu Ala Phe Asp Gln Lys Ser Tyr
35 40 45
Phe Tyr Arg Ser Ser Phe Gln Leu Leu Asn Val Glu Tyr Asn Ser Gln
50 55 60
Leu Asn Ser Pro Ala Thr Gln Glu Tyr Arg Thr Leu Ser Gly Arg Ile
65 70 75 80
Glu Ser Leu Ile Thr Lys Thr Phe Lys Glu Ser Asn Leu Arg Asn Gln
85 90 95
Phe Ile Arg Ala His Val Ala Lys Leu Arg Gln Asp Gly Ser Gly Val
100 105 110
Arg Ala Asp Val Val Met Lys Phe Gln Phe Thr Arg Asn Asn Asn Gly
115 120 125
Ala Ser Met Lys Ser Arg Ile Glu Ser Val Leu Arg Gln Met Leu Asn
130 135 140
Asn Ser Gly Asn Leu Glu Ile Asn Pro Ser Thr Glu Ile Thr Ser Leu
145 150 155 160
Thr Asp Gln Ala Ala Ala Asn Trp Leu Ile Asn Glu Cys Gly Ala Gly
165 170 175
Pro Asp Leu Ile Thr Leu Ser Glu Gln Arg Ile Leu Gly Gly Thr Glu
180 185 190
Ala Glu Glu Gly Ser Trp Pro Trp Gln Val Ser Leu Arg Leu Asn Asn
195 200 205
Ala His His Cys Gly Gly Ser Leu Ile Asn Asn Met Trp Ile Leu Thr
210 215 220
Ala Ala His Cys Phe Arg Ser Asn Ser Asn Pro Arg Asp Trp Ile Ala
225 230 235 240
Thr Ser Gly Ile Ser Thr Thr Phe Pro Lys Leu Arg Met Arg Val Arg
245 250 255
Asn Ile Leu Ile His Asn Asn Tyr Lys Ser Ala Thr His Glu Asn Asp
260 265 270
Ile Ala Leu Val Arg Leu Glu Asn Ser Val Thr Phe Thr Lys Asp Ile
275 280 285
His Ser Val Cys Leu Pro Ala Ala Thr Gln Asn Ile Pro Pro Gly Ser
290 295 300
Thr Ala Tyr Val Thr Gly Trp Gly Ala Gln Glu Tyr Ala Gly His Thr
305 310 315 320
Val Pro Glu Leu Arg Gln Gly Gln Val Arg Ile Ile Ser Asn Asp Val
325 330 335
Cys Asn Ala Pro His Ser Tyr Asn Gly Ala Ile Leu Ser Gly Met Leu
340 345 350
Cys Ala Gly Val Pro Gln Gly Gly Val Asp Ala Cys Gln Gly Asp Ser
355 360 365
Gly Gly Pro Leu Val Gln Glu Asp Ser Arg Arg Leu Trp Phe Ile Val
370 375 380

```
Gly Ile Val Ser Trp Gly Asp Gln Cys Gly Leu Pro Asp Lys Pro Gly
385                 390                 395                 400
Val Tyr Thr Arg Val Thr Ala Tyr Leu Asp Trp Ile Arg Gln Gln Thr
                405                 410                 415
Gly Ile
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<210> 252
<211> 3149
<212> DNA
<213> Homo sapiens

<220>
<223> Matripase

<400> 252

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tgaatggctt ggaggaaggc gtggagttcc tgccagtcaa caacgtcaag aaggtggaaa 180
agcatggccc ggggcgctgg gtggtgctgg cagccgtgct gatcggcctc ctcttggtct 240
tgctggggat cggcttcctg gtgtggcatt tgcagtaccg ggacgtgcgt gtccagaagg 300
tcttcaatgg ctacatgagg atcacaaatg agaattttgt ggatgcctac gagaactcca 360
actccactga gtttgtaagc ctggccagca aggtgaagga cgcgctgaag ctgctgtaca 420
gcggagtccc attcctgggc ccctaccaca aggagtcggc tgtgacggcc ttcagcgagg 480
gcagcgtcat cgcctactac tggtctgagt tcagcatccc gcagcacctg gtggaggagg 540
ccgagcgcgt catggccgag gagcgcgtag tcatgctgcc cccgcgggcg cgctccctga 600
agtcctttgt ggtcacctca gtggtggctt tccccacgga ctccaaaaca gtacagagga 660
cccaggacaa cagctgcagc tttggcctgc acgcccgcgg tgtggagctg atgcgcttca 720
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ccacgcagtg gacggccttc ctgggcttgc acgaccagag ccagcgcagc gcccctgggg 2100
tgcaggagcg caggctcaag cgcatcatct cccacccctt cttcaatgac ttcaccttcg 2160
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tgtgcgtggg cttcctcagc ggcggcgtgg actcctgcca gggtgattcc gggggacccc 2460
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tgtccagcgt ggaggcggat gggcggatct tccaggccgg tgtggtgagc tggggagacg 2520
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aacattttat ttctttttaa aaaaaaaaa                                   3149
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<210> 253
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Matripase

<400> 253

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Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
```

```
          275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
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His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
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<210> 254
<211> 1258
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK13

<400> 254
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tctcaacacc aatgggacca gtgggtttct cccaggtggc tacacctgct tccccactc 180
tcagccctgg caggctgccc tactagtgca agggcggcta ctctgtgggg gagtcctggt 240
ccaccccaaa tgggtcctca ctgccgcaca ctgtctaaag gaggggctca aagtttacct 300
aggcaagcac gccctagggc gtgtggaagc tggtgagcag gtgagggaag ttgtccactc 360
tatcccccac cctgaatacc ggagaagccc cacccacctg aaccacgacc atgacatcat 420
gcttctggag ctgcagtccc cggtccagct cacaggctac atccaaaccc tgccccttc 480
ccacaacaac cgcctaaccc ctggcaccac ctgtcgggtg tctggctggg gcaccaccac 540
cagccccag gtgaattacc ccaaaactct acaatgtgcc aacatccaac ttcgctcaga 600
tgaggagtgt cgtcaagtct acccaggaaa gatcactgac aacatgttgt gtgccggcac 660
aaaagagggt ggcaaagact cctgtgaggg tgactctggg ggccccctgg tctgtaacag 720
aacactgtat ggcatcgtct cctggggaga cttcccatgt gggcaacctg accggcctgg 780
tgtctacacc cgtgtctcaa gatacgtcct gtggatccgt gaaacaatcc gaaaatatga 840
aacccagcag caaaaatggt tgaagggccc acaataaaag ttgagaaatg taccggcttc 900
catcctgtca ccatgacttc ctcacatggt ctgcttagcc cttctctgct ccttattccc 960
agtgttccat ttgaaccagt gatccatgtc ctgaaaaatg ctcaatctca gctaacattc 1020
catgtttcag aagcattcag gcactgccag gcttgcagtc tcccagatgt tgcatccctg 1080
aaacatctca acaacctgaa tgtcccaacc cagacaatgg cccaggtctc tcaacttcat 1140
cagtgtggct tctatgagcc cagatcacca cctgaacgtt ctgtctgtgg cacattctta 1200
aatatttcca tcagcccatc tcaacaatat atgtcctata aatggaccat ccttgaca 1258

<210> 255
<211> 277
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK13

<400> 255
Met Trp Pro Leu Ala Leu Val Ile Ala Ser Leu Thr Leu Ala Leu Ser
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Gly Gly Val Ser Gln Glu Ser Ser Lys Val Leu Asn Thr Asn Gly Thr
            20   25   30
Ser Gly Phe Leu Pro Gly Gly Tyr Thr Cys Phe Pro His Ser Gln Pro
        35   40   45
Trp Gln Ala Ala Leu Leu Val Gln Gly Arg Leu Leu Cys Gly Gly Val
    50   55   60
Leu Val His Pro Lys Trp Val Leu Thr Ala Ala His Cys Leu Lys Glu
65   70   75   80

Gly Leu Lys Val Tyr Leu Gly Lys His Ala Leu Gly Arg Val Glu Ala
                85   90   95
Gly Glu Gln Val Arg Glu Val Val His Ser Ile Pro His Pro Glu Tyr
            100   105   110
Arg Arg Ser Pro Thr His Leu Asn His Asp His Asp Ile Met Leu Leu
        115   120   125
Glu Leu Gln Ser Pro Val Gln Leu Thr Gly Tyr Ile Gln Thr Leu Pro
    130   135   140
Leu Ser His Asn Asn Arg Leu Thr Pro Gly Thr Thr Cys Arg Val Ser
145   150   155   160
Gly Trp Gly Thr Thr Thr Ser Pro Gln Val Asn Tyr Pro Lys Thr Leu
                165   170   175
Gln Cys Ala Asn Ile Gln Leu Arg Ser Asp Glu Glu Cys Arg Gln Val
            180   185   190
Tyr Pro Gly Lys Ile Thr Asp Asn Met Leu Cys Ala Gly Thr Lys Glu
        195   200   205
Gly Gly Lys Asp Ser Cys Glu Gly Asp Ser Gly Gly Pro Leu Val Cys
    210   215   220
Asn Arg Thr Leu Tyr Gly Ile Val Ser Trp Gly Asp Phe Pro Cys Gly
225   230   235   240
Gln Pro Asp Arg Pro Gly Val Tyr Thr Arg Val Ser Arg Tyr Val Leu
                245   250   255
Trp Ile Arg Glu Thr Ile Arg Lys Tyr Glu Thr Gln Gln Gln Lys Trp
            260   265   270
Leu Lys Gly Pro Gln
        275

<210> 256
<211> 1438
<212> DNA
<213> Homo sapiens

<220>
<223> kallikrein hK9

<400> 256
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ctgctggcag ggcatggctg ggcagacacc cgtgccatcg gggccgagga atgtcgcccc 180
aactcccagc cttggcaggc cggcctcttc caccttactc ggctcttctg tggggcgacc 240
ctcatcagtg accgctggct gctcacagct gcccactgcc gcaagccgta tctgtgggtc 300
cgccttggag agcaccacct ctggaaatgg gagggtccgg agcagctgtt ccgggttacg 360
gacttcttcc cccaccctgg cttcaacaag gacctcagcg ccaatgacca caatgatgac 420
atcatgctga tccgcctgcc caggcaggca cgtctgagtc ctgctgtgca gcccctcaac 480

ctcagccaga cctgtgtctc cccaggcatg cagtgtctca tctcaggctg gggggccgtg 540
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aacaaactct gtcactgggc ataccctgga cacatctcgg acagcatgct ctgtgcgggc 660
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acagtcgcgc cccctcggaa cggagcaggg acacgccctt cagagcccgt ctctatgacg 1080
tcaccgacag ccatcacctc cttcttggaa cagcacagcc tgtggctccg ccccaaggaa 1140
ccacttacac aaaatagctc cgcccctcgg aactttgccc agtgggactt cccctcggga 1200
ctccaccccc tgtggccccg cctccttcac cagagatctc gcccctcgtg atgtcagggg 1260
cgcagtagct ccgcccacgt ggagctcggg cggtgtagag ctcagcccct tgtggccccg 1320
tcctgggcgt gtgctgggtt tgaatcctgg cggagacctg gggggaaatt gagggagggt 1380
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<210> 257
<211> 250
<212> PRT
<213> Homo sapiens

<220>
<223> kallikrein hK9

<400> 257
Met Lys Leu Gly Leu Leu Cys Ala Leu Leu Ser Leu Leu Ala Gly His
1 5 10 15
Gly Trp Ala Asp Thr Arg Ala Ile Gly Ala Glu Glu Cys Arg Pro Asn
20 25 30
Ser Gln Pro Trp Gln Ala Gly Leu Phe His Leu Thr Arg Leu Phe Cys
35 40 45
Gly Ala Thr Leu Ile Ser Asp Arg Trp Leu Leu Thr Ala Ala His Cys
50 55 60
Arg Lys Pro Tyr Leu Trp Val Arg Leu Gly Glu His His Leu Trp Lys
65 70 75 80
Trp Glu Gly Pro Glu Gln Leu Phe Arg Val Thr Asp Phe Phe Pro His
85 90 95
Pro Gly Phe Asn Lys Asp Leu Ser Ala Asn Asp His Asn Asp Asp Ile
100 105 110
Met Leu Ile Arg Leu Pro Arg Gln Ala Arg Leu Ser Pro Ala Val Gln
115 120 125
Pro Leu Asn Leu Ser Gln Thr Cys Val Ser Pro Gly Met Gln Cys Leu
130 135 140
Ile Ser Gly Trp Gly Ala Val Ser Ser Pro Lys Ala Leu Phe Pro Val
145 150 155 160
Thr Leu Gln Cys Ala Asn Ile Ser Ile Leu Glu Asn Lys Leu Cys His
165 170 175
Trp Ala Tyr Pro Gly His Ile Ser Asp Ser Met Leu Cys Ala Gly Leu
180 185 190
Trp Glu Gly Gly Arg Gly Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu
195 200 205
Val Cys Asn Gly Thr Leu Ala Gly Val Val Ser Gly Gly Ala Glu Pro
210 215 220
Cys Ser Arg Pro Arg Arg Pro Ala Val Tyr Thr Ser Val Cys His Tyr
225 230 235 240
Leu Asp Trp Ile Gln Glu Ile Met Glu Asn

245 250

<210> 258
<211> 3212
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA035 peptidase

<400> 258
cttgagccag acccagtcca gctctggtgc ctgccctctg gtgcgagctg acctgagatg 60
cacttccctc ctctgtgagc tgtctcggca cccacttgca gtcactgccg cctgatgttg 120
ttactcttcc actccaaaag gatgcccgtg gccgaggccc cccaggtggc tggcgggcag 180
ggggacggag gtgatggcga ggaagcggag ccggagggga tgttcaaggc ctgtgaggac 240
tccaagagaa aagcccgggg ctacctccgc ctggtgcccc tgtttgtgct gctggccctg 300
ctcgtgctgg cttcggcggg ggtgctactc tggtatttcc tagggtacaa ggcggaggtg 360
atggtcagcc aggtgtactc aggcagtctg cgtgtactca atcgccactt ctcccaggat 420
cttacccgcc gggaatctag tgccttccgc agtgaaaccg ccaaagccca gaagatgctc 480
aaggagctca tcaccagcac ccgcctggga acttactaca actccagctc cgtctattcc 540
tttggggagg gaccctcac ctgcttcttc tggttcattc tccaaatccc cgagcaccgc 600
cggctgatgc tgagccccga ggtggtgcag gcactgctgg tggaggagct gctgtccaca 660
gtcaacagct cggctgccgt cccctacagg gccgagtacg aagtggaccc cgagggccta 720
gtgatcctgg aagccagtgt gaaagacata gctgcattga attccacgct gggttgttac 780
cgctacagct acgtgggcca gggccaggtc ctccggctga aggggcctga ccacctggcc 840
tccagctgcc tgtggcacct gcagggcccc aaggacctca tgctcaaact ccggctggag 900
tggacgctgg cagagtgccg ggaccgactg gccatgtatg acgtggccgg gcccctggag 960
aagaggctca tcacctcggt gtacggctgc agccgccagg agcccgtggt ggaggttctg 1020
gcgtcggggg ccatcatggc ggtcgtctgg aagaagggcc tgcacagcta ctacgacccc 1080
ttcgtgctct ccgtgcagcc ggtggtcttc caggcctgtg aagtgaacct gacgctggac 1140
aacaggctcg actcccaggg cgtcctcagc accccgtact tccccagcta ctactcgccc 1200
caaacccact gctcctggca cctcacggtg ccctctctgg actacggctt ggccctctgg 1260
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acgatccaga acaggaggct gtgtggcttg cgcatcctgc agccctacgc cgagaggatc 1380
cccgtggtgg ccacggccgg gatcaccatc aacttcacct cccagatctc cctcaccggg 1440
cccggtgtgc gggtgcacta tggcttgtac aaccagtcgg acccctgccc tggagagttc 1500
ctctgttctg tgaatggact ctgtgtccct gcctgtgatg gggtcaagga ctgccccaac 1560
ggcctggatg agagaaactg cgtttgcaga gccacattcc agtgcaaaga ggacagcaca 1620
tgcatctcac tgcccaaggt ctgtgatggg cagcctgatt gtctcaacgg cagcgacgaa 1680
gagcagtgcc aggaaggggt gccatgtggg acattcacct tccagtgtga ggaccggagc 1740
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gaggagcact gtgactgtgg cctccagggc ccctccagcc gcattgttgg tggagctgtg 1860
tcctccgagg gtgagtggcc atggcaggcc agcctccagg ttcggggtcg acacatctgt 1920
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agcatggcct ccacggtgct gtggaccgtg ttcctgggca aggtgtggca gaactcgcgc 2040
tggcctggag aggtgtcctt caaggtgagc cgcctgctcc tgcacccgta ccacgaagag 2100
gacagccatg actacgacgt ggcgctgctg cagctcgacc acccggtggt gcgctcggcc 2160
gccgtgcgcc ccgtctgcct gcccgcgcgc tcccacttct tcgagcccgg cctgcactgc 2220
tggattacgg gctggggcgc cttgcgcgag ggcggcccca tcagcaacgc tctgcagaaa 2280
gtggatgtgc agttgatccc acaggacctg tgcagcgagg tctatcgcta ccaggtgacg 2340
ccacgcatgc tgtgtgccgg ctaccgcaag ggcaagaagg atgcctgtca gggtgactca 2400
ggtggtccgc tggtgtgcaa ggcactcagt ggccgctggt tcctggcggg gctggtcagc 2460
tggggcctgg gctgtggccg gcctaactac ttcggcgtct acacccgcat cacaggtgtg 2520
atcagctgga tccagcaagt ggtgacctga ggaactgccc ccctgcaaag cagggcccac 2580
ctcctggact cagagagccc agggcaactg ccaagcaggg ggacaagtat tctggcgggg 2640
ggtgggggag agagcaggcc ctgtggtggc aggaggtggc atcttgtctc gtccctgatg 2700

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tctgctccag tgatggcagg aggatggaga agtgccagca gctgggggtc aagacgtccc 2760
ctgaggaccc aggcccacac ccagcccttc tgcctcccaa ttctctctcc tccgtccgct 2820
tcctccactg ctgcctaatg caaggcagtg gctcagcagc aagaatgctg gttctacatc 2880
ccgaggagtg tctgaggtgc gccccactct gtacagaggc tgtttgggca gccttgcctc 2940
cagagagcag attccagctt cggaagcccc tggtctaact tgggatctgg gaatggaagg 3000
tgctcccatc ggaggggacc ctcagagccc tggagactgc caggtgggcc tgctgccact 3060
gtaagccaaa aggtggggaa gtcctgactc cagggtcctt gccccacccc tgcctgccac 3120
ctgggccctc acagcccaga ccctcactgg gaggtgagct cagctgccct ttggaataaa 3180
gctgcctgat caaaaaaaaa aaaaaaaaaa aa                                3212

<210> 259
<211> 811
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA035 peptidase

<400> 259
Met Leu Leu Leu Phe His Ser Lys Arg Met Pro Val Ala Glu Ala Pro
 1               5                  10                  15
Gln Val Ala Gly Gly Gln Gly Asp Gly Gly Asp Gly Glu Glu Ala Glu
            20                  25                  30
Pro Glu Gly Met Phe Lys Ala Cys Glu Asp Ser Lys Arg Lys Ala Arg
        35                  40                  45
Gly Tyr Leu Arg Leu Val Pro Leu Phe Val Leu Leu Ala Leu Leu Val
    50                  55                  60
Leu Ala Ser Ala Gly Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala
65                  70                  75                  80
Glu Val Met Val Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn
                85                  90                  95
Arg His Phe Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg
            100                 105                 110
Ser Glu Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser
        115                 120                 125
Thr Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly
    130                 135                 140
Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro Glu
145                 150                 155                 160
His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu Leu Val
                165                 170                 175
Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val Pro Tyr Arg
            180                 185                 190
Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile Leu Glu Ala Ser
        195                 200                 205
Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu Gly Cys Tyr Arg Tyr
    210                 215                 220
Ser Tyr Val Gly Gln Gly Gln Val Leu Arg Leu Lys Gly Pro Asp His
225                 230                 235                 240
Leu Ala Ser Ser Cys Leu Trp His Leu Gln Gly Pro Lys Asp Leu Met
                245                 250                 255
Leu Lys Leu Arg Leu Glu Trp Thr Leu Ala Glu Cys Arg Asp Arg Leu
            260                 265                 270
Ala Met Tyr Asp Val Ala Gly Pro Leu Glu Lys Arg Leu Ile Thr Ser
        275                 280                 285
Val Tyr Gly Cys Ser Arg Gln Glu Pro Val Val Glu Val Leu Ala Ser
    290                 295                 300
```

```
Gly Ala Ile Met Ala Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr
305                 310                 315                 320
Asp Pro Phe Val Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu
                325                 330                 335
Val Asn Leu Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser
            340                 345                 350
Thr Pro Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp
        355                 360                 365
His Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp
    370                 375                 380
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln Gly
385                 390                 395                 400
Gln Trp Thr Ile Gln Asn Arg Arg Leu Cys Gly Leu Arg Ile Leu Gln
                405                 410                 415
Pro Tyr Ala Glu Arg Ile Pro Val Val Ala Thr Ala Gly Ile Thr Ile
            420                 425                 430
Asn Phe Thr Ser Gln Ile Ser Leu Thr Gly Pro Gly Val Arg Val His
        435                 440                 445
Tyr Gly Leu Tyr Asn Gln Ser Asp Pro Cys Pro Gly Glu Phe Leu Cys
    450                 455                 460
Ser Val Asn Gly Leu Cys Val Pro Ala Cys Asp Gly Val Lys Asp Cys
465                 470                 475                 480
Pro Asn Gly Leu Asp Glu Arg Asn Cys Val Cys Arg Ala Thr Phe Gln
                485                 490                 495
Cys Lys Glu Asp Ser Thr Cys Ile Ser Leu Pro Lys Val Cys Asp Gly
            500                 505                 510
Gln Pro Asp Cys Leu Asn Gly Ser Asp Glu Glu Gln Cys Gln Glu Gly
        515                 520                 525
Val Pro Cys Gly Thr Phe Thr Phe Gln Cys Glu Asp Arg Ser Cys Val
    530                 535                 540
Lys Lys Pro Asn Pro Gln Cys Asp Gly Arg Pro Asp Cys Arg Asp Gly
545                 550                 555                 560
Ser Asp Glu Glu His Cys Asp Cys Gly Leu Gln Gly Pro Ser Ser Arg
                565                 570                 575
Ile Val Gly Gly Ala Val Ser Ser Glu Gly Glu Trp Pro Trp Gln Ala
            580                 585                 590
Ser Leu Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala
        595                 600                 605
Asp Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met
    610                 615                 620
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln Asn
625                 630                 635                 640
Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu Leu Leu
                645                 650                 655
His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val Ala Leu Leu
            660                 665                 670
Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val Arg Pro Val Cys
        675                 680                 685
Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly Leu His Cys Trp Ile
    690                 695                 700
Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly Pro Ile Ser Asn Ala Leu
705                 710                 715                 720
Gln Lys Val Asp Val Gln Leu Ile Pro Gln Asp Leu Cys Ser Glu Val
                725                 730                 735
Tyr Arg Tyr Gln Val Thr Pro Arg Met Leu Cys Ala Gly Tyr Arg Lys
            740                 745                 750
Gly Lys Lys Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
```

```
        755                 760                 765
Lys Ala Leu Ser Gly Arg Trp Phe Leu Ala Gly Leu Val Ser Trp Gly
    770                 775                 780
Leu Gly Cys Gly Arg Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr
785                 790                 795                 800
Gly Val Ile Ser Trp Ile Gln Gln Val Val Thr
                805                 810
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<210> 260
<211> 3750
<212> DNA
<213> Homo sapiens

<220>
<223> umbilical vein proteinase

<400> 260
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gcgctgctcg ccagcttgct cgcactcggc tgtgcggcgg ggcaggcatg ggagccgcgc 60
gctctctccc ggcgcccaca cctgtctgag cggcgcagcg agccgcggcc cgggcgggct 120
gctcggcgcg gaacagtgct cggcatggca gggattccag ggctcctctt ccttctcttc 180
tttctgctct gtgctgttgg gcaagtgagc ccttacagtg ccccctggaa acccacttgg 240
cctgcatacc gcctccctgt cgtcttgccc cagtctaccc tcaatttagc caagccagac 300
tttggagccg aagccaaatt agaagtatct tcttcatgtg gaccccagtg tcataaggga 360
actccactgc ccacttacga agaggccaag caatatctgt cttatgaaac gctctatgcc 420
aatggcagcc gcacagagac gcaggtgggc atctacatcc tcagcagtag tggagatggg 480
gcccaacacc gagactcagg gtcttcagga aagtctcgaa ggaagcggca gatttatggc 540
tatgacagca ggttcagcat ttttgggaag gacttcctgc tcaactaccc tttctcaaca 600
tcagtgaagt tatccacggg ctgcaccggc accctggtgg cagagaagca tgtcctcaca 660
gctgcccact gcatacacga tggaaaaacc tatgtgaaag gaacccagaa gcttcgagtg 720
ggcttcctaa agcccaagtt taaagatggt ggtcgagggg ccaacgactc cacttcagcc 780
atgcccgagc agatgaaatt tcagtggatc cgggtgaaac gcacccatgt gcccaagggt 840
tggatcaagg gcaatgccaa tgacatcggc atggattatg attatgccct cctggaactc 900
aaaaagcccc acaagagaaa atttatgaag attggggtga gccctcctgc taagcagctg 960
ccaggggca gaattcactt ctctggttat gacaatgacc gaccaggcaa tttggtgtat 1020
cgcttctgtg acgtcaaaga cgagacctat gacttgctct accagcaatg cgatgcccag 1080
ccaggggcca gcgggtctgg ggtctatgtg aggatgtgga agagacagca gcagaagtgg 1140
gagcgaaaaa ttattggcat tttttcaggg caccagtggg tggacatgaa tggttcccca 1200
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ttaagggtct tcatgttctt attttaggag aggccaaatt gtttttgtc attggcgtgc 1380
acacgtgtgt gtgtgtgtgt gtgtgtgtgt aaggtgtctt ataatctttt acctatttct 1440
tacaattgca agatgactgg ctttactatt tgaaaactgg tttgtgtatc atatcatata 1500
tcatttaagc agtttgaagg catacttttg catagaaata aaaaaaatac tgatttgggg 1560
caatgaggaa tatttgacaa ttaagttaat cttcacgttt ttgcaaactt tgatttttat 1620
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ttgacagcat ttgttaggca gaatattttg gatttggagg catttgcatg gtagtctttg 1860
aacagtaaaa tgatgtgttg actatactga tacacatatt aaactatacc ttatagtaaa 1920
ccagtatccc aagctgcttt tagttccaaa aatagtttct tttccaaagg ttgttgctct 1980
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agagtgttta tcccaaccct tccatttaac aggatttcac tcacatttct ggaactagct 2100
atttttcaga agacaataat cagggcttaa ttagaacagg ctgtatttcc tcccagcaaa 2160
cagttgtggc cacactaaaa acaatcatag cattttaccc ctggattata gcacatctca 2220
tgttttatca tttggatgga gtaatttaaa atgaattaaa ttccagagaa caatggaagc 2280
attgcctggc agatgtcaca acagaataac cacttgtttg gagcctggca cagtcctcca 2340
```

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gcctgatcaa aaattattct gcatagtttt cagtgtgctt tctgggagct atgtacttct 2400
tcaatttgga aacttttctc tctcatttat agtgaaaata cttggaagtt actttaagaa 2460
aaccagtgtg gccttttttcc ctctagcttt aaaagggccg cttttgctgg aatgctctag 2520
gttatagata aacaattagg tataatagca aaaatgaaaa ttggaagaat gcaaaatgga 2580
tcagaatcat gccttccaat aaaggccttt acacatgttt tatcaatatg attatcaaat 2640
cacagcatat acagaaaaga cttggactta ttgtatgttt ttattttatg gctctcggcc 2700
taagcacttc tttctaaatg tatcggagaa aaaatcaaat ggactacaag cacgtgtttg 2760
ctgtgcttgc accccaggta aacctgcatt gtagcaattt gtaaggatat tcagatggag 2820
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caattttctt tggaatctaa caggaatcta gcctgaggaa gaagggaggt ctccatttct 3060
atgtctggta tttgggggtt ttgtttgttt ttgctttagc ttggtgaaaa aaagttcact 3120
gaacaccaag accagaatgg attttttttaa aaaaatagat gttccttttg tgaagcacct 3180
tgattccttg attttgattt tttgcaaagt tagacaatgg cacaaagtca aaatgaaatc 3240
aatgtttagt tcacaagtag atgtaattta ctaaagaatg atacacccat atgctatata 3300
cagcttaact cacagaactg taaaagaaaa ttataaaata attcaacatg tccatctttt 3360
tagtgataat aaaagaaagc atggtattaa actatcatag aagtagacag aaaaagaaaa 3420
aaggactcat ggcattatta atataattag tgctttacat gtgttagtta tacatattag 3480
aagcatattt gcctagtaag gctagtagaa ccacatttcc caaagtgtgc tccttaaaca 3540
ctcatgcctt atgatttttct accaaaagta aaaagggttg tattaagtca gaggaagatg 3600
cctctccatt ttccctctct ttatcagagg ttcacatgcc tgtctgcaca ttaaaagctc 3660
tgggaagacc tgttgtaaag ggacaagttg aggttgtaaa atctgcattt aaataaacat 3720
ctttgatcac aaaaaaaaaa aaaaaaaaaa                                  3750
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<210> 261
<211> 383
<212> PRT
<213> Homo sapiens

<220>
<223> umbilical vein proteinase

<400> 261

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Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys
 1               5                  10                  15
Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
            20                  25                  30
Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
        35                  40                  45
Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
    50                  55                  60
Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu
65                  70                  75                  80
Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
                85                  90                  95
Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
            100                 105                 110
Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
        115                 120                 125
Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
    130                 135                 140
Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
145                 150                 155                 160
Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys
                165                 170                 175
Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
```

```
            180                 185                 190
Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
        195                 200                 205
Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
    210                 215                 220
Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
225                 230                 235                 240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
                245                 250                 255
Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
            260                 265                 270
Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
        275                 280                 285
Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
    290                 295                 300
Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val
305                 310                 315                 320
Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile
                325                 330                 335
Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
            340                 345                 350
Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
        355                 360                 365
Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
    370                 375                 380
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<210> 262
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<223> LCLP proteinase (LCLP (N-terminus))

<400> 262
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Ile Ile Gly Gly Thr Glu Ser Lys Pro Asp Ser Arg Pro Tyr Met Ala
 1               5                  10                  15
Leu Leu Gln Ile Val Glu Pro Ala Val His
            20                  25
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<210> 263
<211> 2265
<212> DNA
<213> Homo sapiens

<220>
<223> Spinesin

<400> 263
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acgcgggata cagggagggg ccatgtgcga accagggaga cctcatcttc caaccaagct 60
tgctgggctt gcatttaatc aatgcatggc cagagaacag gagcggaaca ttgcctagta 120
gaccctgagg ctttacaaca gtgctactga cccctatgag cctgatgctg gatgaccaac 180
cccctatgga ggcccagtat gcagaggagg gcccaggacc tgggatcttc agagcagagc 240
ctggagacca gcagcatccc atttctcagg cggtgtgctg gcgttccatg cgacgtggct 300
gtgcagtgct gggagccctg gggctgctgg ccggtgcagg tgttggctca tggctcctag 360
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tgctgtatct gtgtcctgct gcctctcagc ccatttccgg gaccttgcag gatgaggaga 420
taactttgag ctgctcagag gccagcgctg aggaagctct gctccctgca ctccccaaaa 480
cagtatcttt cagaataaac agcgaagact tcttgctgga agcgcaagtg agggatcagc 540
cacgctggct cctggtctgc catgagggct ggagccccgc cctggggctg cagatctgct 600
ggagccttgg gcatctcaga ctcactcacc acaagggagt aaacctcact gacatcaaac 660
tcaacagttc ccaggagttt gctcagctct ctcctagact gggaggcttc ctggaggagg 720
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gtggagcgag gcccctggct tcccggatag ttggtgggca gtctgtggct cctgggcgct 840
ggccgtggca ggccagcgtg gccctgggct tccggcacac gtgtgggggc tctgtgctag 900
cgccacgctg ggtggtgact gctgcacatt gtatgcacag tttcaggctg gcccgcctgt 960
ccagctggcg ggttcatgcg gggctggtca gccacagtgc cgtcaggccc caccaagggg 1020
ctctggtgga gaggattatc ccacaccccc tctacagtgc ccagaatcat gactacgacg 1080
tcgccctcct gaggctccag accgctctca acttctcaga cactgtgggc gctgtgtgcc 1140
tgccggccaa ggaacagcat tttccgaagg gctcgcggtg ctgggtgtct ggctggggcc 1200
acacccaccc tagccatact tacagctcgg atatgctcca ggacacggtg gtgcccttgt 1260
tcagcactca gctctgcaac agctcttgcg tgtacagcgg agccctcacc ccccgcatgc 1320
tttgcgctgg ctacctggac ggaagggctg atgcatgcca gggagatagc gggggccccc 1380
tagtgtgccc agatggggac acatggcgcc tagtgggggt ggtcagctgg gggcgtgcgt 1440
gcgcagagcc caatcaccca ggtgtctacg ccaaggtagc tgagtttctg gactggatcc 1500
atgacactgc tcaggactcc ctcctctgag tcctgctgtt tcctccagtc tcactgcaca 1560
ccactgcctc atgcttcctg gggcctccag cagctccact aatggaggag aggcagtagc 1620
ctccgacaca gaacgcatgg acctcctact actgtgtgtg aggaacagtc actacccact 1680
ggccagccac ccagccaaca ggtctctcct cttgggccct gatttcagag tcctctttct 1740
cactagagac tcaatgacag aagagaggct gggacttggt tgggcatgct gtggttgctg 1800
agggatgagg gggaggagag aggtaggagc tggagatgaa gagactgcta gaagcagcag 1860
gaagcctgcc cttctgccct ctcccctccc tgcccctgtg tgagtctttt agggagggtg 1920
actgggaggt gccccccgtc ccacctttt cctgtgctct aggtgggcta agtgcctccc 1980
tagaggactc catggctgag aggctcctgg gcagatgggg tcaaggctgg gccagtccca 2040
gatgaagcct atgggagtca ggaccctctc cactctccct ctccactccc cttcctgttc 2100
tcacctggct gtggctggcc ctgtgtgggg tgggtacact ggaaaacaag aaggttggag 2160
ttggtctagg acattggttt taaatgacag ttctgtgaac tggtccaagg aggttctgtt 2220
attaaagtga tatatggtct tgaaaaaaaa aaaaaaaaaa aaaaa 2265

<210> 264
<211> 457
<212> PRT
<213> Homo sapiens

<220>
<223> Spinesin

<400> 264
Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala
 1   5   10   15
Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln
            20   25   30
Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly
        35   40   45
Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly
    50   55   60
Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile
65   70   75   80
Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala
                85   90   95
Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe
            100   105   110
Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln

```
        115                 120                 125
Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly
    130                 135                 140
Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys
145                 150                 155                 160
Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala
                165                 170                 175
Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro
            180                 185                 190
Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu
        195                 200                 205
Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val
    210                 215                 220
Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg
225                 230                 235                 240
His Thr Cys Gly Gly Ser Val Leu Ala Pro Arg Trp Val Val Thr Ala
                245                 250                 255
Ala His Cys Met His Ser Phe Arg Leu Ala Arg Leu Ser Ser Trp Arg
            260                 265                 270
Val His Ala Gly Leu Val Ser His Ser Ala Val Arg Pro His Gln Gly
        275                 280                 285
Ala Leu Val Glu Arg Ile Ile Pro His Pro Leu Tyr Ser Ala Gln Asn
    290                 295                 300
His Asp Tyr Asp Val Ala Leu Leu Arg Leu Gln Thr Ala Leu Asn Phe
305                 310                 315                 320
Ser Asp Thr Val Gly Ala Val Cys Leu Pro Ala Lys Glu Gln His Phe
                325                 330                 335
Pro Lys Gly Ser Arg Cys Trp Val Ser Gly Trp Gly His Thr His Pro
            340                 345                 350
Ser His Thr Tyr Ser Ser Asp Met Leu Gln Asp Thr Val Val Pro Leu
        355                 360                 365
Phe Ser Thr Gln Leu Cys Asn Ser Ser Cys Val Tyr Ser Gly Ala Leu
    370                 375                 380
Thr Pro Arg Met Leu Cys Ala Gly Tyr Leu Asp Gly Arg Ala Asp Ala
385                 390                 395                 400
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Pro Asp Gly Asp Thr
                405                 410                 415
Trp Arg Leu Val Gly Val Val Ser Trp Gly Arg Ala Cys Ala Glu Pro
            420                 425                 430
Asn His Pro Gly Val Tyr Ala Lys Val Ala Glu Phe Leu Asp Trp Ile
        435                 440                 445
His Asp Thr Ala Gln Asp Ser Leu Leu
    450                 455
```

<210> 265
<211> 1243
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA178 peptidase

<400> 265
atggctgccc ctgcttccgt catgggccca ctcgggccct ctgccctggg ccttctgctg 60
ctgctcctgg tggtggcccc tccccgggtc gcagcattgg tccacagaca gccagagaac 120
cagggaatct ccctaactgg cagcgtggcc tgtggtcggc ccagcatgga ggggaaaatc 180

ctgggcggcg tccctgcgcc cgagaggaag tggccgtggc aggtcagcgt gcactacgca 240
ggcctccacg tctgcggcgg ctccatcctc aatgagtact gggtgctgtc agctgcgcac 300
tgctttcaca gggacaagaa tatcaaaatc tatgacatgt acgtaggcct cgtaaacctc 360
agggtggccg gcaaccacac ccagtggtat gaggtgaaca gggtgatcct gcaccccaca 420
tatgagatgt accaccccat cggaggtgac gtggccctgg tgcagctgaa gacccgcatt 480
gtgttttctg agtccgtgct cccggtttgc cttgcaactc cagaagtgaa ccttaccagt 540
gccaattgct gggctacggg atggggacta gtctcaaaac aaggtgagac ctcagacgag 600
ctgcaggaga tgcagctccc gctgatcctg gagccctggt gccacctgct ctacggacac 660
atgtcctaca tcatgcccga catgctgtgt gctggggaca tcctgaatgc taagaccgtg 720
tgtgagggcg actccggggg cccacttgtc tgtgaattca accgcagctg gttgcagatt 780
ggaattgtga gctggggccg aggctgctcc aaccctctgt accctggagt gtatgccagt 840
gtttcctatt tctcaaaatg gatatgtgat aacatagaaa tcacgcccac tcctgctcag 900
ccagcccctg ctctctctcc agctctgggg cccactctca gcgtcctaat ggccatgctg 960
gctggctggt cagtgctgtg aggtcaggat acccactcta ggattctcat ggctgcacac 1020
cctgccccag cccagctgcc tccagacccc taagcatctc ctgtcctggc ctctctgaag 1080
cagacaaggg ccacctatcc cgggggtgga tgctgagtcc aggaggtgat gagcaagtgt 1140
acaaaagaaa aaagggaagg gggagagggg ctggtcaggg agaacccagc ttgggcagag 1200
tgcacctgag atttgataag atcattaaat atttacaaag caa 1243

<210> 266
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA178 peptidase

<400> 266
Met Ala Ala Pro Ala Ser Val Met Gly Pro Leu Gly Pro Ser Ala Leu
1 5 10 15
Gly Leu Leu Leu Leu Leu Leu Val Val Ala Pro Pro Arg Val Ala Ala
20 25 30
Leu Val His Arg Gln Pro Glu Asn Gln Gly Ile Ser Leu Thr Gly Ser
35 40 45
Val Ala Cys Gly Arg Pro Ser Met Glu Gly Lys Ile Leu Gly Gly Val
50 55 60
Pro Ala Pro Glu Arg Lys Trp Pro Trp Gln Val Ser Val His Tyr Ala
65 70 75 80
Gly Leu His Val Cys Gly Gly Ser Ile Leu Asn Glu Tyr Trp Val Leu
85 90 95
Ser Ala Ala His Cys Phe His Arg Asp Lys Asn Ile Lys Ile Tyr Asp
100 105 110
Met Tyr Val Gly Leu Val Asn Leu Arg Val Ala Gly Asn His Thr Gln
115 120 125
Trp Tyr Glu Val Asn Arg Val Ile Leu His Pro Thr Tyr Glu Met Tyr
130 135 140
His Pro Ile Gly Gly Asp Val Ala Leu Val Gln Leu Lys Thr Arg Ile
145 150 155 160
Val Phe Ser Glu Ser Val Leu Pro Val Cys Leu Ala Thr Pro Glu Val
165 170 175
Asn Leu Thr Ser Ala Asn Cys Trp Ala Thr Gly Trp Gly Leu Val Ser
180 185 190
Lys Gln Gly Glu Thr Ser Asp Glu Leu Gln Glu Met Gln Leu Pro Leu
195 200 205
Ile Leu Glu Pro Trp Cys His Leu Leu Tyr Gly His Met Ser Tyr Ile
210 215 220
Met Pro Asp Met Leu Cys Ala Gly Asp Ile Leu Asn Ala Lys Thr Val

```
225                 230                 235                 240
Cys Glu Gly Asp Ser Gly Gly Pro Leu Val Cys Glu Phe Asn Arg Ser
                245                 250                 255
Trp Leu Gln Ile Gly Ile Val Ser Trp Gly Arg Gly Cys Ser Asn Pro
            260                 265                 270
Leu Tyr Pro Gly Val Tyr Ala Ser Val Ser Tyr Phe Ser Lys Trp Ile
        275                 280                 285
Cys Asp Asn Ile Glu Ile Thr Pro Thr Pro Ala Gln Pro Ala Pro Ala
    290                 295                 300
Leu Ser Pro Ala Leu Gly Pro Thr Leu Ser Val Leu Met Ala Met Leu
305                 310                 315                 320
Ala Gly Trp Ser Val Leu
                325
```

<210> 267
<211> 1695
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA180 peptidase

<400> 267
atgcttataa gcaggaacaa gctgatttta ctactaggaa tagtcttttt tgaacgaggt 60
aaatctgcaa ctctttcgct ccccaaagct cccagttgtg ggcagagtct ggttaaggta 120
cagccttgga attattttaa cattttcagt cgcattcttg gaggaagcca agtggagaag 180
ggttcctatc cctggcaggt atctctgaaa caaaggcaga agcatatttg tggaggaagc 240
atcgtctcac cacagtgggt gatcacggcg gctcactgca ttgcaaacag aaacattgtg 300
tctactttga atgttactgc tggagagtat gacttaagcc agacagaccc aggagagcaa 360
actctcacta ttgaaactgt catcatacat ccacatttct ccaccaagaa accaatggac 420
tatgatattg ccctttgaa gatggctgga gccttccaat ttggccactt tgtggggccc 480
atatgtcttc cagagctgcg ggagcaattt gaggctggtt ttatttgtac aactgcaggc 540
tggggccgct taactgaagg tggcgtcctc tcacaagtct tgcaggaagt gaatctgcct 600
attttgacct gggaagagtg tgtggcagct ctgttaacac taaagaggcc catcagtggg 660
aagacctttc tttgcacagg ttttcctgat ggagggagag acgcatgtca gggagattca 720
ggaggttcac tcatgtgccg gaataagaaa ggggcctgga ctctggctgg tgtgacttcc 780
tggggtttgg gctgtggtcg aggctggaga aacaatgtga ggaaaagtga tcaaggatcc 840
cctgggatct tcacagacat tagtaaagtg cttccctgga tccacgaaca catccaaact 900
ggtaatcgga gaaagagctc cagagcctgg tgcagtgagc aggatgtcat agtcagcggg 960
gctgagggga agctgcactt cccagaaagc ctccacctat attatgagag caagcaacgg 1020
tgtgtctgga ccctgctggt accagaggaa atgcatgtgt tgctcagttt ttcccaccta 1080
gatgttgagt cttgtcacca cagttacctg tcaatgtatt ctttagaaga cagacccatt 1140
ggaaaatttt gtggagaaag cctcccttca tccattctta ttggctctaa ttctctaagg 1200
ctgaaattcg tctctgatgc cacagattat gcagctgggt ttaatcttac ctataaagct 1260
cttaaaccaa actacattcc tgattcaggt tgcagttact taactgtcct ttttgaagaa 1320
ggtctcatac agagtctaaa ctatcctgaa aactacagtg acaaggctaa ctgtgactgg 1380
atttttcaag cctccaaaca tcacctaatt aagctttcat ttcagagtct ggaaatagaa 1440
gaaagtggag actgcacttc cgactatgtg acagtgcaca gcgatgtaga aaggaagaag 1500
gaaatagctc ggctgtgtgg ctatgatgtc cccacccctg tgctgagccc ctccagcatc 1560
atgctcatca gcttccaatc agatgaaaac gggacctgca ggggctttca ggctacagtc 1620
tccttcattc ctaaagcagg taagaagata gagttaccaa ctctttggtt cccagttcta 1680
atccttgtga tgtga 1695

<210> 268
<211> 564
<212> PRT

<213> Homo sapiens

<220>
<223> Mername-AA180 peptidase

<400> 268
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Met Leu Ile Ser Arg Asn Lys Leu Ile Leu Leu Leu Gly Ile Val Phe
 1               5                  10                  15
Phe Glu Arg Gly Lys Ser Ala Thr Leu Ser Leu Pro Lys Ala Pro Ser
            20                  25                  30
Cys Gly Gln Ser Leu Val Lys Val Gln Pro Trp Asn Tyr Phe Asn Ile
        35                  40                  45
Phe Ser Arg Ile Leu Gly Gly Ser Gln Val Glu Lys Gly Ser Tyr Pro
    50                  55                  60
Trp Gln Val Ser Leu Lys Gln Arg Gln Lys His Ile Cys Gly Gly Ser
65                  70                  75                  80
Ile Val Ser Pro Gln Trp Val Ile Thr Ala Ala His Cys Ile Ala Asn
                85                  90                  95
Arg Asn Ile Val Ser Thr Leu Asn Val Thr Ala Gly Glu Tyr Asp Leu
            100                 105                 110
Ser Gln Thr Asp Pro Gly Glu Gln Thr Leu Thr Ile Glu Thr Val Ile
        115                 120                 125
Ile His Pro His Phe Ser Thr Lys Lys Pro Met Asp Tyr Asp Ile Ala
    130                 135                 140
Leu Leu Lys Met Ala Gly Ala Phe Gln Phe Gly His Phe Val Gly Pro
145                 150                 155                 160
Ile Cys Leu Pro Glu Leu Arg Glu Gln Phe Glu Ala Gly Phe Ile Cys
                165                 170                 175
Thr Thr Ala Gly Trp Gly Arg Leu Thr Glu Gly Gly Val Leu Ser Gln
            180                 185                 190
Val Leu Gln Glu Val Asn Leu Pro Ile Leu Thr Trp Glu Glu Cys Val
        195                 200                 205
Ala Ala Leu Leu Thr Leu Lys Arg Pro Ile Ser Gly Lys Thr Phe Leu
    210                 215                 220
Cys Thr Gly Phe Pro Asp Gly Gly Arg Asp Ala Cys Gln Gly Asp Ser
225                 230                 235                 240
Gly Gly Ser Leu Met Cys Arg Asn Lys Lys Gly Ala Trp Thr Leu Ala
                245                 250                 255
Gly Val Thr Ser Trp Gly Leu Gly Cys Gly Arg Gly Trp Arg Asn Asn
            260                 265                 270
Val Arg Lys Ser Asp Gln Gly Ser Pro Gly Ile Phe Thr Asp Ile Ser
        275                 280                 285
Lys Val Leu Pro Trp Ile His Glu His Ile Gln Thr Gly Asn Arg Arg
    290                 295                 300
Lys Ser Ser Arg Ala Trp Cys Ser Glu Gln Asp Val Ile Val Ser Gly
305                 310                 315                 320
Ala Glu Gly Lys Leu His Phe Pro Glu Ser Leu His Leu Tyr Tyr Glu
                325                 330                 335
Ser Lys Gln Arg Cys Val Trp Thr Leu Leu Val Pro Glu Glu Met His
            340                 345                 350
Val Leu Leu Ser Phe Ser His Leu Asp Val Glu Ser Cys His His Ser
        355                 360                 365
Tyr Leu Ser Met Tyr Ser Leu Glu Asp Arg Pro Ile Gly Lys Phe Cys
    370                 375                 380
Gly Glu Ser Leu Pro Ser Ser Ile Leu Ile Gly Ser Asn Ser Leu Arg
385                 390                 395                 400
Leu Lys Phe Val Ser Asp Ala Thr Asp Tyr Ala Ala Gly Phe Asn Leu
```

```
                405                 410                 415
Thr Tyr Lys Ala Leu Lys Pro Asn Tyr Ile Pro Asp Ser Gly Cys Ser
            420                 425                 430
Tyr Leu Thr Val Leu Phe Glu Glu Gly Leu Ile Gln Ser Leu Asn Tyr
        435                 440                 445
Pro Glu Asn Tyr Ser Asp Lys Ala Asn Cys Asp Trp Ile Phe Gln Ala
    450                 455                 460
Ser Lys His His Leu Ile Lys Leu Ser Phe Gln Ser Leu Glu Ile Glu
465                 470                 475                 480
Glu Ser Gly Asp Cys Thr Ser Asp Tyr Val Thr Val His Ser Asp Val
                485                 490                 495
Glu Arg Lys Lys Glu Ile Ala Arg Leu Cys Gly Tyr Asp Val Pro Thr
            500                 505                 510
Pro Val Leu Ser Pro Ser Ser Ile Met Leu Ile Ser Phe Gln Ser Asp
        515                 520                 525
Glu Asn Gly Thr Cys Arg Gly Phe Gln Ala Thr Val Ser Phe Ile Pro
    530                 535                 540
Lys Ala Gly Lys Lys Ile Glu Leu Pro Thr Leu Trp Phe Pro Val Leu
545                 550                 555                 560
Ile Leu Val Met
```

<210> 269
<211> 3420
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA182 peptidase

<400> 269

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atgggcctgc tggccagtgc tggtttgttg ctgttgctgg tcatcggcca ccccagaagc 60
ctaggactga agtgtggaat tcgcatggtc aacatgaaaa gtaaggaacc tgccgtggga 120
tctagattct tctctagaat tagtagttgg agaaattcaa cagtgactgg acatccatgg 180
caggtctccc taaaatcaga tgagcaccac ttctgtggag gaagcttgat tcaagaagat 240
cgggttgtta cagcagcaca ctgcctggac agcctcagtg agaagcagct gaagaatata 300
actgtgactt ctggggagta cagcctcttt cagaaggata agcaagaaca gaatattcct 360
gtctcaaaaa ttattaccca tcctgaatac aacagccgtg aatatatgag tcctgatatt 420
gcactgctgt atctaaaaca caaagtcaag tttggaaatg ctgttcagcc aatctgtctt 480
cctgacagcg atgataaagt tgaaccagga attctttgct tatccagtgg atggggcaag 540
atttccaaaa catcagaata ttcaaatgtc ctacaagaaa tggaacttcc catcatggat 600
gacagagcgt gtaatactgt gctcaagagc atgaacctcc ctcccctggg aaggaccatg 660
ctgtgtgctg gcttccctga ttggggaatg gacgcctgcc agggggactc tggaggacca 720
ctggtttgta gaagaggtgg tggaatctgg attcttgctg ggataacttc ctgggtagct 780
ggttgtgctg gaggttcagt tcccgtaaga aacaaccatg tgaaggcatc acttggcatt 840
ttctccaaag tgtctgagtt gatggatttt atcactcaaa acctgttcac aggtttggat 900
cggggccaac ccctctcaaa agtgggctca aggtatataa caaaggccct gagttctgtc 960
caagaagtga atggaagcca gagaggaaag ggtattttag acatggaaaa gcaagttgga 1020
tgtgatcatg actatgtatc tttacgatca agcagtggag tgctttttaa tcagagatct 1080
ctcatggaag acgatggaaa acaaaacaaa cgtgtctgtg gaaaaatatt gccttcacca 1140
ttgctggcag agaccagtga ggccatggtt ccatttgttt ctgatacaga agacagtggc 1200
agtggctttg agcttaccgt tactgctgta cagaagtcag aagcagggtc aggttgtggg 1260
agtctggcta tattggtaga agaagggaca aatcactctg ccaagtatcc tgatttgtat 1320
cccagtaaca caaggtgtca ttggttcatt tgtgctccag agaagcacat tataaagttg 1380
acatttgagg actttgctgt caaatttagt ccaaactgta tttatgatgc tgttgtgatt 1440
tacggtgatt ctgaagaaaa gcacaagtta gctaaacttt gtggaatgtt gaccatcact 1500
```

```
tcaatattca gttctagtaa catgacggtg atatacttta aaagtgatgg taaaaatcgt 1560
ttacaaggct tcaaggccag atttaccatt ttgccctcag agtctttaaa caaatttgaa 1620
ccaaagttac ctccccaaaa caatcctgta tctaccgtaa aagctattct gcatgatgtc 1680
tgtggcatcc ctccatttag tccccagtgg ctttccagaa gaatcgcagg aggggaagaa 1740
gcctgccccc actgttggcc atggcaggtg ggtctgaggt ttctaggcga ttaccaatgt 1800
ggaggtgcca tcatcaaccc agtgtggatt ctgaccgcag cccactgtgt gcaattgaag 1860
aataatccac tctcctggac tattattgct ggggaccatg acagaaacct gaaggaatca 1920
acagagcagg tgagaagggc caaacacata atagtgcatg aagactttaa cacactaagt 1980
tatgactctg acattgccct aatacaacta agctctcctc tggagtacaa ctcggtggtg 2040
aggccagtat gtctcccaca cagcgcagag cctctatttt cctcggagat ctgtgctgtg 2100
accggatggg gaagcatcag tgcagatggt ggcctagcaa gtcgcctaca gcagattcaa 2160
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ggagactctg gtgggccact agtatgtaga catgaaaatg gtccctttgt cctctatggc 2340
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atgatcttct tggactggat ccaatcaaaa atcaatggtc ctgcttcact tcagacaaat 2460
aataaatgca aaaccttaaa acaacaattg ccaccaccca caccttcacc agacagtgca 2520
tcttggccag gttgttgctc tgaagcagag ctagaaaagc ctagaggctt ttttcccaca 2580
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gcaagcagta tggcaaaatt taccattgag tatctgtcac tcctggggtc tcctgtgtgt 2700
caagactcag ttctaattat ttatgaagaa agacacagta agagaaagac ggcaggtgga 2760
ttacatggaa gaagacttta ctcaatgact ttcatgagtc ctggaccgct ggtgagggtg 2820
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ggtccaaagg acagtaaaat aaccagactt tcccaaagtt caaacagaga gcacttggtc 2940
ccttgtgagg atgttcttct gaccaagcca gaagggatca tgcagatccc aagaaattct 3000
cacagaacta ctatggggtg ccaatggaga ttagtagccc ctttaaatca catcattcag 3060
cttaatatta ttaacttccc gatgaagcca acaacttttg tctgtcatgg tcatctgcgt 3120
gtttacgaag gatttggacc aggaaaaaaa ttaatagctt cattcgctgg aactctggca 3180
atgatactga caaaagacat attaaaaaga gaaaaactga attttattaa cacatatatc 3240
atgcatatat gggaaaattc agtgtatgat aatgtaagaa gtgttggaaa aagaaaacag 3300
aagaaatttg catcaaattt aagttatagt atggaggctg agaagtccag gatccaggtg 3360
ccagcagatt tggtgcctgc taagggctca ctttctggtt cttaggcaca gcccattctc 3420
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<210> 270
<211> 1134
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA182 peptidase

<400> 270

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Met Gly Leu Leu Ala Ser Ala Gly Leu Leu Leu Leu Val Ile Gly
 1               5                  10                  15
His Pro Arg Ser Leu Gly Leu Lys Cys Gly Ile Arg Met Val Asn Met
            20                  25                  30
Lys Ser Lys Glu Pro Ala Val Gly Ser Arg Phe Phe Ser Arg Ile Ser
        35                  40                  45
Ser Trp Arg Asn Ser Thr Val Thr Gly His Pro Trp Gln Val Ser Leu
    50                  55                  60
Lys Ser Asp Glu His His Phe Cys Gly Gly Ser Leu Ile Gln Glu Asp
65                  70                  75                  80
Arg Val Val Thr Ala Ala His Cys Leu Asp Ser Leu Ser Glu Lys Gln
                85                  90                  95
Leu Lys Asn Ile Thr Val Thr Ser Gly Glu Tyr Ser Leu Phe Gln Lys
            100                 105                 110
```

```
Asp Lys Gln Glu Gln Asn Ile Pro Val Ser Lys Ile Ile Thr His Pro
        115                 120                 125
Glu Tyr Asn Ser Arg Glu Tyr Met Ser Pro Asp Ile Ala Leu Leu Tyr
    130                 135                 140
Leu Lys His Lys Val Lys Phe Gly Asn Ala Val Gln Pro Ile Cys Leu
145                 150                 155                 160
Pro Asp Ser Asp Asp Lys Val Glu Pro Gly Ile Leu Cys Leu Ser Ser
                165                 170                 175
Gly Trp Gly Lys Ile Ser Lys Thr Ser Glu Tyr Ser Asn Val Leu Gln
            180                 185                 190
Glu Met Glu Leu Pro Ile Met Asp Asp Arg Ala Cys Asn Thr Val Leu
        195                 200                 205
Lys Ser Met Asn Leu Pro Pro Leu Gly Arg Thr Met Leu Cys Ala Gly
    210                 215                 220
Phe Pro Asp Trp Gly Met Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro
225                 230                 235                 240
Leu Val Cys Arg Arg Gly Gly Gly Ile Trp Ile Leu Ala Gly Ile Thr
                245                 250                 255
Ser Trp Val Ala Gly Cys Ala Gly Gly Ser Val Pro Val Arg Asn Asn
            260                 265                 270
His Val Lys Ala Ser Leu Gly Ile Phe Ser Lys Val Ser Glu Leu Met
        275                 280                 285
Asp Phe Ile Thr Gln Asn Leu Phe Thr Gly Leu Asp Arg Gly Gln Pro
    290                 295                 300
Leu Ser Lys Val Gly Ser Arg Tyr Ile Thr Lys Ala Leu Ser Ser Val
305                 310                 315                 320
Gln Glu Val Asn Gly Ser Gln Arg Gly Lys Gly Ile Leu Asp Met Glu
                325                 330                 335
Lys Gln Val Gly Cys Asp His Asp Tyr Val Ser Leu Arg Ser Ser Ser
            340                 345                 350
Gly Val Leu Phe Asn Gln Arg Ser Leu Met Glu Asp Asp Gly Lys Gln
        355                 360                 365
Asn Lys Arg Val Cys Gly Lys Ile Leu Pro Ser Pro Leu Leu Ala Glu
    370                 375                 380
Thr Ser Glu Ala Met Val Pro Phe Val Ser Asp Thr Glu Asp Ser Gly
385                 390                 395                 400
Ser Gly Phe Glu Leu Thr Val Thr Ala Val Gln Lys Ser Glu Ala Gly
                405                 410                 415
Ser Gly Cys Gly Ser Leu Ala Ile Leu Val Glu Glu Gly Thr Asn His
            420                 425                 430
Ser Ala Lys Tyr Pro Asp Leu Tyr Pro Ser Asn Thr Arg Cys His Trp
        435                 440                 445
Phe Ile Cys Ala Pro Glu Lys His Ile Ile Lys Leu Thr Phe Glu Asp
    450                 455                 460
Phe Ala Val Lys Phe Ser Pro Asn Cys Ile Tyr Asp Ala Val Val Ile
465                 470                 475                 480
Tyr Gly Asp Ser Glu Glu Lys His Lys Leu Ala Lys Leu Cys Gly Met
                485                 490                 495
Leu Thr Ile Thr Ser Ile Phe Ser Ser Ser Asn Met Thr Val Ile Tyr
            500                 505                 510
Phe Lys Ser Asp Gly Lys Asn Arg Leu Gln Gly Phe Lys Ala Arg Phe
        515                 520                 525
Thr Ile Leu Pro Ser Glu Ser Leu Asn Lys Phe Glu Pro Lys Leu Pro
    530                 535                 540
Pro Gln Asn Asn Pro Val Ser Thr Val Lys Ala Ile Leu His Asp Val
545                 550                 555                 560
Cys Gly Ile Pro Pro Phe Ser Pro Gln Trp Leu Ser Arg Arg Ile Ala
```

```
                565                 570                 575
Gly Gly Glu Glu Ala Cys Pro His Cys Trp Pro Trp Gln Val Gly Leu
            580                 585                 590
Arg Phe Leu Gly Asp Tyr Gln Cys Gly Gly Ala Ile Ile Asn Pro Val
        595                 600                 605
Trp Ile Leu Thr Ala Ala His Cys Val Gln Leu Lys Asn Asn Pro Leu
    610                 615                 620
Ser Trp Thr Ile Ile Ala Gly Asp His Asp Arg Asn Leu Lys Glu Ser
625                 630                 635                 640
Thr Glu Gln Val Arg Arg Ala Lys His Ile Ile Val His Glu Asp Phe
                645                 650                 655
Asn Thr Leu Ser Tyr Asp Ser Asp Ile Ala Leu Ile Gln Leu Ser Ser
            660                 665                 670
Pro Leu Glu Tyr Asn Ser Val Val Arg Pro Val Cys Leu Pro His Ser
        675                 680                 685
Ala Glu Pro Leu Phe Ser Ser Glu Ile Cys Ala Val Thr Gly Trp Gly
    690                 695                 700
Ser Ile Ser Ala Asp Gly Gly Leu Ala Ser Arg Leu Gln Gln Ile Gln
705                 710                 715                 720
Val His Val Leu Glu Arg Glu Val Cys Glu His Thr Tyr Tyr Ser Ala
                725                 730                 735
His Pro Gly Gly Ile Thr Glu Lys Met Ile Cys Ala Gly Phe Ala Ala
            740                 745                 750
Ser Gly Glu Lys Asp Phe Cys Gln Gly Asp Ser Gly Gly Pro Leu Val
        755                 760                 765
Cys Arg His Glu Asn Gly Pro Phe Val Leu Tyr Gly Ile Val Ser Trp
    770                 775                 780
Gly Ala Gly Cys Val Gln Pro Trp Lys Pro Gly Val Phe Ala Arg Val
785                 790                 795                 800
Met Ile Phe Leu Asp Trp Ile Gln Ser Lys Ile Asn Gly Pro Ala Ser
                805                 810                 815
Leu Gln Thr Asn Asn Lys Cys Lys Thr Leu Lys Gln Gln Leu Pro Pro
            820                 825                 830
Pro Thr Pro Ser Pro Asp Ser Ala Ser Trp Pro Gly Cys Cys Ser Glu
        835                 840                 845
Ala Glu Leu Glu Lys Pro Arg Gly Phe Phe Pro Thr Pro Arg Tyr Leu
    850                 855                 860
Leu Asp Tyr Arg Gly Arg Leu Glu Cys Ser Trp Val Leu Arg Val Ser
865                 870                 875                 880
Ala Ser Ser Met Ala Lys Phe Thr Ile Glu Tyr Leu Ser Leu Leu Gly
                885                 890                 895
Ser Pro Val Cys Gln Asp Ser Val Leu Ile Ile Tyr Glu Glu Arg His
            900                 905                 910
Ser Lys Arg Lys Thr Ala Gly Gly Leu His Gly Arg Arg Leu Tyr Ser
        915                 920                 925
Met Thr Phe Met Ser Pro Gly Pro Leu Val Arg Val Thr Phe His Ala
    930                 935                 940
Leu Val Arg Gly Ala Phe Gly Ile Ser Tyr Ile Asp Leu Lys Val Leu
945                 950                 955                 960
Gly Pro Lys Asp Ser Lys Ile Thr Arg Leu Ser Gln Ser Ser Asn Arg
                965                 970                 975
Glu His Leu Val Pro Cys Glu Asp Val Leu Leu Thr Lys Pro Glu Gly
            980                 985                 990
Ile Met Gln Ile Pro Arg Asn Ser His Arg Thr Thr Met Gly Cys Gln
        995                 1000                1005
Trp Arg Leu Val Ala Pro Leu Asn His Ile Ile Gln Leu Asn Ile Ile
    1010                1015                1020
```

```
Asn Phe Pro Met Lys Pro Thr Thr Phe Val Cys His Gly His Leu Arg
1025                1030                1035                1040
Val Tyr Glu Gly Phe Gly Pro Gly Lys Lys Leu Ile Ala Ser Phe Ala
                1045                1050                1055
Gly Thr Leu Ala Met Ile Leu Thr Lys Asp Ile Leu Lys Arg Glu Lys
            1060                1065                1070
Leu Asn Phe Ile Asn Thr Tyr Ile Met His Ile Trp Glu Asn Ser Val
        1075                1080                1085
Tyr Asp Asn Val Arg Ser Val Gly Lys Arg Lys Gln Lys Lys Phe Ala
    1090                1095                1100
Ser Asn Leu Ser Tyr Ser Met Glu Ala Glu Lys Ser Arg Ile Gln Val
1105                1110                1115                1120
Pro Ala Asp Leu Val Pro Ala Lys Gly Ser Leu Ser Gly Ser
                1125                1130
```

<210> 271
<211> 2810
<212> DNA
<213> Homo sapiens

<220>
<223> Mername-AA122 peptidase

<400> 271

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acttggctct gcctccgctg actctagcgc catggcccgg cacctgctcc tccccttgt 60
gatgcttgtc atcagtccca tcccaggagc cttccaggac tcagctctca gtcctaccca 120
ggaagaacct gaagatctgg actgcgggcg ccctgagccc tcggcccgca tcgtgggggg 180
gctcaaacgc gcagccgggc acctggcctt ggcaagtgag cctgcaccat ggaggtggcc 240
acatctgcgg gggctccctc atcgcccccc cctgggtcct ctccgctgct cactgtttca 300
tgacgaatgg gacgctggag cccgcggccg agtggtcggt actgctgggc gtgcactccc 360
aggacgggcc cctggacggc gcgcacaccc gcgcagtggc cgccatcgtg gtgccggcca 420
actacagcca agtggagctg ggcgccgacc tggccctgct gcgcctggcc tcacccgcca 480
gcctgggccc cgccgtgtgg cctgtctgcc tgccccgcgc ctcacaccgc ttcgtgcacg 540
gcaccgcctg ctgggccacc ggctggggag acgtccagga ggcagatcct ctgcctctcc 600
cctgggtgct acaggaagtg gagctaaggc tgctgggcga ggccacctgt caatgtctct 660
acagccagcc cggtcccttc aacctcactc tccagatatt gccagggatg ctgtgtgctg 720
gctacccaga gggccgcagg gacacctgcc agggcgactc tgggggccc ctggtctgtg 780
aggaaggcgg ccgctggttc caggcaggaa tcaccagctt tggctttggc tgtggacgga 840
gaaaccgccc tggagttttc actgctgtgg ctacctatga ggcatggata cgggagcagg 900
tgatgggttc agagcctggg cctgcctttc ccacccagcc ccagaagacc cagtcagatc 960
cccaggagcc cagggaggag aactgcacca ttgccctgcc tgagtgcggg aaggccccgc 1020
ggccaggggc ctggccctgg gaggcccagg tgatggtgcc aggatccaga ccctgccatg 1080
gggcgctggt gtctgaaagc tgggtcttgg cacctgccag ctgctttctg gacccgaaca 1140
gctccgacag cccaccccgc gacctcgacg cctggcgcgt gctgctgccc tcgcgcccgc 1200
gcgcggagcg ggtggcgcgc ctggtgcagc acgagaacgc ttcgtgggac aacgcctcgg 1260
acctggcgct gctgcagctg cgcacgcccg tgaacctgag tgcggcttcg cggcccgtgt 1320
gcctacccca cccggaacac tacttcctgc ccgggagccg ctgccgcctg gcccgctggg 1380
gccgcgggga acccgcgctt ggcccaggcg cgctgctgga ggcggagctg ttaggcggct 1440
ggtggtgcca ctgcctgtac ggccgccagg gggcggcagt accgctgccc ggagacccgc 1500
cgcacgcgct ctgccctgcc taccaggaaa aggaggaggt gggcagctgc tggaatgact 1560
cgcgttggag ccttttgtgc caggaggagg ggacctggtt tctggctgga atcagagact 1620
ttcccagtgg ctgtctacgt ccccgagcct tcttccctct gcagactcat ggcccatgga 1680
tcagccatgt gactcgggga gcctacctgg aggaccagct agcctgggac tggggccctg 1740
atggggagga gactgagaca cagacttgtc ccccacacac agagcatggt gcctgtggcc 1800
tgcggctgga ggctgctcca gtgggggtcc tgtggccctg gctggcagag gtgcatgtgg 1860
ctggtgatcg agtctgcact gggatcctcc tggccccagg ctgggtcctg gcagccactc 1920
```

```
actgtgtcct caggccaggc tctacaacag tgccttacat tgaagtgtat ctgggccggg 1980
caggggccag ctccctccca cagggccacc aggtatcccg cttggtcatc agcatccggc 2040
tgccccagca cctgggactc aggccccccc tggccctcct ggagctgagc tcccgggtgg 2100
agccctcccc atcagccctg cccatctgtc tccacccggc gggtatcccc ccgggggcca 2160
gctgctgggt gttgggctgg aaagaacccc aggaccgagt ccctgtggct gctgctgtct 2220
ccatcttgac acaacgaatc tgtgactgcc tctatcaggg catcctgccc cctggaaccc 2280
tctgtgtcct gtatgcagag gggcaggaga acaggtgtga gatgacctca gcaccgcccc 2340
tcctgtgcca gatgacggaa gggtcctgga tcctcgtggg catggctgtt caagggagcc 2400
gggagctgtt tgctgccatt ggtcctgaag aggcctggat ctcccagaca gtgggagagg 2460
ccaacctcct gccccccagt ggctccccac actggcccac tggaggcagc aatctctgcc 2520
ccccagaact ggccaaggcc tcgggatccc cgcatgcagt ctacttcctg ctcctgctga 2580
ctctcctgat ccagagctga ggggctaggg tcccagcacc acttcccccc tctccaccct 2640
ctacttcccg cccagtgggg ctggaatgtg gcccagccgg ctggaacctc aagggcccca 2700
cccaccgaga ttgcagcggc tctggctaat tgggcctctg tgcccgggct attttgaacc 2760
caggaatcct tgggggtggt gggaggagcg gacaataaag gtgtaaacac            2810
```

<210> 272
<211> 766
<212> PRT
<213> Homo sapiens

<220>
<223> Mername-AA122 peptidase

<400> 272

```
Met Thr Asn Gly Thr Leu Glu Pro Ala Ala Glu Trp Ser Val Leu Leu
 1               5                  10                  15
Gly Val His Ser Gln Asp Gly Pro Leu Asp Gly Ala His Thr Arg Ala
            20                  25                  30
Val Ala Ala Ile Val Val Pro Ala Asn Tyr Ser Gln Val Glu Leu Gly
        35                  40                  45
Ala Asp Leu Ala Leu Leu Arg Leu Ala Ser Pro Ala Ser Leu Gly Pro
    50                  55                  60
Ala Val Trp Pro Val Cys Leu Pro Arg Ala Ser His Arg Phe Val His
65                  70                  75                  80
Gly Thr Ala Cys Trp Ala Thr Gly Trp Gly Asp Val Gln Glu Ala Asp
                85                  90                  95
Pro Leu Pro Leu Pro Trp Val Leu Gln Glu Val Glu Leu Arg Leu Leu
            100                 105                 110
Gly Glu Ala Thr Cys Gln Cys Leu Tyr Ser Gln Pro Gly Pro Phe Asn
        115                 120                 125
Leu Thr Leu Gln Ile Leu Pro Gly Met Leu Cys Ala Gly Tyr Pro Glu
    130                 135                 140
Gly Arg Arg Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
145                 150                 155                 160
Glu Glu Gly Gly Arg Trp Phe Gln Ala Gly Ile Thr Ser Phe Gly Phe
                165                 170                 175
Gly Cys Gly Arg Arg Asn Arg Pro Gly Val Phe Thr Ala Val Ala Thr
            180                 185                 190
Tyr Glu Ala Trp Ile Arg Glu Gln Val Met Gly Ser Glu Pro Gly Pro
        195                 200                 205
Ala Phe Pro Thr Gln Pro Gln Lys Thr Gln Ser Asp Pro Gln Glu Pro
    210                 215                 220
Arg Glu Glu Asn Cys Thr Ile Ala Leu Pro Glu Cys Gly Lys Ala Pro
225                 230                 235                 240
Arg Pro Gly Ala Trp Pro Trp Glu Ala Gln Val Met Val Pro Gly Ser
                245                 250                 255
```

```
Arg Pro Cys His Gly Ala Leu Val Ser Glu Ser Trp Val Leu Ala Pro
            260                 265                 270
Ala Ser Cys Phe Leu Asp Pro Asn Ser Ser Asp Ser Pro Pro Arg Asp
        275                 280                 285
Leu Asp Ala Trp Arg Val Leu Leu Pro Ser Arg Pro Arg Ala Glu Arg
    290                 295                 300
Val Ala Arg Leu Val Gln His Glu Asn Ala Ser Trp Asp Asn Ala Ser
305                 310                 315                 320
Asp Leu Ala Leu Leu Gln Leu Arg Thr Pro Val Asn Leu Ser Ala Ala
                325                 330                 335
Ser Arg Pro Val Cys Leu Pro His Pro Glu His Tyr Phe Leu Pro Gly
            340                 345                 350
Ser Arg Cys Arg Leu Ala Arg Trp Gly Arg Gly Glu Pro Ala Leu Gly
        355                 360                 365
Pro Gly Ala Leu Leu Glu Ala Glu Leu Leu Gly Gly Trp Trp Cys His
    370                 375                 380
Cys Leu Tyr Gly Arg Gln Gly Ala Ala Val Pro Leu Pro Gly Asp Pro
385                 390                 395                 400
Pro His Ala Leu Cys Pro Ala Tyr Gln Glu Lys Glu Glu Val Gly Ser
                405                 410                 415
Cys Trp Asn Asp Ser Arg Trp Ser Leu Leu Cys Gln Glu Glu Gly Thr
            420                 425                 430
Trp Phe Leu Ala Gly Ile Arg Asp Phe Pro Ser Gly Cys Leu Arg Pro
        435                 440                 445
Arg Ala Phe Phe Pro Leu Gln Thr His Gly Pro Trp Ile Ser His Val
    450                 455                 460
Thr Arg Gly Ala Tyr Leu Glu Asp Gln Leu Ala Trp Asp Trp Gly Pro
465                 470                 475                 480
Asp Gly Glu Glu Thr Glu Thr Gln Thr Cys Pro Pro His Thr Glu His
                485                 490                 495
Gly Ala Cys Gly Leu Arg Leu Glu Ala Ala Pro Val Gly Val Leu Trp
            500                 505                 510
Pro Trp Leu Ala Glu Val His Val Ala Gly Asp Arg Val Cys Thr Gly
        515                 520                 525
Ile Leu Leu Ala Pro Gly Trp Val Leu Ala Ala Thr His Cys Val Leu
    530                 535                 540
Arg Pro Gly Ser Thr Thr Val Pro Tyr Ile Glu Val Tyr Leu Gly Arg
545                 550                 555                 560
Ala Gly Ala Ser Ser Leu Pro Gln Gly His Gln Val Ser Arg Leu Val
                565                 570                 575
Ile Ser Ile Arg Leu Pro Gln His Leu Gly Leu Arg Pro Pro Leu Ala
            580                 585                 590
Leu Leu Glu Leu Ser Ser Arg Val Glu Pro Ser Pro Ser Ala Leu Pro
        595                 600                 605
Ile Cys Leu His Pro Ala Gly Ile Pro Pro Gly Ala Ser Cys Trp Val
    610                 615                 620
Leu Gly Trp Lys Glu Pro Gln Asp Arg Val Pro Val Ala Ala Ala Val
625                 630                 635                 640
Ser Ile Leu Thr Gln Arg Ile Cys Asp Cys Leu Tyr Gln Gly Ile Leu
                645                 650                 655
Pro Pro Gly Thr Leu Cys Val Leu Tyr Ala Glu Gly Gln Glu Asn Arg
            660                 665                 670
Cys Glu Met Thr Ser Ala Pro Pro Leu Leu Cys Gln Met Thr Glu Gly
        675                 680                 685
Ser Trp Ile Leu Val Gly Met Ala Val Gln Gly Ser Arg Glu Leu Phe
    690                 695                 700
Ala Ala Ile Gly Pro Glu Glu Ala Trp Ile Ser Gln Thr Val Gly Glu
```

```
705                 710                 715                 720
Ala Asn Leu Leu Pro Pro Ser Gly Ser Pro His Trp Pro Thr Gly Gly
                725                 730                 735
Ser Asn Leu Cys Pro Pro Glu Leu Ala Lys Ala Ser Gly Ser Pro His
            740                 745                 750
Ala Val Tyr Phe Leu Leu Leu Leu Thr Leu Leu Ile Gln Ser
        755                 760                 765
```

<210> 273
<211> 1575
<212> DNA
<213> Homo sapiens

<220>
<223> Cathepsin L

<400> 273
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agaaccgcga cctccgcaac cttgagcggc atccgtggag tgcgcctgca gctacgaccg 60
cagcaggaaa gcgccgccgg ccaggcccag ctgtggccgg acagggactg gaagagagga 120
cgcggtcgag taggtgtgca ccagccctgg caacgagagc gtctaccccg aactctgctg 180
gccttgaggt ggggaagccg gggagggcag ttgaggaccc cgcggaggcg cgtgactggt 240
tgagcgggca ggccagcctc cgagccgggt ggacacaggt tttaaaacat gaatcctaca 300
ctcatccttg ctgccttttg cctgggaatt gcctcagcta ctctaacatt tgatcacagt 360
ttagaggcac agtggaccaa gtggaaggcg atgcacaaca gattatacgg catgaatgaa 420
gaaggatgga ggagagcagt gtgggagaag aacatgaaga tgattgaact gcacaatcag 480
gaatacaggg aagggaaaca cagcttcaca atggccatga acgcctttgg agacatgacc 540
agtgaagaat tcaggcaggt gatgaatggc tttcaaaacc gtaagcccag gaaggggaaa 600
gtgttccagg aacctctgtt ttatgaggcc cccagatctg tggattggag agagaaaggc 660
tacgtgactc ctgtgaagaa tcagggtcag tgtggttctt gttgggcttt tagtgctact 720
ggtgctcttg aaggacagat gttccggaaa actgggaggc ttatctcact gagtgagcag 780
aatctggtag actgctctgg gcctcaaggc aatgaaggct gcaatggtgg cctaatggat 840
tatgctttcc agtatgttca ggataatgga ggcctggact ctgaggaatc ctatccatat 900
gaggcaacag aagaatcctg taagtacaat cccaagtatt ctgttgctaa tgacaccggc 960
tttgtggaca tccctaagca ggagaaggcc ctgatgaagg cagttgcaac tgtggggccc 1020
atttctgttg ctattgatgc aggtcatgag tccttcctgt tctataaaga aggcatttat 1080
tttgagccag actgtagcag tgaagacatg gatcatggtg tgctggtggt tggctacgga 1140
tttgaaagca cagaatcaga taacaataaa tattggctgg tgaagaacag ctggggtgaa 1200
gaatggggca tgggtggcta cgtaaagatg gccaaagacc ggagaaacca ttgtggaatt 1260
gcctcagcag ccagctaccc cactgtgtga gctggtggac ggtgatgagg aaggacttga 1320
ctggggatgg cgcatgcatg ggaggaattc atcttcagtc taccagcccc cgctgtgtcg 1380
gatacacact cgaatcattg aagatccgag tgtgatttga attctgtgat attttcacac 1440
tggtaaatgt tacctctatt ttaattactg ctataaatag gtttatatta ttgattcact 1500
tactgacttt gcattttcgt ttttaaaagg atgtataaat ttttacctgt ttaaataaaa 1560
tttaatttca aatgt                                                  1575
```

<210> 274
<211> 333
<212> PRT
<213> Homo sapiens

<220>
<223> Cathepsin L

<400> 274
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Met Asn Pro Thr Leu Ile Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 1               5                  10                  15
```

```
Ala Thr Leu Thr Phe Asp His Ser Leu Glu Ala Gln Trp Thr Lys Trp
            20                  25                  30
Lys Ala Met His Asn Arg Leu Tyr Gly Met Asn Glu Glu Gly Trp Arg
        35                  40                  45
Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gln
    50                  55                  60
Glu Tyr Arg Glu Gly Lys His Ser Phe Thr Met Ala Met Asn Ala Phe
65                  70                  75                  80
Gly Asp Met Thr Ser Glu Glu Phe Arg Gln Val Met Asn Gly Phe Gln
                85                  90                  95
Asn Arg Lys Pro Arg Lys Gly Lys Val Phe Gln Glu Pro Leu Phe Tyr
            100                 105                 110
Glu Ala Pro Arg Ser Val Asp Trp Arg Glu Lys Gly Tyr Val Thr Pro
        115                 120                 125
Val Lys Asn Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
    130                 135                 140
Gly Ala Leu Glu Gly Gln Met Phe Arg Lys Thr Gly Arg Leu Ile Ser
145                 150                 155                 160
Leu Ser Glu Gln Asn Leu Val Asp Cys Ser Gly Pro Gln Gly Asn Glu
                165                 170                 175
Gly Cys Asn Gly Gly Leu Met Asp Tyr Ala Phe Gln Tyr Val Gln Asp
            180                 185                 190
Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Glu Ala Thr Glu
        195                 200                 205
Glu Ser Cys Lys Tyr Asn Pro Lys Tyr Ser Val Ala Asn Asp Thr Gly
    210                 215                 220
Phe Val Asp Ile Pro Lys Gln Glu Lys Ala Leu Met Lys Ala Val Ala
225                 230                 235                 240
Thr Val Gly Pro Ile Ser Val Ala Ile Asp Ala Gly His Glu Ser Phe
                245                 250                 255
Leu Phe Tyr Lys Glu Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser Glu
            260                 265                 270
Asp Met Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Ser Thr
        275                 280                 285
Glu Ser Asp Asn Asn Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly Glu
    290                 295                 300
Glu Trp Gly Met Gly Gly Tyr Val Lys Met Ala Lys Asp Arg Arg Asn
305                 310                 315                 320
His Cys Gly Ile Ala Ser Ala Ala Ser Tyr Pro Thr Val
                325                 330
```

<210> 275
<211> 1342
<212> DNA
<213> Homo sapiens

<220>
<223> Cathepsin V

<400> 275
cggctgtaat ctcagaggct tgtttgctga gggtgcctgc gcacgtgcga cggctgctgg 60
ttttgaaaca tgaatctttc gctcgtcctg gctgcctttt gcttgggaat agcctccgct 120
gttccaaaat ttgaccaaaa tttggataca aagtggtacc agtggaaggc aacacacaga 180
agattatatg gcgcgaatga agaaggatgg aggagagcag tgtgggaaaa gaatatgaaa 240
atgattgaac tgcacaatgg ggaatacagc caagggaaac atggcttcac aatggccatg 300
aatgcttttc ctgacatgac caatgaagaa ttcaggcaga tgatgggttg ctttcgaaac 360

```
cagaaattca ggaaggggaa agtgttccgt gagcctctgt ttcttgatct tcccaaatct 420
gtggattgga gaaagaaagg ctacgtgacg ccagtgaaga atcagaaaca gtgtggttct 480
tgttgggctt ttagtgcgac tggtgctctt gaaggacaga tgttccggaa aactgggaaa 540
cttgtctcac tgagcgagca gaatctggtg gactgttcgc gtcctcaagg caatcagggc 600
tgcaatggtg gcttcatggc tagggccttc cagtatgtca aggagaacgg aggcctggac 660
tctgaggaat cctatccata tgtagcagtg gatgaaatct gtaagtacag acctgagaat 720
tctgttgcta atgacactgg cttcacagtg gtcgcacctg gaaaggagaa ggccctgatg 780
aaagcagtcg caactgtggg gcccatctcc gttgctatgg atgcaggcca ttcgtccttc 840
cagttctaca aatcaggcat ttattttgaa ccagactgca gcagcaaaaa cctggatcat 900
ggtgttctgg tggttggcta cggctttgaa ggagcaaatt cgaataacag caagtattgg 960
ctcgtcaaaa acagctgggg tccagaatgg ggctcgaatg gctatgtaaa aatagccaaa 1020
gacaagaaca accactgtgg aatcgccaca gcagccagct accccaatgt gtgagctgat 1080
ggatggtgag gaggaaggac ttaaggacag catgtctggg gaaatttttat cttgaaactg 1140
accaaacgct tattgtgtaa gataaaccag ttgaatcatt gaggatccaa gttgagattt 1200
taattctgtg acatttttac aagggtaaaa tgttaccact actttaatta ttgttataca 1260
cagctttatg atatcaaaga ctcattgctt aattctaaga cttttgaatt ttcatttttt 1320
aaaaagatgt acaaaacagt tt                                          1342
```

<210> 276
<211> 334
<212> PRT
<213> Homo sapiens

<220>
<223> Cathepsin V

<400> 276

```
Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
 1               5                  10                  15
Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
            20                  25                  30
Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly Trp Arg
        35                  40                  45
Arg Ala Val Trp Glu Lys Asn Met Lys Met Ile Glu Leu His Asn Gly
    50                  55                  60
Glu Tyr Ser Gln Gly Lys His Gly Phe Thr Met Ala Met Asn Ala Phe
65                  70                  75                  80
Gly Asp Met Thr Asn Glu Glu Phe Arg Gln Met Met Gly Cys Phe Arg
                85                  90                  95
Asn Gln Lys Phe Arg Lys Gly Lys Val Phe Arg Glu Pro Leu Phe Leu
            100                 105                 110
Asp Leu Pro Lys Ser Val Asp Trp Arg Lys Lys Gly Tyr Val Thr Pro
        115                 120                 125
Val Lys Asn Gln Lys Gln Cys Gly Ser Cys Trp Ala Phe Ser Ala Thr
    130                 135                 140
Gly Ala Leu Glu Gly Gln Met Phe Arg Lys Thr Gly Lys Leu Val Ser
145                 150                 155                 160
Leu Ser Glu Gln Asn Leu Val Asp Cys Ser Arg Pro Gln Gly Asn Gln
                165                 170                 175
Gly Cys Asn Gly Gly Phe Met Ala Arg Ala Phe Gln Tyr Val Lys Glu
            180                 185                 190
Asn Gly Gly Leu Asp Ser Glu Glu Ser Tyr Pro Tyr Val Ala Val Asp
        195                 200                 205
Glu Ile Cys Lys Tyr Arg Pro Glu Asn Ser Val Ala Asn Asp Thr Gly
    210                 215                 220
Phe Thr Val Val Ala Pro Gly Lys Glu Lys Ala Leu Met Lys Ala Val
225                 230                 235                 240
```

```
Ala Thr Val Gly Pro Ile Ser Val Ala Met Asp Ala Gly His Ser Ser
                245                 250                 255
Phe Gln Phe Tyr Lys Ser Gly Ile Tyr Phe Glu Pro Asp Cys Ser Ser
            260                 265                 270
Lys Asn Leu Asp His Gly Val Leu Val Val Gly Tyr Gly Phe Glu Gly
        275                 280                 285
Ala Asn Ser Asn Asn Ser Lys Tyr Trp Leu Val Lys Asn Ser Trp Gly
    290                 295                 300
Pro Glu Trp Gly Ser Asn Gly Tyr Val Lys Ile Ala Lys Asp Lys Asn
305                 310                 315                 320
Asn His Cys Gly Ile Ala Thr Ala Ala Ser Tyr Pro Asn Val
                325                 330
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<210> 277
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<223> Cathepsin K

<400> 277

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attcggcacg agccgcaatc ccgatggaat aaatctagca cccctgatgg tgtgcccaca 60
ctttgctgcc gaaacgaagc cagacaacag atttccatca gcaggatgtg ggggctcaag 120
gttctgctgc tacctgtggt gagctttgct ctgtaccctg aggagatact ggacacccac 180
tgggagctat ggaagaagac ccacaggaag caatataaca acaaggtgga tgaaatctct 240
cggcgtttaa tttgggaaaa aaacctgaag tatatttcca tccataacct tgaggcttct 300
cttggtgtcc atacatatga actggctatg aaccacctgg gggacatgac cagtgaagag 360
gtggttcaga agatgactgg actcaaagta cccctgtctc attcccgcag taatgacacc 420
ctttatatcc cagaatggga aggtagagcc ccagactctg tcgactatcg aaagaaagga 480
tatgttactc ctgtcaaaaa tcagggtcag tgtggttcct gttgggcttt tagctctgtg 540
ggtgccctgg agggccaact caagaagaaa actggcaaac tcttaaatct gagtccccag 600
aacctagtgg attgtgtgtc tgagaatgat ggctgtggag ggggctacat gaccaatgcc 660
ttccaatatg tgcagaagaa ccggggtatt gactctgaag atgcctaccc atatgtggga 720
caggaagaga gttgtatgta caacccaaca ggcaaggcag ctaaatgcag agggtacaga 780
gagatccccg aggggaatga gaaagccctg aagagggcag tggcccgagt gggacctgtc 840
tctgtggcca ttgatgcaag cctgacctcc ttccagtttt acagcaaagg tgtgtattat 900
gatgaaagct gcaatagcga taatctgaac catgcggttt tggcagtggg atatggaatc 960
cagaagggaa acaagcactg gataattaaa aacagctggg gagaaaactg gggaaacaaa 1020
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ttccccaaga tgtgactcca gccagccaaa tccatcctgc tcttccattt cttccacgat 1140
ggtgcagtgt aacgatgcac tttggaaggg agttggtgtg ctatttttga agcagatgtg 1200
gtgatactga gattgtctgt tcagtttccc catttgtttg tgcttcaaat gatccttcct 1260
actttggttc tctcctccca tgacctttt cactgtggcc atcaggactt tccctgacag 1320
ctgtgtactc ttaggctaag agatgtgact acagcctgcc cctgactgtg ttgtcccagg 1380
gctgatgctg tacaggtaca ggctggagat tttcacatag gttagattct cattcacggg 1440
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cccttcaata tcctcaaggt agaaatgtct atgttttcta ctccaattca taaatctatt 1560
cataagtctt tggtacaagt ttacatgata aaaagaaatg tgatttgtct tcccttcttt 1620
gcacttttga aataaagtat ttatctcctg tctacagttt a                    1661
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<210> 278
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<223> Cathepsin K

<400> 278
Met Trp Gly Leu Lys Val Leu Leu Leu Pro Val Val Ser Phe Ala Leu
 1   5   10   15
Tyr Pro Glu Glu Ile Leu Asp Thr His Trp Glu Leu Trp Lys Lys Thr
            20   25   30
His Arg Lys Gln Tyr Asn Asn Lys Val Asp Glu Ile Ser Arg Arg Leu
        35   40   45
Ile Trp Glu Lys Asn Leu Lys Tyr Ile Ser Ile His Asn Leu Glu Ala
    50   55   60
Ser Leu Gly Val His Thr Tyr Glu Leu Ala Met Asn His Leu Gly Asp
65   70   75   80
Met Thr Ser Glu Glu Val Val Gln Lys Met Thr Gly Leu Lys Val Pro
                85   90   95
Leu Ser His Ser Arg Ser Asn Asp Thr Leu Tyr Ile Pro Glu Trp Glu
            100   105   110
Gly Arg Ala Pro Asp Ser Val Asp Tyr Arg Lys Lys Gly Tyr Val Thr
        115   120   125
Pro Val Lys Asn Gln Gly Gln Cys Gly Ser Cys Trp Ala Phe Ser Ser
    130   135   140
Val Gly Ala Leu Glu Gly Gln Leu Lys Lys Lys Thr Gly Lys Leu Leu
145   150   155   160
Asn Leu Ser Pro Gln Asn Leu Val Asp Cys Val Ser Glu Asn Asp Gly
                165   170   175
Cys Gly Gly Gly Tyr Met Thr Asn Ala Phe Gln Tyr Val Gln Lys Asn
            180   185   190
Arg Gly Ile Asp Ser Glu Asp Ala Tyr Pro Tyr Val Gly Gln Glu Glu
        195   200   205
Ser Cys Met Tyr Asn Pro Thr Gly Lys Ala Ala Lys Cys Arg Gly Tyr
    210   215   220
Arg Glu Ile Pro Glu Gly Asn Glu Lys Ala Leu Lys Arg Ala Val Ala
225   230   235   240
Arg Val Gly Pro Val Ser Val Ala Ile Asp Ala Ser Leu Thr Ser Phe
                245   250   255
Gln Phe Tyr Ser Lys Gly Val Tyr Tyr Asp Glu Ser Cys Asn Ser Asp
            260   265   270
Asn Leu Asn His Ala Val Leu Ala Val Gly Tyr Gly Ile Gln Lys Gly
        275   280   285
Asn Lys His Trp Ile Ile Lys Asn Ser Trp Gly Glu Asn Trp Gly Asn
    290   295   300
Lys Gly Tyr Ile Leu Met Ala Arg Asn Lys Asn Asn Ala Cys Gly Ile
305   310   315   320
Ala Asn Leu Ala Ser Phe Pro Lys Met
                325

<210> 279
<211> 1255
<212> DNA
<213> Homo sapiens

<220>
<223> Cathepsin S

<400> 279

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ctaaagatga aacggctggt ttgtgtgctc ttggtgtgct cctctgcagt ggcacagttg 60
cataaagatc ctaccctgga tcaccactgg catctctgga agaaaaccta tggcaaacaa 120
tacaaggaaa agaatgaaga agcagtacga cgtctcatct gggaaaagaa tctaaagttt 180
gtgatgcttc acaacctgga gcattcaatg ggaatgcact catacgatct gggcatgaac 240
cacctgggag acatgaccag tgaagaagtg atgtctttga cgagttccct gagagttccc 300
agccagtggc agagaaatat cacatataag tcaaacccta atcggatatt gcctgattct 360
gtggactgga gagagaaagg gtgtgttact gaagtgaaat atcaaggttc ttgtggtgct 420
tgctgggctt tcagtgctgt gggggcccтg gaagcacagc tgaagctgaa aacaggaaag 480
ctggtgactc tcagtgccca gaacctggtg gattgctcaa ctgaaaaata tggaaacaaa 540
ggctgcaatg gtggcttcat gacaacggct ttccagtaca tcattgataa caagggcatc 600
gactcagacg cttcctatcc ctacaaagcc atggatcaga aatgtcaata tgactcaaaa 660
tatcgtgctg ccacatgttc aaagtacact gaacttcctt atgggagaga agatgtcctg 720
aaagaagctg tggccaataa aggcccagtg tctgttggtg tagatgcgcg tcatccttct 780
ttcttcctct acagaagtgg tgtctactat gaaccatcct gtactcagaa tgtgaatcat 840
ggtgtacttg tggttggcta tggtgatctt aatgggaaag aatactggct tgtgaaaaac 900
agctggggcc acaactttgg tgaagaagga tatattcgga tggcaagaaa taaaggaaat 960
cattgtggga ttgctagctt tccctcttac ccagaaatct agaggatctc tccttttttat 1020
aacaaatcaa gaaatatgaa gcactttctc ttaacttaat ttttcctgct gtatccagaa 1080
gaaataattg tgtcatgatt aatgtgtatt tactgtacta atagaaaata tagtttgagg 1140
ccgggcactg tctggctcac gcctgtaatc ccagtacttg ggaggccaag gaggcatatc 1200
aacttgaggc caggagttaa agagcagcct ggctaactgt gaaaccctct ctact      1255

<210> 280
<211> 331
<212> PRT
<213> Homo sapiens

<220>
<223> Cathepsin S

<400> 280
Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala Val Ala
 1               5                  10                  15
Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu Trp Lys
            20                  25                  30

Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala Val Arg
        35                  40                  45
Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His Asn Leu
    50                  55                  60
Glu His Ser Met Gly Met His Ser Tyr Asp Leu Gly Met Asn His Leu
65                  70                  75                  80
Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser Leu Arg
                85                  90                  95
Val Pro Ser Gln Trp Gln Arg Asn Ile Thr Tyr Lys Ser Asn Pro Asn
            100                 105                 110
Arg Ile Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val Thr
        115                 120                 125
Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser Ala
    130                 135                 140
Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu Val
145                 150                 155                 160
Thr Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr Gly
                165                 170                 175
Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr Ile
            180                 185                 190
Ile Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr Lys Ala
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        195                 200                 205
Met Asp Gln Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala Thr Cys
    210                 215                 220
Ser Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu Lys Glu
225                 230                 235                 240
Ala Val Ala Asn Lys Gly Pro Val Ser Val Gly Val Asp Ala Arg His
                245                 250                 255
Pro Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro Ser Cys
            260                 265                 270
Thr Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly Asp Leu
        275                 280                 285
Asn Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His Asn Phe
    290                 295                 300
Gly Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn His Cys
305                 310                 315                 320
Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile
                325                 330
```

<210> 281
<211> 1517
<212> DNA
<213> Homo sapiens

<220>
<223> Cathepsin F

<400> 281
gaattccggg tctgttgggt ccgggccgcc ggcttcgccc tcgccatggc gccctggctg 60
cagctcctgt cgctgctggg gctgctcccg ggcgcagtgg ccgcccccgc ccagccccga 120
gccgccagct ttcaggcctg ggggccgccg tccccggagc tgctggcgcc cacccgcttc 180
gcgctggaga tgttcaaccg cggccgggct gcggggacgc gggccgtgct gggccttgtg 240
cgcggccgcg tccgccgggc gggtcagggg tcgctgtact ccctggaggc caccctggag 300
gagccaccct gcaacgaccc catggtgtgc cggctccccg tgtccaagaa aaccctgctc 360
tgcagcttcc aagtcctgga tgagctcgga agacacgtgc tgctgcggaa ggactgtggc 420
ccagtggaca ccaaggttcc aggtgctggg gagcccaagt cagccttcac tcagggctca 480
gccatgattt cttctctgtc ccaaaaccat ccagacaaca gaaacgagac tttcagctca 540
gtcatttccc tgttgaatga ggatcccctg tcccaggact tgcctgtgaa gatggcttca 600
atcttcaaga actttgtcat tacctataac cggacatatg agtcaaagga agaagcccgg 660

tggcgcctgt ccgtctttgt caataacatg gtgcgagcac agaagatcca ggccctggac 720
cgtgggacag ctcagtatgg agtcaccaag ttcagtgatc tcacagagga ggagttccgc 780
actatctacc tgaatactct cctgaggaaa gagcctggca acaagatgaa gcaagccaag 840
tctgtgggtg acctcgcccc acctgaatgg gactggagga gtaaggggc tgtcacaaaa 900
gtcaaagacc agggcatgtg tggctcctgc tgggccttct cagtcacagg caatgtggag 960
ggccagtggt ttctcaacca ggggaccctg ctctccctct ctgaacagga gctcttggac 1020
tgtgacaaga tggacaaggc ctgcatgggc ggcttgccct ccaatgccta ctcggccata 1080
aagaatttgg gagggctgga gacagaggat gactacagct accagggtca catgcagtcc 1140
tgcaacttct cagcagagaa ggccaaggtc tacatcaatg actccgtgga gctgagccag 1200
aacgagcaga agctggcagc ctggctggcc aagagaggcc caatctccgt ggccatcaat 1260
gcctttggca tgcagtttta ccgccacggg atctcccgcc ctctccggcc cctctgcagc 1320
ccttggctca ttgaccatgc ggtgttgctt gtgggctacg gcaaccgctc tgacgttccc 1380
ttttgggcca tcaagaacag ctggggcact gactggggtg agaagggtta ctactacttg 1440
catcgtgggt ccggggcctg tggcgtgaac accatggcca gctcggcggt ggtggactga 1500
agaggggccc cgaattc   1517

<210> 282

<211> 484
<212> PRT
<213> Homo sapiens

<220>
<223> Cathepsin F

<400> 282
Met Ala Pro Trp Leu Gln Leu Leu Ser Leu Leu Gly Leu Leu Pro Gly
1 5 10 15
Ala Val Ala Ala Pro Ala Gln Pro Arg Ala Ala Ser Phe Gln Ala Trp
20 25 30
Gly Pro Pro Ser Pro Glu Leu Leu Ala Pro Thr Arg Phe Ala Leu Glu
35 40 45
Met Phe Asn Arg Gly Arg Ala Ala Gly Thr Arg Ala Val Leu Gly Leu
50 55 60
Val Arg Gly Arg Val Arg Arg Ala Gly Gln Gly Ser Leu Tyr Ser Leu
65 70 75 80
Glu Ala Thr Leu Glu Glu Pro Pro Cys Asn Asp Pro Met Val Cys Arg
85 90 95
Leu Pro Val Ser Lys Lys Thr Leu Leu Cys Ser Phe Gln Val Leu Asp
100 105 110
Glu Leu Gly Arg His Val Leu Leu Arg Lys Asp Cys Gly Pro Val Asp
115 120 125
Thr Lys Val Pro Gly Ala Gly Glu Pro Lys Ser Ala Phe Thr Gln Gly
130 135 140
Ser Ala Met Ile Ser Ser Leu Ser Gln Asn His Pro Asp Asn Arg Asn
145 150 155 160
Glu Thr Phe Ser Ser Val Ile Ser Leu Leu Asn Glu Asp Pro Leu Ser
165 170 175
Gln Asp Leu Pro Val Lys Met Ala Ser Ile Phe Lys Asn Phe Val Ile
180 185 190
Thr Tyr Asn Arg Thr Tyr Glu Ser Lys Glu Glu Ala Arg Trp Arg Leu
195 200 205
Ser Val Phe Val Asn Asn Met Val Arg Ala Gln Lys Ile Gln Ala Leu
210 215 220
Asp Arg Gly Thr Ala Gln Tyr Gly Val Thr Lys Phe Ser Asp Leu Thr
225 230 235 240
Glu Glu Glu Phe Arg Thr Ile Tyr Leu Asn Thr Leu Leu Arg Lys Glu
245 250 255
Pro Gly Asn Lys Met Lys Gln Ala Lys Ser Val Gly Asp Leu Ala Pro
260 265 270
Pro Glu Trp Asp Trp Arg Ser Lys Gly Ala Val Thr Lys Val Lys Asp
275 280 285
Gln Gly Met Cys Gly Ser Cys Trp Ala Phe Ser Val Thr Gly Asn Val
290 295 300
Glu Gly Gln Trp Phe Leu Asn Gln Gly Thr Leu Leu Ser Leu Ser Glu
305 310 315 320
Gln Glu Leu Leu Asp Cys Asp Lys Met Asp Lys Ala Cys Met Gly Gly
325 330 335
Leu Pro Ser Asn Ala Tyr Ser Ala Ile Lys Asn Leu Gly Gly Leu Glu
340 345 350
Thr Glu Asp Asp Tyr Ser Tyr Gln Gly His Met Gln Ser Cys Asn Phe
355 360 365
Ser Ala Glu Lys Ala Lys Val Tyr Ile Asn Asp Ser Val Glu Leu Ser
370 375 380
Gln Asn Glu Gln Lys Leu Ala Ala Trp Leu Ala Lys Arg Gly Pro Ile

```
385                 390                 395                 400
Ser Val Ala Ile Asn Ala Phe Gly Met Gln Phe Tyr Arg His Gly Ile
                405                 410                 415
Ser Arg Pro Leu Arg Pro Leu Cys Ser Pro Trp Leu Ile Asp His Ala
            420                 425                 430
Val Leu Leu Val Gly Tyr Gly Asn Arg Ser Asp Val Pro Phe Trp Ala
        435                 440                 445
Ile Lys Asn Ser Trp Gly Thr Asp Trp Gly Glu Lys Gly Tyr Tyr Tyr
    450                 455                 460
Leu His Arg Gly Ser Gly Ala Cys Gly Val Asn Thr Met Ala Ser Ser
465                 470                 475                 480
Ala Val Val Asp
```

<210> 283
<211> 2002
<212> DNA
<213> Homo sapiens

<220>
<223> Cathepsin B

<400> 283

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aattccgcgg caaccgctcc ggcaacgcca accgctccgc tgcgcgcagg ctgggctgca 60
ggctctcggc tgcagcgctg ggctggtgtg cagtggtgcg accacggctc acggcagcct 120

cagccaccca gatgtaagcg atctggttcc cacctcagcc ttccgagtag tggatctagg 180
atctggcttc caacatgtgg cagctctggg cctccctctg ctgcctgctg gtgttggcca 240
atgcccggag caggccctct ttccatcccg tgtcggatga gctggtcaac tatgtcaaca 300
aacggaatac cacgtggcag gccgggcaca acttctacaa cgtggacatg agctacttga 360
agaggctatg tggtaccttc ctgggtgggc ccaagccacc ccagagagtt atgtttaccg 420
aggacctgaa gctgcctgca agcttcgatg cacgggaaca atggccacag tgtcccacca 480
tcaaagagat cagagaccag ggctcctgtg gctcctgctg ggccttcggg gctgtggaag 540
ccatctctga ccgcatctgc atccacacca atgcgcacgt cagcgtggag gtgtcggcgg 600
aggacctgct cacctgctgt ggcagcatgt gtggggacgg ctgtaatggt ggctatcctg 660
ctgaagcttg gaacttctgg acaagaaaag gcctggtttc tggtggcctc tatgaatccc 720
atgtagggtg cagaccgtac tccatccctc cctgtgagca ccacgtcaac ggctcccggc 780
ccccatgcac gggggaggga gataccccca agtgtagcaa gatctgtgag cctggctaca 840
gcccgaccta caaacaggac aagcactacg gatacaattc ctacagcgtc tccaatagcg 900
agaaggacat catggccgag atctacaaaa acggccccgt ggagggagct ttctctgtgt 960
attcggactt cctgctctac aagtcaggag tgtaccaaca cgtcaccgga gagatgatgg 1020
gtggccatgc catccgcatc ctgggctggg gagtggagaa tggcacaccc tactggctgg 1080
ttgccaactc ctggaacact gactggggtg acaatggctt ctttaaaata ctcagaggac 1140
aggatcactg cggaatcgaa tcagaagtgg tggctggaat tccacgcacc gatcagtact 1200
gggaaaagat ctaatctgcc gtgggcctgt cgtgccagtc ctgggggcga gatcggggta 1260
gaaagtcatt ttattcttta agttcacgta agatacaagt ttcaggcagg gtctgaagga 1320
ctggattggc caaagtcctc caaggagacc aagtcctggc tacatcccag cctgtggtta 1380
cagtgcagac aggccatgtg agccaccgct gccagcacag agcgtccttc cccctgtaga 1440
ctagtgccgt gggagtacct gctgcccagc tgctgtggcc ccctccgtga tccatccatc 1500
tccagggagc aagacagaga cgcaggatgg aaagcggagt tcctaacagg atgaaagttc 1560
ccccatcagt tcccccagta cctccaagca agtagctttc cacatttgtc acagaaatca 1620
gaggagagat ggtgttggga gcccttgga gaacgccagt ctccaggtcc ccctgcatct 1680
atcgagtttg caatgtcaca acctctctga tcttgtgctc agcatgattc tttaatagaa 1740
gttttatttt tcgtgcactc tgctaatcat gtgggtgagc cagtggaaca gcgggagcct 1800
gtgctggttt gcagattgcc tcctaatgac gcggctcaaa aggaaaccaa gtggtcagga 1860
gttgtttctg acccactgat ctctactacc acaaggaaaa tagtttagga gaaaccagct 1920
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tttactgttt ttgaaaaatt acagcttcac cctgtcaagt taacaaggaa tgcctgtgcc 1980
aataaaaggt ttctccaact tg 2002

<210> 284
<211> 339
<212> PRT
<213> Homo sapiens

<220>
<223> Cathepsin B

<400> 284
Met Trp Gln Leu Trp Ala Ser Leu Cys Cys Leu Leu Val Leu Ala Asn
1 5 10 15
Ala Arg Ser Arg Pro Ser Phe His Pro Leu Ser Asp Glu Leu Val Asn
20 25 30
Tyr Val Asn Lys Arg Asn Thr Thr Trp Gln Ala Gly His Asn Phe Tyr
35 40 45
Asn Val Asp Met Ser Tyr Leu Lys Arg Leu Cys Gly Thr Phe Leu Gly
50 55 60
Gly Pro Lys Pro Pro Gln Arg Val Met Phe Thr Glu Asp Leu Lys Leu
65 70 75 80
Pro Ala Ser Phe Asp Ala Arg Glu Gln Trp Pro Gln Cys Pro Thr Ile
85 90 95
Lys Glu Ile Arg Asp Gln Gly Ser Cys Gly Ser Cys Trp Ala Phe Gly
100 105 110
Ala Val Glu Ala Ile Ser Asp Arg Ile Cys Ile His Thr Asn Ala His
115 120 125
Val Ser Val Glu Val Ser Ala Glu Asp Leu Leu Thr Cys Cys Gly Ser
130 135 140
Met Cys Gly Asp Gly Cys Asn Gly Gly Tyr Pro Ala Glu Ala Trp Asn
145 150 155 160
Phe Trp Thr Arg Lys Gly Leu Val Ser Gly Gly Leu Tyr Glu Ser His
165 170 175
Val Gly Cys Arg Pro Tyr Ser Ile Pro Pro Cys Glu His His Val Asn
180 185 190
Gly Ser Arg Pro Pro Cys Thr Gly Glu Gly Asp Thr Pro Lys Cys Ser
195 200 205
Lys Ile Cys Glu Pro Gly Tyr Ser Pro Thr Tyr Lys Gln Asp Lys His
210 215 220
Tyr Gly Tyr Asn Ser Tyr Ser Val Ser Asn Ser Glu Lys Asp Ile Met
225 230 235 240
Ala Glu Ile Tyr Lys Asn Gly Pro Val Glu Gly Ala Phe Ser Val Tyr
245 250 255
Ser Asp Phe Leu Leu Tyr Lys Ser Gly Val Tyr Gln His Val Thr Gly
260 265 270
Glu Met Met Gly Gly His Ala Ile Arg Ile Leu Gly Trp Gly Val Glu
275 280 285
Asn Gly Thr Pro Tyr Trp Leu Val Ala Asn Ser Trp Asn Thr Asp Trp
290 295 300
Gly Asp Asn Gly Phe Phe Lys Ile Leu Arg Gly Gln Asp His Cys Gly
305 310 315 320
Ile Glu Ser Glu Val Val Ala Gly Ile Pro Arg Thr Asp Gln Tyr Trp
325 330 335
Glu Lys Ile

<210> 285
<211> 1292
<212> DNA
<213> Carica papaya

<220>
<223> Papain

<400> 285
atccattccc acttaagaag taaaaagata tagctagtgt cacaatggct atgatacctt 60
caatttcaaa gttgcttttt gttgcaatat gtctttttgt ttatatgggt ttgtcatttg 120
gtgatttttc tattgtgggt tattctcaaa atgacttgac atccactgaa agacttattc 180
agctatttga atcgtggatg ttgaagcaca ataagattta taagaatatt gatgaaaaaa 240
tctacagatt tgaaattttt aaagataatc ttaaatatat tgatgagaca aataagaaaa 300
ataacagtta ttggcttgga ttaaatgtgt ttgctgatat gagcaatgat gaattcaaag 360
aaaagtatac tggttctatt gctggaaatt atacaacaac cgaactatca tacgaagaag 420
tgcttaatga tggtgatgta aatatcccgg agtatgtcga ttggagacaa aaaggagctg 480
tcactcctgt aaaaaatcag ggttcttgtg gtagttgttg ggcattctca gctgttgtaa 540
ctatagaggg aataattaag attagaactg ggaacttaaa tgaatactca gagcaagaac 600
tgcttgactg cgacagacgt agctacgggt gcaatggagg ttacccttgg agtgcacttc 660
aattagtggc tcaatatggt attcactaca gaaatactta cccatatgag ggagtgcaac 720
gttattgtcg ctcaagggag aaaggtcctt atgcagccaa aaccgatggg gttcgacaag 780
tgcaaccata taatgaaggg gctctcttat attcaattgc aaaccaacct gtgagcgttg 840
tccttgaagc tgctggaaaa gatttccaat tatatagagg gggaatattt gtggggccat 900
gcggaaacaa agtagatcat gcagtcgcag cagttgggta tggaccaaat tacatactca 960
taaagaattc atggggtaca ggatggggtg aaaatggata tataagaatc aaaagaggca 1020
ctggaaactc ctatggagta tgtggacttt atacaagctc attctatcct gttaaaaact 1080
gatgagatca cggctttcat aaaatccctt atatatatat atatatatag aacttgtata 1140
ctcatcgtgt gttgaaataa taaatgagag gattaataat ttgtgtaatc ctatatatca 1200
cagtttgttg tgacaaactt ttgcatcgct tgttatatta tttgtaataa tgtttgtttt 1260
gattgaataa acttttacat atacttttat gc 1292

<210> 286
<211> 345
<212> PRT
<213> Carica papaya

<220>
<223> Papain

<400> 286
Met Ala Met Ile Pro Ser Ile Ser Lys Leu Leu Phe Val Ala Ile Cys
 1   5   10   15
Leu Phe Val Tyr Met Gly Leu Ser Phe Gly Asp Phe Ser Ile Val Gly
            20   25   30
Tyr Ser Gln Asn Asp Leu Thr Ser Thr Glu Arg Leu Ile Gln Leu Phe
        35   40   45
Glu Ser Trp Met Leu Lys His Asn Lys Ile Tyr Lys Asn Ile Asp Glu
    50   55   60
Lys Ile Tyr Arg Phe Glu Ile Phe Lys Asp Asn Leu Lys Tyr Ile Asp
65   70   75   80
Glu Thr Asn Lys Lys Asn Asn Ser Tyr Trp Leu Gly Leu Asn Val Phe
                85   90   95
Ala Asp Met Ser Asn Asp Glu Phe Lys Glu Lys Tyr Thr Gly Ser Ile
            100   105   110
Ala Gly Asn Tyr Thr Thr Thr Glu Leu Ser Tyr Glu Glu Val Leu Asn

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        115                 120                 125
Asp Gly Asp Val Asn Ile Pro Glu Tyr Val Asp Trp Arg Gln Lys Gly
    130                 135                 140
Ala Val Thr Pro Val Lys Asn Gln Gly Ser Cys Gly Ser Cys Trp Ala
145                 150                 155                 160
Phe Ser Ala Val Val Thr Ile Glu Gly Ile Ile Lys Ile Arg Thr Gly
                165                 170                 175
Asn Leu Asn Glu Tyr Ser Glu Gln Glu Leu Leu Asp Cys Asp Arg Arg
            180                 185                 190
Ser Tyr Gly Cys Asn Gly Gly Tyr Pro Trp Ser Ala Leu Gln Leu Val
        195                 200                 205
Ala Gln Tyr Gly Ile His Tyr Arg Asn Thr Tyr Pro Tyr Glu Gly Val
    210                 215                 220
Gln Arg Tyr Cys Arg Ser Arg Glu Lys Gly Pro Tyr Ala Ala Lys Thr
225                 230                 235                 240
Asp Gly Val Arg Gln Val Gln Pro Tyr Asn Glu Gly Ala Leu Leu Tyr
                245                 250                 255
Ser Ile Ala Asn Gln Pro Val Ser Val Val Leu Glu Ala Ala Gly Lys
            260                 265                 270
Asp Phe Gln Leu Tyr Arg Gly Gly Ile Phe Val Gly Pro Cys Gly Asn
        275                 280                 285
Lys Val Asp His Ala Val Ala Ala Val Gly Tyr Gly Pro Asn Tyr Ile
    290                 295                 300
Leu Ile Lys Asn Ser Trp Gly Thr Gly Trp Gly Glu Asn Gly Tyr Ile

305                 310                 315                 320
Arg Ile Lys Arg Gly Thr Gly Asn Ser Tyr Gly Val Cys Gly Leu Tyr
                325                 330                 335
Thr Ser Ser Phe Tyr Pro Val Lys Asn
            340                 345
```

<210> 287
<211> 1845
<212> DNA
<213> Trypanosoma cruzi

<220>
<223> Cruzain (Cruzapain)

<400> 287

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atgtctggct gggcgcgtgc gctgttgctc gcggccgtcc tggtcgtcat ggcgtgcctc 60
gtccccgcgg cgacggcgag cctgcatgcg gaggagacgc tgacgtcgca attcgcagaa 120
ttcaagcaga agcatggcag ggtgtacgag agcgccgcgg aggaggcgtt ccgcctgagc 180
gtgttcaggg agaacctgtt tcttgcgagg ctgcacgccg cggcaaaccc acacgcgacc 240
ttcggcgtca cgcccttctc ggacctcacg cgcgaggaat tccggtcccg ctaccacaac 300
ggcgcggcgc actttgcggc ggcgcaggag cgcgcgagag tgccggtgaa ggtggaggta 360
gttggcgcgc ccgcggcagt ggattggcgt gcgagaggcg ccgtgacagc cgtcaaggac 420
cagggccaat gcggttcgtg ctgggccttc tccgccattg gcaacgttga gtgccagtgg 480
tttcttgccg gccacccgct gacgaacctg tcggagcaga tgctcgtgtc gtgcgacaaa 540
acggactctg gctgcagtgg tggcctgatg aacaacgcct ttgagtggat tgtgcaggag 600
aataacggcg ccgtgtacac ggaggacagc tacccttatg cgtcgggcga ggggatatcg 660
ccgccgtgca cgacgtcagg ccacacggtg ggtgccacga ttaccggtca cgttgaatta 720
cctcaggacg aggcccaaat agccgcatgg cttgcagtca atggcccggt tgccgttgcc 780
gtcgacgcca gcagctggat gacctacacg ggcggcgtta tgacgagctg cgtctccgag 840
cagctggatc acggcgttct tctcgtcggc tacaatgaca gcgccgcagt gccgtactgg 900
atcatcaaga actcgtggac cacgcagtgg ggcgaggaag gctacatccg cattgcaaag 960
```

ggctcgaacc agtgccttgt caaggaggag gcgagctccg cggtggtcgg tggtcccgga 1020
cccactcccg agccaaccac cacgacaacc acaagtgccc caggaccgtc cccatcgtac 1080
tttgtgcaga tgtcctgcac tgacgctgcg tgcattgtcg ggtgcgagaa cgtgacgtta 1140
ccgaccggtc agtgtctcct gaccaccagc ggcgtctctg ccattgtcac gtgcggtgct 1200
gagactctca cagaagaagt cttccttacg agtacgcact gcagcggccc atcggtgagg 1260
tcctctgttc ctctcaacaa atgcaaccgg cttttaagag gctccgttga gttcttctgc 1320
ggctccagct ccagtggccg actggccgac gtggacaggc agcgtcgcca tcagccatac 1380
cacagccgtc atcgccgcct ctgagggcac tctttgtttc tgatgctgcc ttttctctca 1440
ttttactttt ttattattat tgagcgagcg tcggtgctgc ggcacactgg gcaaataagt 1500
cccagtggag tggattgttt attgatttgc tccatgtatg tgttttcttt tttgtgcaca 1560
actgcaaata tgtgtccgcg atcgacgtct cagccacgcg tgtgtttttt ctattatatg 1620
cttctgttga gcgcccgagc attccccact gtggctgaac ccaccgccgt ccccgactgt 1680
cacccgacca tgcggggcgg ggtggcgtgg caacgctcct ttgccgcggc gtgcacatac 1740
acgcgcgcat gcttcttctc tccacgtcaa cgccgacacc accacagtct gaaggtgacg 1800
ctgttgaagg cacacaagga aggaaacaca cccacacaag cagta 1845

<210> 288
<211> 467
<212> PRT
<213> Trypanosoma cruzi

<220>
<223> Cruzain (Cruzapain)

<400> 288
Met Ser Gly Trp Ala Arg Ala Leu Leu Leu Ala Ala Val Leu Val Val
1 5 10 15
Met Ala Cys Leu Val Pro Ala Ala Thr Ala Ser Leu His Ala Glu Glu
20 25 30
Thr Leu Thr Ser Gln Phe Ala Glu Phe Lys Gln Lys His Gly Arg Val
35 40 45
Tyr Glu Ser Ala Ala Glu Glu Ala Phe Arg Leu Ser Val Phe Arg Glu
50 55 60
Asn Leu Phe Leu Ala Arg Leu His Ala Ala Ala Asn Pro His Ala Thr
65 70 75 80
Phe Gly Val Thr Pro Phe Ser Asp Leu Thr Arg Glu Glu Phe Arg Ser
85 90 95
Arg Tyr His Asn Gly Ala Ala His Phe Ala Ala Ala Gln Glu Arg Ala
100 105 110
Arg Val Pro Val Lys Val Glu Val Val Gly Ala Pro Ala Ala Val Asp
115 120 125
Trp Arg Ala Arg Gly Ala Val Thr Ala Val Lys Asp Gln Gly Gln Cys
130 135 140
Gly Ser Cys Trp Ala Phe Ser Ala Ile Gly Asn Val Glu Cys Gln Trp
145 150 155 160
Phe Leu Ala Gly His Pro Leu Thr Asn Leu Ser Glu Gln Met Leu Val
165 170 175
Ser Cys Asp Lys Thr Asp Ser Gly Cys Ser Gly Gly Leu Met Asn Asn
180 185 190
Ala Phe Glu Trp Ile Val Gln Glu Asn Asn Gly Ala Val Tyr Thr Glu
195 200 205
Asp Ser Tyr Pro Tyr Ala Ser Gly Glu Gly Ile Ser Pro Pro Cys Thr
210 215 220
Thr Ser Gly His Thr Val Gly Ala Thr Ile Thr Gly His Val Glu Leu
225 230 235 240
Pro Gln Asp Glu Ala Gln Ile Ala Ala Trp Leu Ala Val Asn Gly Pro

```
                245                 250                 255
Val Ala Val Ala Val Asp Ala Ser Ser Trp Met Thr Tyr Thr Gly Gly
            260                 265                 270
Val Met Thr Ser Cys Val Ser Glu Gln Leu Asp His Gly Val Leu Leu
        275                 280                 285
Val Gly Tyr Asn Asp Ser Ala Ala Val Pro Tyr Trp Ile Ile Lys Asn
    290                 295                 300
Ser Trp Thr Thr Gln Trp Gly Glu Glu Gly Tyr Ile Arg Ile Ala Lys
305                 310                 315                 320
Gly Ser Asn Gln Cys Leu Val Lys Glu Glu Ala Ser Ser Ala Val Val
                325                 330                 335
Gly Gly Pro Gly Pro Thr Pro Glu Pro Thr Thr Thr Thr Thr Thr Ser
            340                 345                 350
Ala Pro Gly Pro Ser Pro Ser Tyr Phe Val Gln Met Ser Cys Thr Asp
        355                 360                 365
Ala Ala Cys Ile Val Gly Cys Glu Asn Val Thr Leu Pro Thr Gly Gln
    370                 375                 380
Cys Leu Leu Thr Thr Ser Gly Val Ser Ala Ile Val Thr Cys Gly Ala
385                 390                 395                 400
Glu Thr Leu Thr Glu Glu Val Phe Leu Thr Ser Thr His Cys Ser Gly
                405                 410                 415
Pro Ser Val Arg Ser Ser Val Pro Leu Asn Lys Cys Asn Arg Leu Leu
            420                 425                 430
Arg Gly Ser Val Glu Phe Phe Cys Gly Ser Ser Ser Ser Gly Arg Leu
        435                 440                 445
Ala Asp Val Asp Arg Gln Arg Arg His Gln Pro Tyr His Ser Arg His
    450                 455                 460
Arg Arg Leu
465
```

<210> 289
<211> 379
<212> PRT
<213> Bacillus licheniformis

<220>
<223> Subtilisin Carlsberg precursor S08.001

```
<400> 289
Met Met Arg Lys Lys Ser Phe Trp Leu Gly Met Leu Thr Ala Phe Met
 1               5                  10                  15
Leu Val Phe Thr Met Ala Phe Ser Asp Ser Ala Ser Ala Ala Gln Pro
            20                  25                  30
Ala Lys Asn Val Glu Lys Asp Tyr Ile Val Gly Phe Lys Ser Gly Val
        35                  40                  45
Lys Thr Ala Ser Val Lys Lys Asp Ile Ile Lys Glu Ser Gly Gly Lys
    50                  55                  60
Val Asp Lys Gln Phe Arg Ile Ile Asn Ala Ala Lys Ala Lys Leu Asp
65                  70                  75                  80
Lys Glu Ala Leu Lys Glu Val Lys Asn Asp Pro Asp Val Ala Tyr Val
                85                  90                  95
Glu Glu Asp His Val Ala His Ala Leu Ala Gln Thr Val Pro Tyr Gly
            100                 105                 110
Ile Pro Leu Ile Lys Ala Asp Lys Val Gln Ala Gln Gly Phe Lys Gly
        115                 120                 125
Ala Asn Val Lys Val Ala Val Leu Asp Thr Gly Ile Gln Ala Ser His
```

```
    130                 135                 140
Pro Asp Leu Asn Val Val Gly Gly Ala Ser Phe Val Ala Gly Glu Ala
145                 150                 155                 160
Tyr Asn Thr Asp Gly Asn Gly His Gly Thr His Val Ala Gly Thr Val
                165                 170                 175
Ala Ala Leu Asp Asn Thr Thr Gly Val Leu Gly Val Ala Pro Ser Val
            180                 185                 190
Ser Leu Tyr Ala Val Lys Val Leu Asn Ser Ser Gly Ser Gly Thr Tyr
        195                 200                 205
Ser Gly Ile Val Ser Gly Ile Glu Trp Ala Thr Thr Asn Gly Met Asp
    210                 215                 220
Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Thr Ala Met Lys
225                 230                 235                 240
Gln Ala Val Asp Asn Ala Tyr Ala Arg Gly Val Val Val Val Ala Ala
                245                 250                 255
Ala Gly Asn Ser Gly Ser Ser Gly Asn Thr Asn Thr Ile Gly Tyr Pro
            260                 265                 270
Ala Lys Tyr Asp Ser Val Ile Ala Val Gly Ala Val Asp Ser Asn Ser
        275                 280                 285
Asn Arg Ala Ser Phe Ser Ser Val Gly Ala Glu Leu Glu Val Met Ala
    290                 295                 300
Pro Gly Ala Gly Val Tyr Ser Thr Tyr Pro Thr Ser Thr Tyr Ala Thr
305                 310                 315                 320
Leu Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Ala Ala
                325                 330                 335
Leu Ile Leu Ser Lys His Pro Asn Leu Ser Ala Ser Gln Val Arg Asn
            340                 345                 350
Arg Leu Ser Ser Thr Ala Thr Tyr Leu Gly Ser Ser Phe Tyr Tyr Gly
        355                 360                 365
Lys Gly Leu Ile Asn Val Glu Ala Ala Ala Gln
    370                 375
```

<210> 290
<211> 1588
<212> DNA
<213> Bacillus licheniformis

<220>
<223> Subtilisin Carlsberg precursor S08.001

<400> 290
gatcgacaag accgcaacct ccttcgacaa aaaatgatct cttaaaataa atgaatagta 60
ttttcataaa atgaatcaga tggagcaatc tcctgtcatt cgcggccctc gggacctctt 120
tccctgccag gctgaagcgg tctattcata ctttcgaact gaacatttttt ctaaaacagt 180
tattaataac caaaaaattt taaattggtc ctccaaaaaa ataggcctac catataattc 240
attttttttc tataataaat taacagaata attggaatag attatattat ccttctattt 300
aaattattct gaataaagag gaggagagtg agtaatgatg aggaaaaaga gtttttggct 360
tgggatgctg acggccttca tgctcgtgtt cacgatggca ttcagcgatt ccgcttctgc 420
tgctcaaccg gcgaaaaatg ttgaaaagga ttatattgtc ggatttaagt caggagtgaa 480
aaccgcatct gtcaaaaagg acatcatcaa agagagcggc ggaaaagtgg acaagcagtt 540
tagaatcatc aacgcggcaa aagcgaagct agacaaagaa gcgcttaagg aagtcaaaaa 600
tgatccggat gtcgcttatg tggaagagga tcatgtggcc catgccttgg cgcaaaccgt 660
tccttacggc attcctctca ttaaagcgga caaagtgcag gctcaaggct ttaagggagc 720
gaatgtaaaa gtagccgtcc tggatacagg aatccaagct tctcatccgg acttgaacgt 780
agtcggcgga gcaagctttg tggctggcga agcttataac accgacggca acggacacgg 840

```
cacacatgtt gccggtacag tagctgcgct tgacaataca acgggtgtat taggcgttgc 900
gccaagcgta tccttgtacg cggttaaagt actgaattca agcggaagcg gaacttacag 960
cggcattgta agcggaatcg agtgggcgac gacaaacggc atggatgtta tcaacatgag 1020
tcttggagga ccatcaggct caacagcgat gaaacaggcg gttgacaatg catatgcaag 1080
aggggttgtc gttgtggcgg ctgctgggaa cagcggatct tcaggaaaca cgaatacaat 1140
cggctatcct gcgaaatacg actctgtcat cgcagttggc gcggtagact ctaacagcaa 1200
cagagcttca ttttccagcg tcggagcaga gcttgaagtc atggctcctg gcgcaggcgt 1260
gtacagcact tacccaacca gcacttatgc aacattgaac ggaacgtcaa tggcttctcc 1320
tcatgtagcg ggagcagcag ctttgatctt gtcaaaacat ccgaaccttt cagcttcaca 1380
agtccgcaac cgtctctcca gtacggcgac ttatttggga agctccttct actatggaaa 1440
aggtctgatc aatgtcgaag ctgccgctca ataacatatt ctaacaaatg gcatatagaa 1500
aaagctagtg tttttagcac tagctttttc ttcattcagt tgaagactgt tcaatatttt 1560
gaatccgttc cattatggtc ggatggcc                                    1588
```

<210> 291
<211> 275
<212> PRT
<213> Bacillus pumilus

<220>
<223> Subtilisin (Alkaline mesentericopeptidase) S08.002

<400> 291

```
Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu
 1               5                  10                  15
His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys Val Ala Val Ile Asp
            20                  25                  30
Ser Gly Ile Asp Ser Ser His Pro Asp Leu Asn Val Arg Gly Gly Ala
        35                  40                  45
Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln Asp Gly Ser Ser His
    50                  55                  60
Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly
65                  70                  75                  80
Val Leu Gly Val Ala Pro Ser Ser Ala Leu Tyr Ala Val Lys Val Leu
                85                  90                  95
Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu
            100                 105                 110
Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn Met Ser Leu Gly Gly
        115                 120                 125
Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val Asp Lys Ala Val Ser
    130                 135                 140
Ser Gly Ile Val Val Ala Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly
145                 150                 155                 160
Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala
                165                 170                 175
Val Gly Ala Val Asn Ser Ala Asn Gln Arg Ala Ser Phe Ser Ser Ala
            180                 185                 190
Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val Ser Ile Gln Ser Thr
        195                 200                 205
Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr
    210                 215                 220
Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu Ser Lys His Pro Thr
225                 230                 235                 240
Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr
                245                 250                 255
Leu Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala
```

260 265 270
Ala Ala Gln
275

<210> 292
<211> 269
<212> PRT
<213> Bacillus lentus

<220>
<223> Subtilisin Savinase (Alkaline protease) S08.003

<400> 292
Ala Gln Ser Val Pro Trp Gly Ile Ser Arg Val Gln Ala Pro Ala Ala
1 5 10 15
His Asn Arg Gly Leu Thr Gly Ser Gly Val Lys Val Ala Val Leu Asp
20 25 30
Thr Gly Ile Ser Thr His Pro Asp Leu Asn Ile Arg Gly Gly Ala Ser
35 40 45
Phe Val Pro Gly Glu Pro Ser Thr Gln Asp Gly Asn Gly His Gly Thr
50 55 60
His Val Ala Gly Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu
65 70 75 80
Gly Val Ala Pro Ser Ala Glu Leu Tyr Ala Val Lys Val Leu Gly Ala
85 90 95
Ser Gly Ser Gly Ser Val Ser Ser Ile Ala Gln Gly Leu Glu Trp Ala
100 105 110
Gly Asn Asn Gly Met His Val Ala Asn Leu Ser Leu Gly Ser Pro Ser
115 120 125
Pro Ser Ala Thr Leu Glu Gln Ala Val Asn Ser Ala Thr Ser Arg Gly
130 135 140
Val Leu Val Val Ala Ala Ser Gly Asn Ser Gly Ala Gly Ser Ile Ser
145 150 155 160
Tyr Pro Ala Arg Tyr Ala Asn Ala Met Ala Val Gly Ala Thr Asp Gln
165 170 175
Asn Asn Asn Arg Ala Ser Phe Ser Gln Tyr Gly Ala Gly Leu Asp Ile
180 185 190
Val Ala Pro Gly Val Asn Val Gln Ser Thr Tyr Pro Gly Ser Thr Tyr
195 200 205
Ala Ser Leu Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
210 215 220
Ala Ala Leu Val Lys Gln Lys Asn Pro Ser Trp Ser Asn Val Gln Ile
225 230 235 240
Arg Asn His Leu Lys Asn Thr Ala Thr Ser Leu Gly Ser Thr Asn Leu
245 250 255
Tyr Gly Ser Gly Leu Val Asn Ala Glu Ala Ala Thr Arg
260 265

<210> 293
<211> 279
<212> PRT
<213> Thermoactinomyces vulgaris

<220>
<223> Thermitase S08.007

<400> 293
Tyr Thr Pro Asn Asp Pro Tyr Phe Ser Ser Arg Gln Tyr Gly Pro Gln
1 5 10 15
Lys Ile Gln Ala Pro Gln Ala Trp Asp Ile Ala Glu Gly Ser Gly Ala
20 25 30
Lys Ile Ala Ile Val Asp Thr Gly Val Gln Ser Asn His Pro Asp Leu
35 40 45
Ala Gly Lys Val Val Gly Gly Trp Asp Phe Val Asp Asn Asp Ser Thr
50 55 60
Pro Gln Asn Gly Asn Gly His Gly Thr His Cys Ala Gly Ile Ala Ala
65 70 75 80
Ala Val Thr Asn Asn Ser Thr Gly Ile Ala Gly Thr Ala Pro Lys Ala
85 90 95
Ser Ile Leu Ala Val Arg Val Leu Asp Asn Ser Gly Ser Gly Thr Trp
100 105 110
Thr Ala Val Ala Asn Gly Ile Thr Tyr Ala Ala Asp Gln Gly Ala Lys
115 120 125
Val Ile Ser Leu Ser Leu Gly Gly Thr Val Gly Asn Ser Gly Leu Gln
130 135 140
Gln Ala Val Asn Tyr Ala Trp Asn Lys Gly Ser Val Val Val Ala Ala
145 150 155 160
Ala Gly Asn Ala Gly Asn Thr Ala Pro Asn Tyr Pro Ala Tyr Tyr Ser
165 170 175
Asn Ala Ile Ala Val Ala Ser Thr Asp Gln Asn Asp Asn Lys Ser Ser
180 185 190
Phe Ser Thr Tyr Gly Ser Val Val Asp Val Ala Ala Pro Gly Ser Trp
195 200 205
Ile Tyr Ser Thr Tyr Pro Thr Ser Thr Tyr Ala Ser Leu Ser Gly Thr
210 215 220
Ser Met Ala Thr Pro His Val Ala Gly Val Ala Gly Leu Leu Ala Ser
225 230 235 240
Gln Gly Arg Ser Ala Ser Asn Ile Arg Ala Ala Ile Glu Asn Thr Ala
245 250 255
Asp Lys Ile Ser Gly Thr Gly Thr Tyr Trp Ala Lys Gly Arg Val Asn
260 265 270
Ala Tyr Lys Ala Val Gln Tyr
275

<210> 294
<211> 401
<212> PRT
<213> Bacillus sp. AK1

<220>
<223> Thermophilic serine proteinase precursor (Ak.1 protease) S08.009

<400> 294
Met Lys Phe Lys Ala Ile Val Ser Leu Ser Leu Ala Val Ser Met Ser
1 5 10 15
Leu Phe Pro Phe Leu Val Glu Ala Ala Ser Asn Asp Gly Val Glu Ser
20 25 30
Pro Lys Thr Val Ser Glu Ile Asn Val Ser His Glu Lys Gly Ala Tyr
35 40 45
Val Gln Gly Glu Val Ile Val Gln Phe Lys Glu Gln Val Asn Ala Glu

```
    50                  55                  60
Glu Lys Ala Lys Ala Leu Lys Glu Val Gly Ala Thr Ala Val Pro Asp
65                  70                  75                  80
Asn Asp Arg Val Lys Ser Lys Phe Asn Val Leu Lys Val Gly Asn Val
                85                  90                  95
Glu Ala Val Val Lys Ala Leu Asn Asn Asn Pro Leu Val Glu Tyr Ala
            100                 105                 110
Glu Pro Asn Tyr Leu Phe Asn Ala Ala Trp Thr Pro Asn Asp Thr Tyr
        115                 120                 125
Tyr Gln Gly Tyr Gln Tyr Gly Pro Gln Asn Thr Tyr Thr Asp Tyr Ala
    130                 135                 140
Trp Asp Val Thr Lys Gly Ser Ser Gly Gln Glu Ile Ala Val Ile Asp
145                 150                 155                 160
Thr Gly Val Asp Tyr Thr His Pro Asp Leu Asp Gly Lys Val Ile Lys
                165                 170                 175
Gly Tyr Asp Phe Val Asp Asn Asp Tyr Asp Pro Met Asp Leu Asn Asn
            180                 185                 190
His Gly Thr His Val Ala Gly Ile Ala Ala Ala Glu Thr Asn Asn Ala
        195                 200                 205
Thr Gly Ile Ala Gly Met Ala Pro Asn Thr Arg Ile Leu Ala Val Arg
    210                 215                 220
Ala Leu Asp Arg Asn Gly Ser Gly Thr Leu Ser Asp Ile Ala Asp Ala
225                 230                 235                 240
Ile Ile Tyr Ala Ala Asp Ser Gly Ala Glu Val Ile Asn Leu Ser Leu
                245                 250                 255
Gly Cys Asp Cys His Thr Thr Thr Leu Glu Asn Ala Val Asn Tyr Ala
            260                 265                 270
Trp Asn Lys Gly Ser Val Val Val Ala Ala Ala Gly Asn Asn Gly Ser
        275                 280                 285
Ser Thr Thr Phe Glu Pro Ala Ser Tyr Glu Asn Val Ile Ala Val Gly
    290                 295                 300
Ala Val Asp Gln Tyr Asp Arg Leu Ala Ser Phe Ser Asn Tyr Gly Thr
305                 310                 315                 320
Trp Val Asp Val Val Ala Pro Gly Val Asp Ile Val Ser Thr Ile Thr
                325                 330                 335
Gly Asn Arg Tyr Ala Tyr Met Ser Gly Thr Ser Met Ala Ser Pro His
            340                 345                 350
Val Ala Gly Leu Ala Ala Leu Leu Ala Ser Gln Gly Arg Asn Asn Ile
        355                 360                 365
Glu Ile Arg Gln Ala Ile Glu Gln Thr Ala Asp Lys Ile Ser Gly Thr
    370                 375                 380
Gly Thr Tyr Phe Lys Tyr Gly Arg Ile Asn Ser Tyr Asn Ala Val Thr
385                 390                 395                 400
Tyr
```

<210> 295
<211> 1591
<212> DNA
<213> Bacillus sp

<220>
<223> Thermophilic serine proteinase precursor (Ak.1 protease) S08.009

<400> 295

```
gcatgctacg attaaatatc taagaatccc caattaaata ccattatttt acaaaattat 60
attatattaa aataaatgtc gagatttttg agaaaaaatt tttcattcct ccccttcct 120
caacgtaaaa ttaataccgc aattccattt aaaggggaa tatttccatg aagtttaaag 180
cgattgtaag tttatccctc gctgtttcca tgtcacttt tccattcctt gtggaagcag 240
cctctaatga tggggtagaa tctccaaaaa ccgtttccga aattaacgtg tctcatgaaa 300
aaggagcata tgtccaggga gaagtcattg tccaattcaa agaacaagta aatgctgaag 360
aaaaggcaaa ggcattaaaa gaagttgggg caacggcggt tccagataat gatcgagtta 420
aatctaaatt taatgtacta aaagtaggaa atgtggaagc tgttgtgaaa gcattaaata 480
ataacccgtt agtagaatac gcagagccaa actatttatt taatgcagct tggactccaa 540
atgatacgta ctatcagggt tatcaatatg gtccacaaaa tacgtatacc gactatgctt 600
gggatgttac aaaaggcagt agcggtcaag agattgctgt tattgataca ggtgtagatt 660
atacacatcc tgatttagat ggaaaagtca tcaaaggata tgatttcgta gataatgatt 720
acgacccaat ggatttgaat aatcatggta cgcacgtagc tggaatagca gctgcggaaa 780
caaacaatgc tacaggtatt gccggcatgg ccccaaacac aagaattttg gctgtgcgcg 840
ctttagatcg aaatggcagt ggtactctaa gtgatattgc cgatgcgatc atttatgctg 900
ctgattcagg cgctgaagtc attaacctgt cacttggttg tgattgtcat acaaccacat 960
tggagaatgc tgtaaactat gcatggaata agggttctgt agtagttgcc gcagccggaa 1020

ataatggatc ctctacaaca tttgaaccgg cttcttatga aaatgtaatt gcagttggcg 1080
cagtagatca atatgatcgg ttagcatcat tctcgaacta tggaacatgg gtagatgtcg 1140
tagctccagg tgtagacatt gtctcaacta ttactggtaa ccgatatgcc tatatgtcgg 1200
gcacttccat ggcatccct catgtagccg gtcttgcagc cttactagcg agtcaaggac 1260
ggaataacat agaaattcgt caagccatcg agcaaacagc agacaaaatc tccggaactg 1320
gaacatactt caaatatgga agaatcaatt cttataatgc tgtaacatat taaatagatt 1380
taaataacga caccgtgcca acgccaaggg cacggtgtct taattcaagc tttttggaaa 1440
atcacgacat acaaattatg taagaaagct tattctccca taggaattga agaggaaaac 1500
caatattatt cttttatctc agcaaaaata aaaaaactgc caaatggcag actctaacta 1560
actatttttt gcttccttct ttctgctgca g                                1591
```

<210> 296
<211> 1167
<212> PRT
<213> Streptococcus pyogenes

<220>
<223> C5a peptidase precursor (SCP) S08.020

<400> 296

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Met Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
 1               5                  10                  15
Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
            20                  25                  30
Thr Val Thr Glu Asp Thr Pro Val Thr Glu Gln Ala Val Glu Thr Pro
        35                  40                  45
Gln Pro Thr Ala Val Ser Glu Glu Val Pro Ser Ser Lys Glu Thr Lys
    50                  55                  60
Thr Pro Gln Thr Pro Asp Asp Ala Glu Glu Thr Ile Ala Asp Asp Ala
65                  70                  75                  80
Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
                85                  90                  95
Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
            100                 105                 110
Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
        115                 120                 125
Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
    130                 135                 140
Lys Thr Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
```

```
145                 150                 155                 160
Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
                165                 170                 175
Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
            180                 185                 190
His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
        195                 200                 205
Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
    210                 215                 220
Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
225                 230                 235                 240
Asn Tyr Ala Gln Ala Ile Arg Asp Ala Val Asn Leu Gly Ala Lys Val
                245                 250                 255
Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
            260                 265                 270
Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
        275                 280                 285
Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
    290                 295                 300
Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
305                 310                 315                 320
Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
                325                 330                 335
Leu Thr Glu Thr Ala Met Val Lys Thr Asp Asp Gln Gln Asp Lys Glu
            340                 345                 350
Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
        355                 360                 365
Tyr Ala Tyr Ala Asn Arg Gly Met Lys Glu Asp Asp Phe Lys Asp Val
    370                 375                 380
Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
385                 390                 395                 400
Lys Val Ala Asn Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
                405                 410                 415
Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
            420                 425                 430
Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
        435                 440                 445
Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
    450                 455                 460
Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
465                 470                 475                 480
Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
                485                 490                 495
Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
            500                 505                 510
Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
        515                 520                 525
Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
    530                 535                 540
Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
545                 550                 555                 560
Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
                565                 570                 575
Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
            580                 585                 590
Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
        595                 600                 605
```

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Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
    610                 615                 620
Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
625                 630                 635                 640
Ala Pro Lys Val Leu Tyr Glu Ala Ser Trp Gln Lys Ile Thr Ile Pro
                645                 650                 655
Ala Asn Ser Ser Lys Gln Val Thr Val Pro Ile Asp Ala Ser Arg Phe
            660                 665                 670
Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
        675                 680                 685
Phe Val Arg Phe Lys Gln Asp Pro Thr Lys Glu Glu Leu Met Ser Ile
    690                 695                 700
Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Val Glu
705                 710                 715                 720
Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
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Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
            740                 745                 750
Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
        755                 760                 765
Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
    770                 775                 780
Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
785                 790                 795                 800
Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Glu
                805                 810                 815
Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
            820                 825                 830
Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
        835                 840                 845
Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
    850                 855                 860
Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
865                 870                 875                 880
Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys
                885                 890                 895
Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
            900                 905                 910
Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
        915                 920                 925
Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
    930                 935                 940
Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr
945                 950                 955                 960
Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
                965                 970                 975
Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
            980                 985                 990
Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
        995                 1000                1005
Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro Val
    1010                1015                1020
Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp Gly Ser
1025                1030                1035                1040
Gly Gln Thr Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp Gly
                1045                1050                1055
Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu Gln Asp
```

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            1060                1065                1070
Gly Ser Gly Gln Thr Pro Asp Lys Lys Pro Glu Thr Lys Pro Glu Lys
        1075                1080                1085
Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln Lys Gly Gln Pro
    1090                1095                1100
Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg Ala Leu Ala Thr Lys
1105                1110                1115                1120
Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr Asn Asp Lys Asp Thr Asn
            1125                1130                1135
Arg Leu His Leu Leu Lys Leu Val Met Thr Thr Phe Phe Phe Gly Leu
            1140                1145                1150
Val Ala His Ile Phe Lys Thr Lys Arg Gln Lys Glu Thr Lys Lys
        1155                1160                1165
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<210> 297
<211> 4637
<212> DNA
<213> Streptococcus pyogenes

<220>
<223> C5a peptidase precursor (SCP) S08.020

<400> 297

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gaaactgcta tggtcaaaac agacgatcag caagataaag aaatgcctgt tctttcaaca 1920
```

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gatgatttta aggatgtcaa aggcaagatt gcccttattg aacgtggcga tattgatttc 2040
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caggacaagg gcttcccgat tgaattgcca aatgttgatc agatgcctgc ggcctttatc 2160
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<210> 298
<211> 699
<212> PRT
<213> Fervidobacterium pennivorans

<220>
<223> fervidolysin S08.020

<400> 298

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            20                  25                  30
Asp Leu Ala Ser Leu Pro Glu Ile Lys Ser Gln Gly Tyr His Ile Leu
        35                  40                  45
Phe Gly Glu Leu Arg Asp Gly Glu Tyr Thr Glu Gly Lys Ile Leu Val
    50                  55                  60
Gly Tyr Asn Asp Arg Ser Glu Val Asp Lys Ile Val Lys Ala Val Asn
65                  70                  75                  80
Gly Lys Val Val Leu Glu Leu Pro Gln Ile Lys Val Val Ser Ile Lys
                85                  90                  95
Leu Asn Gly Met Thr Val Lys Gln Ala Tyr Asp Lys Ile Lys Ala Leu
            100                 105                 110
Ala Leu Lys Gly Ile Arg Tyr Val Glu Pro Ser Tyr Lys Arg Glu Leu
        115                 120                 125
Ile Lys Pro Thr Val Val Lys Pro Asn Pro Asp Met Tyr Lys Ile Arg
    130                 135                 140
Lys Pro Gly Leu Asn Ser Thr Ala Arg Asp Tyr Gly Glu Glu Leu Ser
145                 150                 155                 160
Asn Glu Leu Trp Gly Leu Glu Ala Ile Gly Val Thr Gln Gln Leu Trp
                165                 170                 175
Glu Glu Ala Ser Gly Thr Asn Ile Ile Val Ala Val Val Asp Thr Gly
            180                 185                 190
Val Asp Gly Thr His Pro Asp Leu Glu Gly Gln Val Ile Ala Gly Tyr
        195                 200                 205
Arg Pro Ala Phe Asp Glu Glu Leu Pro Ala Gly Thr Asp Ser Ser Tyr
    210                 215                 220
Gly Gly Ser His Gly Thr His Val Ala Gly Thr Ile Ala Ala Lys Lys
225                 230                 235                 240
Asp Gly Lys Gly Ile Val Gly Val Ala Pro Gly Ala Lys Ile Met Pro
                245                 250                 255
Ile Val Ile Phe Asp Asp Pro Ala Leu Val Gly Gly Asn Gly Tyr Val
            260                 265                 270
Gly Asp Asp Tyr Val Ala Ala Gly Ile Ile Trp Ala Thr Asp His Gly
        275                 280                 285
Ala Lys Val Met Asn His Ser Trp Gly Gly Trp Gly Tyr Ser Tyr Thr
    290                 295                 300
Met Lys Glu Ala Phe Asp Tyr Ala Met Glu His Gly Val Val Met Val
305                 310                 315                 320
Val Ser Ala Gly Asn Asn Thr Ser Asp Ser His His Gln Tyr Pro Ala
                325                 330                 335
Gly Tyr Pro Gly Val Ile Gln Val Ala Ala Leu Asp Tyr Tyr Gly Gly
            340                 345                 350
Thr Phe Arg Val Ala Gly Phe Ser Ser Arg Ser Asp Gly Val Ser Val
        355                 360                 365
Gly Ala Pro Gly Val Thr Ile Leu Ser Thr Val Pro Gly Glu Asp Ser
    370                 375                 380
Ile Gly Tyr Glu Gly His Asn Glu Asn Val Pro Ala Thr Asn Gly Gly
385                 390                 395                 400
Thr Tyr Asp Tyr Tyr Gln Gly Thr Ser Met Ala Ala Pro His Val Thr
                405                 410                 415
Gly Val Val Ala Val Leu Leu Gln Lys Phe Pro Asn Ala Lys Pro Trp
            420                 425                 430
Gln Ile Arg Lys Leu Leu Glu Asn Thr Ala Phe Asp Phe Asn Gly Asn
        435                 440                 445
Gly Trp Asp His Asp Thr Gly Tyr Gly Leu Val Lys Leu Asp Ala Ala
```

```
    450                 455                 460
Leu Gln Gly Pro Leu Pro Thr Gln Gly Gly Val Glu Glu Phe Gln Val
465                 470                 475                 480
Val Val Thr Asp Ala Lys Gly Asn Phe Gly Val Pro Thr Val Phe Val
                485                 490                 495
Ser Met Met Arg Asp Asn Gly Ser Cys Tyr Tyr Ala Lys Thr Gly Pro
            500                 505                 510
Asp Gly Ile Ala Arg Phe Pro His Ile Asp Ser Gly Thr Tyr Asp Ile
        515                 520                 525
Phe Val Gly Gly Pro Asp His Trp Asp Arg Ala Leu Ala Pro Tyr Asp
    530                 535                 540
Gly Glu Ser Ile Pro Gly Gly Tyr Ala Ile Ala Leu Arg Met Ala Glu
545                 550                 555                 560
Glu Arg Gln Ala Ser Phe Val Gly Phe Gly Val Ser Pro Asp Ala Thr
                565                 570                 575
Gln Leu Asn Val Asn Phe Asn Ser Thr Leu Gln Val Lys Phe Ser Thr
            580                 585                 590
Asn Leu Ser Thr Leu Lys Asp Pro Gln Phe Val Val Val Asp Pro Leu
        595                 600                 605
Leu Arg Gly Val Tyr Gly Arg Val Ala Tyr Ala Arg Asn Gln Thr Tyr
    610                 615                 620
Asp Leu Ser Leu Leu Ser Gly Gln Ile Ser Phe Gly Ile Gln Thr Leu
625                 630                 635                 640
Leu Pro Ala Ala Thr Asp Ile Thr Ile Gln Gly Thr Val Thr Leu Asn
                645                 650                 655
Gly Glu Asp Ile Pro Val Tyr Gly Val Leu Lys Ala Gly Thr Thr Trp
            660                 665                 670
Thr Ile Ile Asp Asp Phe Gly Gly Leu Asn Leu Gly Thr Asp Ser Gln
        675                 680                 685
Pro Ile Tyr Val Trp Trp Thr Ile Phe Gly Gln
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<210> 299
<211> 2227
<212> DNA
<213> Fervidobacterium pennivorans

<220>
<223> fervidolysin S08.020

<400> 299
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aaatccgagt tttgagccaa ggagcaaagc aaaagattta gcatcgttac cggagataaa 180
atctcagggt taccatatac tcttcggtga attgagggac ggggaatata ccgagggtaa 240
aatcctcgtt ggttacaacg ataggtcgga agtagataaa atagtcaaag cagttaacgg 300
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ggttaaacaa gcatacgaca agataaaggc acttgcactt aaaggtatca ggtatgttga 420
accaagttac aagagggagc tcataaaacc aacagttgtg aagccaaatc ctgatatgta 480
caaaatcaga aaacctgggt tgaacagtac tgcaagagat tacggtgaag aactttccaa 540
cgaactctgg ggccttgagg caattggtgt aacacaacag ctttgggaag aagcatcggg 600
aacaaatatt atcgttgcgg ttgttgatac tggtgtcgac ggcacccatc cagatttgga 660
agggcaagtt atcgcaggat acagaccggc atttgatgaa gaactcccag caggaacaga 720
ttcatcctac ggtggttcac atggaacaca cgttgctgga acgattgcgg caaagaaaga 780
tggaaaaggt atcgttggtg ttgcacctgg tgcaaagata atgccgatag ttatattcga 840
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<210> 300
<211> 381
<212> PRT
<213> Geobacillus stearothermophilus

<220>
<223> Subtilisin J precursor S08.035

<400> 300

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Ile Phe Thr Met Ala Phe Ser Asn Met Ser Val Gln Ala Ala Gly Lys
            20                  25                  30
Ser Ser Thr Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser
        35                  40                  45
Ala Met Ser Ser Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly
    50                  55                  60
Lys Val Gln Lys Gln Phe Lys Tyr Val Asn Ala Ala Ala Ala Thr Leu
65                  70                  75                  80
Asp Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr
                85                  90                  95
Val Glu Glu Asp His Ile Ala His Glu Tyr Ala Gln Ser Val Pro Tyr
            100                 105                 110
Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr
        115                 120                 125
Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser
    130                 135                 140
His Pro Asp Leu Asn Val Arg Gly Gly Ala Ser Phe Val Pro Ser Glu
145                 150                 155                 160
Thr Asn Pro Tyr Gln Asp Gly Ser Ser His Gly Thr His Val Ala Gly
                165                 170                 175
Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ser Pro
```

```
            180                 185                 190
Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Asp Ser Thr Gly Ser Gly
        195                 200                 205
Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ser Asn Asn
    210                 215                 220
Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Ser Gly Ser Thr Ala
225                 230                 235                 240
Leu Lys Thr Val Val Asp Lys Ala Val Ser Ser Gly Ile Val Val Ala
                245                 250                 255
Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly Ser Ser Ser Thr Val Gly
            260                 265                 270
Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala Val Gly Ala Val Asn Ser
        275                 280                 285
Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala Gly Ser Glu Leu Asp Val
    290                 295                 300
Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Gly Thr Tyr
305                 310                 315                 320
Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
                325                 330                 335
Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val
            340                 345                 350
Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Asn Ser Phe Tyr
        355                 360                 365
Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
    370                 375                 380
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<210> 301
<211> 2494
<212> DNA
<213> Geobacillus stearothermophilus

<220>
<223> Subtilisin J precursor S08.035

<400> 301
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caataaattc acagaatagt cttttaagta agtctactct gaatttttttt aaaaggagag 600
ggtaaagagt gagaagcaaa aaattgtgga tcagcttgtt gtttgcgtta acgttaatct 660
ttacgatggc gttcagcaac atgtctgtgc aggctgccgg aaaaagcagt acagaaaaga 720
aatacattgt cggatttaaa cagacaatga gtgccatgag ttccgccaag aaaaaggatg 780
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gcacttacgg tgcttacaac ggcacgtcca tggcgactcc tcacgttgcc ggagcagcag 1620
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cattcagcgc atttgttttt tctgacatgt tcacttcata tacatggtca gccggaatat 2400
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<210> 302
<211> 381
<212> PRT
<213> Bacillus subtilis

<220>
<223> Subtilisin E precursor S08.036

<400> 302

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Ser Ser Thr Glu Lys Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser
        35                  40                  45
Ala Met Ser Ser Ala Lys Lys Lys Asp Val Ile Ser Glu Lys Gly Gly
    50                  55                  60
Lys Val Gln Lys Gln Phe Lys Tyr Val Asn Ala Ala Ala Ala Thr Leu
65                  70                  75                  80
Asp Glu Lys Ala Val Lys Glu Leu Lys Lys Asp Pro Ser Val Ala Tyr
                85                  90                  95
Val Glu Glu Asp His Ile Ala His Glu Tyr Ala Gln Ser Val Pro Tyr
            100                 105                 110
Gly Ile Ser Gln Ile Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr
        115                 120                 125
Gly Ser Asn Val Lys Val Ala Val Ile Asp Ser Gly Ile Asp Ser Ser
    130                 135                 140
His Pro Asp Leu Asn Val Arg Gly Gly Ala Ser Phe Val Pro Ser Glu
145                 150                 155                 160
Thr Asn Pro Tyr Gln Asp Gly Ser Ser His Gly Thr His Val Ala Gly
                165                 170                 175
Thr Ile Ala Ala Leu Asn Asn Ser Ile Gly Val Leu Gly Val Ser Pro
            180                 185                 190
Ser Ala Ser Leu Tyr Ala Val Lys Val Leu Asp Ser Thr Gly Ser Gly
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        195                 200                 205
Gln Tyr Ser Trp Ile Ile Asn Gly Ile Glu Trp Ala Ile Ser Asn Asn
    210                 215                 220
Met Asp Val Ile Asn Met Ser Leu Gly Gly Pro Thr Gly Ser Thr Ala
225                 230                 235                 240
Leu Lys Thr Val Val Asp Lys Ala Val Ser Ser Gly Ile Val Val Ala
                245                 250                 255
Ala Ala Ala Gly Asn Glu Gly Ser Ser Gly Ser Thr Ser Thr Val Gly
            260                 265                 270
Tyr Pro Ala Lys Tyr Pro Ser Thr Ile Ala Val Gly Ala Val Asn Ser
        275                 280                 285
Ser Asn Gln Arg Ala Ser Phe Ser Ser Ala Gly Ser Glu Leu Asp Val
    290                 295                 300
Met Ala Pro Gly Val Ser Ile Gln Ser Thr Leu Pro Gly Gly Thr Tyr
305                 310                 315                 320
Gly Ala Tyr Asn Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ala
                325                 330                 335
Ala Ala Leu Ile Leu Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val
            340                 345                 350
Arg Asp Arg Leu Glu Ser Thr Ala Thr Tyr Leu Gly Asn Ser Phe Tyr
        355                 360                 365
Tyr Gly Lys Gly Leu Ile Asn Val Gln Ala Ala Ala Gln
    370                 375                 380
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<210> 303
<211> 1500
<212> DNA
<213> Bacillus subtilis

<220>
<223> Subtilisin E precursor S08.036

<400> 303
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aaggagaggg taaagagtga gaagcaaaaa attgtggatc agcttgttgt ttgcgttaac 180
gttaatcttt acgatggcgt tcagcaacat gtctgcgcag gctgccggaa aaagcagtac 240
agaaaagaaa tacattgtcg gatttaaaca gacaatgagt gccatgagtt ccgccaagaa 300
aaaggatgtt atttctgaaa aaggcggaaa ggttcaaaag caatttaagt atgttaacgc 360
ggccgcagca acattggatg aaaaagctgt aaaagaattg aaaaaagatc cgagcgttgc 420
atatgtggaa gaagatcata ttgcacatga atatgcgcaa tctgttcctt atggcatttc 480
tcaaattaaa gcgccggctc ttcactctca aggctacaca ggctctaacg taaaagtagc 540
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cttcgtacct tctgaaacaa acccatacca ggacggcagt tctcacggta cgcatgtagc 660
cggtacgatt gccgctctta ataactcaat cggtgttctg ggcgttagcc caagcgcatc 720
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<210> 304
<211> 274
<212> PRT
<213> Bacillus licheniformis

<220>
<223> Subtilisin DY S08.037

<400> 304

Ala	Gln	Thr	Val	Pro	Tyr	Gly	Ile	Pro	Leu	Ile	Lys	Ala	Asp	Lys	Val
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Gln	Ala	Gln	Gly	Tyr	Lys	Gly	Ala	Asn	Val	Lys	Val	Gly	Ile	Ile	Asp
		20					25					30			
Thr	Gly	Ile	Ala	Ala	Ser	His	Thr	Asp	Leu	Lys	Val	Val	Gly	Gly	Ala
	35					40					45				
Ser	Phe	Val	Ser	Gly	Glu	Ser	Tyr	Asn	Thr	Asp	Gly	Asn	Gly	His	Gly
50					55					60					
Thr	His	Val	Ala	Gly	Thr	Val	Ala	Ala	Leu	Asp	Asn	Thr	Thr	Gly	Val
65				70					75					80	
Leu	Gly	Val	Ala	Pro	Asn	Val	Ser	Leu	Tyr	Ala	Ile	Lys	Val	Leu	Asn
			85					90					95		
Ser	Ser	Gly	Ser	Gly	Thr	Tyr	Ser	Ala	Ile	Val	Ser	Gly	Ile	Glu	Trp
		100					105					110			
Ala	Thr	Gln	Asn	Gly	Leu	Asp	Val	Ile	Asn	Met	Ser	Leu	Gly	Gly	Pro
	115					120					125				
Ser	Gly	Ser	Thr	Ala	Leu	Lys	Gln	Ala	Val	Asp	Lys	Ala	Tyr	Ala	Ser
130					135					140					
Gly	Ile	Val	Val	Val	Ala	Ala	Ala	Gly	Asn	Ser	Gly	Ser	Ser	Gly	Ser
145				150					155					160	
Gln	Asn	Thr	Ile	Gly	Tyr	Pro	Ala	Lys	Tyr	Asp	Ser	Val	Ile	Ala	Val
			165					170					175		
Gly	Ala	Val	Asp	Ser	Asn	Lys	Asn	Arg	Ala	Ser	Phe	Ser	Ser	Val	Gly
		180					185					190			
Ala	Glu	Leu	Glu	Val	Met	Ala	Pro	Gly	Val	Ser	Val	Tyr	Ser	Thr	Tyr
	195					200					205				
Pro	Ser	Asn	Thr	Tyr	Thr	Ser	Leu	Asn	Gly	Thr	Ser	Met	Ala	Ser	Pro
210					215					220					
His	Val	Ala	Gly	Ala	Ala	Ala	Leu	Ile	Leu	Ser	Lys	Tyr	Pro	Thr	Leu
225				230					235					240	
Ser	Ala	Ser	Gln	Val	Arg	Asn	Arg	Leu	Ser	Ser	Thr	Ala	Thr	Asn	Leu
			245					250					255		
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<210> 305
<211> 384
<212> PRT
<213> Engyodontium album

<220>
<223> Proteinase K precursor S08.054

<400> 305

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Gly Glu Met Val Ala Asn Lys Tyr Ile Val Lys Phe Lys Glu Gly Ser
        35                  40                  45
Ala Leu Ser Ala Leu Asp Ala Ala Met Glu Lys Ile Ser Gly Lys Pro
    50                  55                  60
Asp His Val Tyr Lys Asn Val Phe Ser Gly Phe Ala Ala Thr Leu Asp
65                  70                  75                  80
Glu Asn Met Val Arg Val Leu Arg Ala His Pro Asp Val Glu Tyr Ile
                85                  90                  95
Glu Gln Asp Ala Val Val Thr Ile Asn Ala Ala Gln Thr Asn Ala Pro
            100                 105                 110
Trp Gly Leu Ala Arg Ile Ser Ser Thr Ser Pro Gly Thr Ser Thr Tyr
        115                 120                 125
Tyr Tyr Asp Glu Ser Ala Gly Gln Gly Ser Cys Val Tyr Val Ile Asp
    130                 135                 140
Thr Gly Ile Glu Ala Ser His Pro Glu Phe Glu Gly Arg Ala Gln Met
145                 150                 155                 160
Val Lys Thr Tyr Tyr Tyr Ser Ser Arg Asp Gly Asn Gly His Gly Thr
                165                 170                 175
His Cys Ala Gly Thr Val Gly Ser Arg Thr Tyr Gly Val Ala Lys Lys
            180                 185                 190
Thr Gln Leu Phe Gly Val Lys Val Leu Asp Asp Asn Gly Ser Gly Gln
        195                 200                 205
Tyr Ser Thr Ile Ile Ala Gly Met Asp Phe Val Ala Ser Asp Lys Asn
    210                 215                 220
Asn Arg Asn Cys Pro Lys Gly Val Val Ala Ser Leu Ser Leu Gly Gly
225                 230                 235                 240
Gly Tyr Ser Ser Ser Val Asn Ser Ala Ala Ala Arg Leu Gln Ser Ser
                245                 250                 255
Gly Val Met Val Ala Val Ala Ala Gly Asn Asn Asn Ala Asp Ala Arg
            260                 265                 270
Asn Tyr Ser Pro Ala Ser Glu Pro Ser Val Cys Thr Val Gly Ala Ser
        275                 280                 285
Asp Arg Tyr Asp Arg Arg Ser Ser Phe Ser Asn Tyr Gly Ser Val Leu
    290                 295                 300
Asp Ile Phe Gly Pro Gly Thr Ser Ile Leu Ser Thr Trp Ile Gly Gly
305                 310                 315                 320
Ser Thr Arg Ser Ile Ser Gly Thr Ser Met Ala Thr Pro His Val Ala
                325                 330                 335
Gly Leu Ala Ala Tyr Leu Met Thr Leu Gly Lys Thr Thr Ala Ala Ser
            340                 345                 350
Ala Cys Arg Tyr Ile Ala Asp Thr Ala Asn Lys Gly Asp Leu Ser Asn
        355                 360                 365
Ile Pro Phe Gly Thr Val Asn Leu Leu Ala Tyr Asn Asn Tyr Gln Ala
    370                 375                 380
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<210> 306
<211> 2347

<212> DNA
<213> Engyodontium album

<220>
<223> Proteinase K precursor S08.054

<400> 306
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tctggtttgt caaggttctc attaccctct tggctttctc ctcttttcgc gacattgtgc 180
ttgtggtgtg cctatgtatg ttgtagtcaa tgctatatgt caatggtttt tgtcaaatgc 240
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cttgattaag caccgctttc tcattcatca acaacagcca aaatgcgttt gtctgttctt 660
ctgagtcttc ttcccctcgc tctcggcgct cctgccgttg agcagcgctc cgaggctgct 720
cctctgatcg aggcccgcgg cgagatggtt gccaacaagt acattgtcaa gttcaaggag 780
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aacttgtgag ctaacaacgg catctcgagg aaacgttcaa ctatgagccg aaagacaagt 2340
acttaat 2347

<210> 307
<211> 534
<212> PRT
<213> Vibrio alginolyticus

<220>
<223> Alkaline serine exoprotease A precursor S08.050

<400> 307
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His Ser Ser Leu Ala Phe Ser Gln Pro Asn Glu Ile Ala Asp Ser Ala
20 25 30
Glu Leu Gln Gln Ala Pro Asp Thr Leu Pro Ala Thr Leu Met Leu Ala
35 40 45
Pro Asp Asp Ile Ala Ile Ala Asp Arg Tyr Ile Val Val Phe Gln Gln
50 55 60
Pro Gln Met Met Ala Ser Ser Ser Pro Glu Phe Glu Gln Phe Thr Gln
65 70 75 80
Gln Ser Val Asp Arg Met Ser Gly Leu Tyr Ser Ile Gln Val Glu Ser
85 90 95
Val Phe Asp His Ser Ile Ser Gly Phe Val Ala Asn Leu Ser Pro Glu
100 105 110
Gln Leu Lys Asp Leu Arg Ser Asp Pro Arg Val Asp Tyr Ile Glu Gln
115 120 125
Asp Arg Ile Leu Ser Leu Asp Pro Ile Val Ser Ala Asp Ala Asn Gln
130 135 140
Thr Asn Ala Ile Trp Gly Leu Asp Arg Ile Asp Gln Arg Asn Leu Pro
145 150 155 160
Leu Asp Asn Asn Tyr Ser Ala Asn Phe Asp Gly Thr Gly Val Thr Ala
165 170 175
Tyr Val Ile Asp Thr Gly Val Asn Asn Ala His Val Glu Phe Gly Gly
180 185 190
Arg Ser Val Ser Gly Tyr Asp Phe Val Asp Asn Asp Ala Asp Ala Ser
195 200 205
Asp Cys Asn Gly His Gly Thr His Val Ala Gly Thr Ile Gly Gly Ser
210 215 220
Leu Tyr Gly Val Ala Lys Asn Val Asn Leu Val Gly Val Arg Val Leu
225 230 235 240
Ser Cys Ser Gly Ser Gly Ser Thr Ser Gly Val Ile Ala Gly Val Asp
245 250 255
Trp Val Ala Ala Asn Ala Ser Gly Pro Ser Val Ala Asn Met Ser Leu
260 265 270
Gly Gly Gly Gln Ser Val Ala Leu Asp Ser Ala Val Gln Ser Ala Val
275 280 285
Gln Ser Gly Val Ser Phe Met Leu Ala Ala Gly Asn Ser Asn Ala Asp
290 295 300
Ala Cys Asn Tyr Ser Pro Ala Arg Val Ala Thr Gly Val Thr Val Gly
305 310 315 320
Ser Thr Thr Ser Thr Asp Ala Arg Ser Ser Phe Ser Asn Trp Gly Ser
325 330 335
Cys Val Asp Val Phe Ala Pro Gly Ser Gln Ile Lys Ser Ala Trp Tyr
340 345 350
Asp Gly Gly Tyr Lys Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His
355 360 365
Val Ala Gly Val Ala Ala Leu Tyr Leu Gln Glu Asn Ser Ser Val Ser
370 375 380
Pro Ser Gln Val Glu Ala Leu Ile Val Ser Arg Ala Ser Thr Gly Lys
385 390 395 400
Val Thr Asp Thr Arg Gly Ser Val Asn Lys Leu Leu Tyr Ser Leu Thr
405 410 415
Asp Ala Asp Cys Gly Gln Asp Cys Gly Gly Pro Asp Pro Thr Pro Asp
420 425 430
Pro Glu Gly Lys Leu Thr Ser Gly Val Pro Val Ser Gly Leu Ser Gly

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        435                 440                 445
Ser Ser Gly Gln Val Ala Tyr Tyr Tyr Val Asp Val Glu Ala Gly Gln
    450                 455                 460
Arg Leu Thr Val Gln Met Tyr Gly Gly Ser Gly Asp Ala Asp Leu Tyr
465                 470                 475                 480
Leu Arg Phe Gly Ala Lys Pro Thr Leu Asn Ala Trp Asp Cys Arg Pro
                485                 490                 495
Phe Lys Tyr Gly Asn Asn Glu Thr Cys Thr Val Ser Ala Thr Gln Ser
            500                 505                 510
Gly Arg Tyr His Val Met Ile Gln Gly Tyr Ser Asn Tyr Ser Gly Val
        515                 520                 525
Ser Ile Gln Ala Asn Tyr
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<210> 308
<211> 1856
<212> DNA
<213> Vibrio alginolyticus

<220>
<223> Alkaline serine exoprotease A precursor S08.050

<400> 308
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gagattgcgg acagtgcaga gttacaacaa gctcccgaca cattgcctgc cactttgatg 240
cttgcaccgg acgacatcgc cattgcagat cgatatatag tggtatttca acaaccgcaa 300
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gagcaagaca gaatcctatc gcttgaccca atagtctcgg cagacgcaaa tcaaaccaat 540
gccatttggg gactagatcg aatcgaccaa cgtaacttgc cactcgataa caactacagt 600
gccaactttg atgggactgg tgtaacggct tatgttatcg atactggtgt gaacaatgca 660
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gcaagtgact gtaatggaca cggcacacac gtggcgggca ccattggcgg cagcttgtat 780
ggtgttgcga aaaacgtcaa ccttgtcggc gtgagagtat tgagctgtag cggatcgggg 840
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gttgccaata tgagtttagg tggcggtcaa tctgtcgctc tcgatagtgc ggtgcaaagt 960
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<220>
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<400> 309

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Val Ala Leu Val Asp Ser Gly Val Asn Ser Ser His Thr Asp Leu Lys
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Asn His Gly Thr Leu Val Ala Gly Gln Ile Gly Ala Asn Gly Asn Leu
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Lys Gly Val Asn Pro Gly Val Glu Met Asn Val Tyr Arg Val Phe Gly
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Ser Lys Lys Ser Glu Met Leu Trp Val Ser Lys Gly Ile Ile Asp Ala
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Val Lys Glu Ile Asn Lys Lys Arg Asn Leu Asn Ser Lys Thr Ser Lys
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Asp Lys Tyr Gln Leu Lys Asp Gln Pro Glu Thr Ala Ile Glu Leu Phe
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<212> PRT
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S08.063

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Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe
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Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
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Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asp Pro Ile
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Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
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Pro Leu Arg Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
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His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
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Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
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Val Ile Phe Ser Asp Trp Tyr Asn Thr Ser Val Met Arg Lys Val Lys
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His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Leu Ala Pro
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Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
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Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
        915                 920                 925
His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
    930                 935                 940
Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
945                 950                 955                 960
Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
                965                 970                 975
Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
            980                 985                 990
Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu
        995                 1000                1005
Gly Ala Met Val Ala Leu Ala Phe Phe Val Val Gln Ile Ser Lys Ala
    1010                1015                1020
Lys Ser Arg Pro Lys Arg Arg Arg Pro Arg Ala Lys Arg Pro Gln Leu
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Thr Gln Gln Thr His Pro Pro Arg Thr Pro Ser Val
                1045                1050
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<210> 312
<211> 4198
<212> DNA
<213> Cricetulus griseus

<220>
<223> Site-1 protease (Subtilisin/kexin-isozyme
1) S08.063

<400> 312
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aggttttctt tacgttggac aagtctgtag gatggctgat cagtaaggtt gcagctttta 300
gccaaaacag aaattcactt ctgatcaagg aagaacctag tgcgatttga atttatgcaa 360
ttttatgacc atattcactt aggaccatga agctcatcaa catctggctt cttctgctgg 420
tggttttgct ctgtggaaag aagcatctgg gtgacaggct ggggaagaaa gcgtttgaaa 480
aggcatcatg ccctagctgt tcccacctga ctttgaaggt ggaattctcc tcaactgtgg 540

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ttatttcaag tgctctgaaa agcagtgaag tagacaactg gagaattata cctcggaaca 660
acccatccag tgactaccct agtgattttg aggtgattca gataaaagag aagcagaagg 720
ccgggctgct cacacttgaa gatcatccaa acatcaagcg ggtgacacct caacgcaaag 780
tctttcgttc cttgaagttt gctgaatctg accccattgt gccatgtaat gaaactcggt 840
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<210> 313
<211> 409
<212> PRT
<213> Hypocrea lixii

<220>
<223> Alkaline proteinase precursor (ALP) S08.066

<400> 313
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1 5 10 15
Ala Val Leu Ala Ala Pro Ala Ala Leu His Lys Lys Pro Glu Ala Val
20 25 30
Pro Asn Lys Phe Ile Val Thr Leu Lys Glu Gly Ala Ser Ile Asp Thr
35 40 45
Asp Ser His Leu Ala Trp Val Thr Asp Ile His Thr Arg Ser Leu Thr
50 55 60
Lys Arg Ser Thr Ala Gly Val Glu Lys Thr Tyr Asn Ile His Thr Trp
65 70 75 80
Asn Ala Tyr Ala Gly Glu Phe Asp Glu Glu Thr Ile Glu Gln Ile Lys
85 90 95
Ser Asn Pro Asp Val Ala Ser Val Glu Pro Asp Tyr Ile Met His Leu
100 105 110
Ser Asp Ile Val Glu Asp Lys Arg Ala Leu Thr Thr Gln Ser Gly Ala
115 120 125
Pro Trp Gly Leu Gly Thr Val Ser His Arg Thr Ser Gly Ser Thr Ser
130 135 140
Tyr Ile Tyr Asp Ser Ser Ala Gly Ala Gly Thr Phe Ala Tyr Val Val
145 150 155 160
Asp Ser Gly Ile Asn Thr Ser His Gln Gln Phe Gly Gly Arg Ala Ser
165 170 175
Leu Gly Tyr Asn Ala Ala Gly Gly Gln His Val Asp Thr Leu Gly His
180 185 190
Gly Thr His Val Ser Gly Thr Ile Gly Gly Ser Thr Tyr Gly Val Ala
195 200 205
Lys Gln Ala Ser Leu Ile Ser Val Lys Val Phe Ala Gly Glu Ser Ala
210 215 220
Ser Thr Ser Val Ile Leu Asp Gly Tyr Asn Trp Ala Val Asn Asp Ile
225 230 235 240
Val Ser Lys Ser Arg Ala Ser Lys Ser Ala Ile Asn Met Ser Leu Gly
245 250 255
Gly Pro Ala Ser Ser Thr Trp Thr Thr Ala Ile Asn Ala Ala Phe Asn
260 265 270
Gln Gly Val Leu Thr Ile Val Ala Ala Gly Asn Gly Asp Ser Leu Gly
275 280 285
Asn Pro Gln Pro Val Ser Gly Thr Ser Pro Ala Asn Val Pro Asn Ala
290 295 300
Ile Thr Val Ala Ala Leu Asp Ile Asn Trp Arg Thr Ala Ser Phe Thr
305 310 315 320
Asn Tyr Gly Ala Gly Val Asp Val Phe Ala Pro Gly Val Asn Ile Leu
325 330 335
Ser Ser Trp Ile Gly Ser Asn Thr Ala Thr Asn Thr Ile Ser Gly Thr

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            340                 345                 350
Ser Met Ala Thr Pro His Val Val Gly Leu Ala Leu Tyr Leu Gln Ser
        355                 360                 365
Leu Glu Gly Leu Thr Ser Pro Thr Ala Val Thr Asn Arg Ile Lys Ala
    370                 375                 380
Leu Ala Thr Ser Gly Arg Val Thr Gly Ser Leu Asn Gly Ser Pro Asn
385                 390                 395                 400
Val Ile Ile Phe Asn Gly Asn Ser Ser
                405
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<210> 314
<211> 1458
<212> DNA
<213> Hypocrea lixii

<220>
<223> Alkaline proteinase precursor (ALP) S08.066

<400> 314
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gccgtaccca acaagttcat cgtcactctt aaagagggtg cttctattga taccgactct 180
catctcgcct gggtaacgga catccacacc cgttcgttga ccaagcgtag cactgctggt 240
gttgaaaaga cttataacat tcatacttgg aatgcttatg cgggcgagtt tgacgaggag 300
acaattgagc agatcaagtc caaccccgat gttgcgtctg ttgagccaga ctacatcatg 360
catctgtcgg acattgttga agacaagcgt gctctgacca cacaatctgg tgctccttgg 420
ggtctcggca ctgtgtccca tcgcacatct ggatccacaa gctacattta tgatagctca 480
gccggcgccg gcacctttgc ctatgtggtt gactctggta tcaacacttc tcatcagcaa 540
ttcggcgggc gtgccagcct tggctacaat gctgcaggag gacagcatgt cgatactctt 600
ggccatggta ctcatgtttc cggaacaatt ggtggatcta catacggtgt tgctaagcag 660
gcgagcctaa tctctgtcaa ggtctttgct ggtgaaagtg cttccacctc tgttatcctt 720
gacggctata actgggctgt aaacgacatc gtctcgaaaa gccgtgctag caagtctgct 780
attaacatgt cgcttggagg acctgcctca tctacctgga cgaccgccat taacgcagcc 840
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cagccagtct ccggcacttc tcctgctaac gttcctaacg ccataaccgt tgccgcattg 960
gacatcaact ggcgcactgc ttccttcacc aactatggtg ctggcgttga tgtttttgcc 1020
cctggcgtca acattctgtc gtcatggatt ggatccaaca ctgctaccaa cacaatcagc 1080
ggtacttcca tggctacacc tcacgttgtt ggcctggccc tctatcttca atctctcgag 1140
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gtaaccggaa gcctcaacgg cagccccaac gttatcatct tcaacggaaa cagttcttaa 1260
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tggcttgctt agctcattta agaagctaat caccatgatg gagtgcgatg ggtatataag 1380
cttctacagc gttttcaact tagctagatg accctctata gatcgctaaa acaaaaagat 1440
atgacagata cctgtgct 1458

<210> 315
<211> 1045
<212> PRT
<213> Serratia marcescens

<220>
<223> Extracellular serine protease precursor S08.094

<400> 315
Met Ile Leu Asn Lys Arg Leu Lys Leu Ala Tyr Cys Val Phe Leu Gly

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 1               5                  10                  15
Cys Tyr Gly Leu Ser Ile His Ser Ser Leu Ala Ala Tyr Gln Asp Pro
            20                  25                  30
Gly Arg Leu Gly Ala Pro Asp Ser Trp Lys Thr Ala Glu Phe Asn Arg
        35                  40                  45
Gln Trp Gly Leu Glu Ala Ile Ser Ala Glu Phe Ala Tyr Ala Arg Gly
    50                  55                  60
Tyr Thr Gly Lys Gly Ile Thr Ile Gly Val Ile Asp Asn Ala Ile Leu
65                  70                  75                  80
Ser His Ser Glu Phe Ser Gly Lys Leu Thr Arg Leu Asp Asn Gly Ser
                85                  90                  95
Tyr Asn Phe Ser Tyr Asp Lys Gln Asp Asn Met Ser Phe Gly Asp His
            100                 105                 110
Gly Thr His Val Ala Gly Ile Ala Ala Ala Lys Arg Asp Gly Ala Gly
        115                 120                 125
Met His Gly Val Ala Phe Asp Ala Asp Ile Ile Gly Thr Lys Leu Asn
    130                 135                 140
Asp Tyr Gly Asn Arg Asn Gly Arg Glu Glu Leu Ile Gln Ser Ala Ala
145                 150                 155                 160
Arg Val Ile Asn Asn Ser Trp Gly Ile Ala Pro Asp Ile Arg Arg Asp
                165                 170                 175
Ala Lys Gly Asp Ile Ile Trp Leu Pro Asn Gly Arg Pro Asp Tyr Val
            180                 185                 190
Ala Phe Val Lys Ser Glu Val Ile Ala Glu Met Met Arg Ser Lys Ser
        195                 200                 205
Ser Val Glu Trp Gly Ser Glu Gln Pro Val Pro Thr Gly Gly His Ser
    210                 215                 220
Ala Met Ser Thr Leu Leu Arg Ala Ala Arg His Gly Lys Leu Ile Val
225                 230                 235                 240
Phe Ser Ala Gly Asn Tyr Asn Asn Tyr Asn Ile Pro Glu Ala Gln Lys
                245                 250                 255
Ser Leu Pro Tyr Ala Phe Pro Asp Val Leu Asn Asn Tyr Leu Ile Val
            260                 265                 270
Thr Asn Leu Ser Asp Glu Asn Gln Leu Ser Val Ser Ser Thr Ser Cys
        275                 280                 285
Gly Gln Thr Ala Ser Tyr Cys Val Ser Ala Pro Gly Ser Asp Ile Tyr
    290                 295                 300
Ser Thr Val Gly Arg Leu Glu Ser Asn Thr Gly Gly Ala Val Asn Arg
305                 310                 315                 320
Glu Ala Tyr Asn Lys Gly Glu Leu Ser Leu Asn Pro Gly Tyr Gly Asn
                325                 330                 335
Lys Ser Gly Thr Ser Met Ala Ala Pro His Val Thr Gly Val Ala Ala
            340                 345                 350
Val Leu Met Gln Arg Phe Pro Tyr Met Ser Ala Asp Gln Ile Ser Ala
        355                 360                 365
Val Ile Lys Thr Thr Ala Thr Asp Leu Gly Val Ala Gly Ile Asp Asn
    370                 375                 380
Leu Phe Gly Trp Gly Arg Val Asn Leu Arg Asp Ala Ile Asn Gly Pro
385                 390                 395                 400
Lys Met Phe Ile Thr Lys Glu Asp Ile Pro Gln Glu Tyr Tyr Val Pro
                405                 410                 415
Gly Ser Tyr Ser Glu Lys Gln Phe Val Val Asn Ile Pro Gly Leu Gly
            420                 425                 430
Asn Ile Val Glu Pro Gly Thr Pro Val Glu Arg Arg Cys Thr Ser Ser
        435                 440                 445
Glu Cys Ser Phe Asp Ser Trp Ser Asn Asp Ile Ser Gly His Gly Gly
    450                 455                 460
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Leu Thr Lys Thr Gly Ala Gly Thr Leu Ala Leu Leu Gly Asn Asn Thr
465                 470                 475                 480
Tyr Arg Gly Asp Thr Trp Val Lys Gln Gly Val Leu Ala Ile Asp Gly
                485                 490                 495
Ser Val Ala Ser Asn Val Tyr Ile Glu Asn Ser Gly Thr Leu Ser Gly
            500                 505                 510
Glu Gly Thr Val Gly Ala Phe Arg Ala Ala Arg Ser Gly Ser Val Ala
        515                 520                 525
Pro Gly Asn Gly Ile Gly Thr Leu His Val Leu His Asp Ala Ile Phe
    530                 535                 540
Asp Arg Gly Ser Gln Tyr Asn Val Glu Val Ala Asp Asn Gly Arg Ser
545                 550                 555                 560
Asp Lys Ile Ala Ala Arg Arg Ala Phe Leu Asn Gly Gly Ser Val Asn
                565                 570                 575
Val Ser Leu Glu Arg Ser Gln Asn Leu Leu Ser Gln Asn Glu Ala Gln
            580                 585                 590
Ser Leu Leu Gly Asn Lys Tyr Thr Ile Leu Thr Thr Thr Asp Gly Val
        595                 600                 605
Thr Gly Arg Phe Glu Asn Ala Asn Pro Ser Tyr Pro Phe Val Lys Val
    610                 615                 620
Ala Leu Asp Tyr Arg Gly Asn Asp Val Gly Leu Gly Ile Thr Arg Thr
625                 630                 635                 640
Asp Ala Ser Phe Asp Ser Leu Ala Ser Thr Glu Asn Glu Lys Ala Val
                645                 650                 655
Ala Arg Ala Val Glu Thr Leu Asn Ala Thr Glu Pro Val Thr Glu Thr
            660                 665                 670
Ala Lys Arg Ser Val Ala Ile Pro Ala Ala Glu Glu Ala Asn Leu Leu
        675                 680                 685
Gln Ser Asp Gly Gly Glu Ala Gln Ala Val Asn Glu Glu Ala Ser Ile
    690                 695                 700
Val Ala Gly His Pro Ile Tyr Glu Ser Phe Leu Gly Phe Thr Ser Ala
705                 710                 715                 720
Arg Glu Leu Gln Gln Ala Thr Arg Gln Leu Ser Gly Gln Ile His Ala
                725                 730                 735
Asp Met Ala Ser Ala Gln Ile Asn Glu Ser Arg Tyr Leu Arg Asp Thr
            740                 745                 750
Ala Thr Glu Arg Leu Arg Gln Ala Glu Gly Arg Arg Thr Ala Thr Asp
        755                 760                 765
Ile Lys Ala Asp Asp Asn Gly Ala Trp Ala Lys Leu Leu Gly Ser Trp
    770                 775                 780
Gly His Ala Ser Gly Asn Asp Asn Ala Thr Gly Tyr Gln Thr Ser Thr
785                 790                 795                 800
Tyr Gly Val Leu Leu Gly Leu Asp Ser Glu Leu Phe Gly Asp Gly Arg
                805                 810                 815
Leu Gly Met Met Thr Gly Tyr Thr Arg Thr Ser Leu Asp Gly Gly Tyr
            820                 825                 830
Gln Ser Asp Ala His Ser Asp Asn Tyr His Leu Gly Leu Tyr Gly Asp
        835                 840                 845
Lys Arg Phe Gly Ala Leu Ala Leu Arg Ala Gly Gly Thr Tyr Thr Trp
    850                 855                 860
His Arg Ile Asp Thr Ser Arg Ser Val Asn Tyr Gly Ala Gln Ser Asp
865                 870                 875                 880
Arg Glu Lys Ala Lys Tyr Asn Ala Arg Thr Gly Gln Leu Phe Ile Glu
                885                 890                 895
Ser Gly Tyr Asp Trp Thr Ser Asp Ala Val Asn Leu Glu Pro Phe Ala
            900                 905                 910
Asn Leu Ala Tyr Thr His Tyr Arg Asn Glu Glu Ile Asn Glu Gln Gly
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        915                 920                 925
Gly Ala Ala Ala Leu Arg Gly Asp Lys Gln Ser Gln Ser Ala Thr Ala
    930                 935                 940
Ser Thr Leu Gly Leu Arg Ala Asp Thr Glu Trp Gln Thr Asp Ser Val
945                 950                 955                 960
Ala Ile Ala Leu Arg Gly Glu Leu Gly Trp Gln His Gln Tyr Gly Lys
                965                 970                 975
Leu Glu Arg Lys Thr Gln Leu Met Phe Lys Arg Thr Asp Ala Ala Phe
            980                 985                 990
Asp Val Asn Ser Val Pro Val Ser Arg Asp Gly Ala Ile Leu Lys Ala
        995                 1000                1005
Gly Val Asp Val Ser Ile Asn Lys Asn Ala Val Leu Ser Leu Gly Tyr
    1010                1015                1020
Gly Gly Gln Leu Ser Ser Asn His Gln Asp Asn Ser Val Asn Ala Gly
1025                1030                1035                1040
Leu Thr Trp Arg Phe
                1045
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<210> 316
<211> 3675
<212> DNA
<213> Serratia marcescens

<220>
<223> Extracellular serine protease precursor S08.094

<400> 316

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gcgcccattt gcatctctca gcatgtctgt tcgtgcggcc cgcgccgggt ccgcatgtgt 180
tatccgtcgt ttcacgatca taggaggttt cagcgcggtt aaaacgtaag ttttcttctg 240
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cgtttttctg ggttgttatg gcttatccat tcattcttct cttgccgctt atcaggatcc 360
cggtcgattg ggcgcgcctg acagttggaa aaccgcggag tttaatcgcc aatgggggct 420
tgaagctatt tccgccgaat tcgcctatgc cagaggctat accggaaaag gtataaccat 480
cggcgttatc gataacgcta ttctttccca ttctgaattc tccggtaaac tgacgcgcct 540
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cggcacgcac gtagccggta tcgctgcggc taaaagagat ggcgcaggca tgcacggcgt 660
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cgattcgtgg agtaacgaca tcagcgggca cggcggcttg accaaaacgg gcgccggtac 1680
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gctggcgctg ttgggtaata acacctatcg cggtgatacc tgggtgaaac agggcgtgtt 1740
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cgagggcacc gtaggcgcct tcagagcggc tcggagcggc agcgtcgcgc cgggcaacgg 1860
catcggcacg ctgcatgtgt tgcacgatgc cattttgat cgcggttcgc agtataacgt 1920
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gggcgaggcg caagccgtga acgaagaggc gagcatcgtg gcgggccatc cgatctatga 2400
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<210> 317
<211> 1441
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Tripeptidyl-peptidase II (TPP-II)
S08.090

<400> 317

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Asn Phe Gly Leu Leu Gly Gln Lys Ala Ser Val Gly Leu Thr Leu Pro
            20                  25                  30
Ile Ile Ser Leu Ser Arg Pro Tyr Met Ala Tyr Met Gly Thr Glu Arg
        35                  40                  45
Ser Val Val Met Ile Thr Ala Pro Ala Thr Lys Glu Phe Ala Glu Ser
    50                  55                  60
Ser Glu Arg Ser Asn Ser Ser Lys Lys Thr Thr Asn Lys Glu Gln Ser
65                  70                  75                  80
Asp Lys Ser Ala Glu Ser Arg Met Ala Thr Ser Gly Ile Val Glu Ser
                85                  90                  95
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Phe Pro Thr Gly Ala Leu Val Pro Lys Ala Glu Thr Gly Val Leu Asn
                100                 105                 110
Phe Leu Gln Lys Tyr Pro Glu Tyr Asp Gly Arg Asp Val Thr Ile Ala
        115                 120                 125
Ile Phe Asp Ser Gly Val Asp Pro Arg Ala Thr Gly Leu Glu Thr Leu
    130                 135                 140
Cys Asp Gly Lys Thr Val Lys Val Ile Glu Arg Tyr Asp Cys Ser Gly
145                 150                 155                 160
Cys Gly Asp Val Asp Met Lys Lys Lys Val Thr Pro Asp Glu Asn Gly
                165                 170                 175
Asn Ile Lys Gly Leu Ser Gly Asn Ser Leu Lys Leu Ser Pro Glu Leu
            180                 185                 190
Met Ala Leu Asn Thr Asp Pro Glu Lys Ala Val Arg Val Gly Leu Lys
        195                 200                 205
Ser Phe Ser Asp Leu Leu Pro Ser Lys Val Arg Asn Asn Ile Val Ala
    210                 215                 220
Gln Ala Lys Leu Lys His Trp Asp Lys Pro His Lys Thr Ala Thr Ala
225                 230                 235                 240
Asn Ala Ser Arg Lys Ile Val Glu Phe Glu Ser Gln Asn Pro Gly Glu
                245                 250                 255
Ala Ser Lys Leu Pro Trp Asp Lys Lys Ile Leu Lys Glu Asn Leu Asp
            260                 265                 270
Phe Glu Leu Glu Met Leu Asn Ser Tyr Glu Lys Val Tyr Gly Asp Ile
        275                 280                 285
Lys Thr Ser Tyr Asp Cys Ile Leu Phe Pro Thr Ala Asp Gly Trp Leu
    290                 295                 300
Thr Ile Val Asp Thr Thr Glu Gln Gly Asp Leu Asp Gln Ala Leu Arg
305                 310                 315                 320
Ile Gly Glu Tyr Ser Arg Thr His Glu Thr Arg Asn Val Asp Asp Phe
                325                 330                 335
Leu Ser Ile Ser Val Asn Val His Asp Glu Gly Asn Val Leu Glu Val
            340                 345                 350
Val Gly Met Ser Ser Pro His Gly Thr His Val Ser Ser Ile Ala Ser
        355                 360                 365
Gly Asn His Ser Ser Arg Asp Val Asp Gly Val Ala Pro Asn Ala Lys
    370                 375                 380
Ile Val Ser Met Thr Ile Gly Asp Gly Arg Leu Gly Ser Met Glu Thr
385                 390                 395                 400
Gly Thr Ala Leu Val Arg Ala Met Thr Lys Val Met Glu Leu Cys Arg
                405                 410                 415
Asp Gly Arg Arg Ile Asp Val Ile Asn Met Ser Tyr Gly Glu His Ala
            420                 425                 430
Asn Trp Ser Asn Ser Gly Arg Ile Gly Glu Leu Met Asn Glu Val Val
        435                 440                 445
Asn Lys Tyr Gly Val Val Trp Val Ala Ser Ala Gly Asn His Gly Pro
    450                 455                 460
Ala Leu Cys Thr Val Gly Thr Pro Pro Asp Ile Ser Gln Pro Ser Leu
465                 470                 475                 480
Ile Gly Val Gly Ala Tyr Val Ser Pro Gln Met Met Glu Ala Glu Tyr
                485                 490                 495
Ala Met Arg Glu Lys Leu Pro Gly Asn Val Tyr Thr Trp Thr Ser Arg
            500                 505                 510
Asp Pro Cys Ile Asp Gly Gly Gln Gly Val Thr Val Cys Ala Pro Gly
        515                 520                 525
Gly Ala Ile Ala Ser Val Pro Gln Phe Thr Met Ser Lys Ser Gln Leu
    530                 535                 540
Met Asn Gly Thr Ser Met Ala Ala Pro His Val Ala Gly Ala Val Ala
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545                 550                 555                 560
Leu Leu Ile Ser Gly Leu Lys Gln Gln Asn Ile Glu Tyr Ser Pro Tyr
                565                 570                 575
Ser Ile Lys Arg Ala Ile Ser Val Thr Ala Thr Lys Leu Gly Tyr Val
            580                 585                 590
Asp Pro Phe Ala Gln Gly His Gly Leu Leu Asn Val Glu Lys Ala Phe
        595                 600                 605
Glu His Leu Thr Glu His Arg Gln Ser Lys Asp Asn Met Leu Arg Phe
    610                 615                 620
Ser Val Arg Val Gly Asn Asn Ala Asp Lys Gly Ile His Leu Arg Gln
625                 630                 635                 640
Gly Val Gln Arg Asn Ser Ile Asp Tyr Asn Val Tyr Ile Glu Pro Ile
                645                 650                 655
Phe Tyr Asn Asp Lys Glu Ala Asp Pro Lys Asp Lys Phe Asn Phe Asn
            660                 665                 670
Val Arg Leu Asn Leu Ile Ala Ser Gln Pro Trp Val Gln Cys Gly Ala
        675                 680                 685
Phe Leu Asp Leu Ser Tyr Gly Thr Arg Ser Ile Ala Val Arg Val Asp
    690                 695                 700
Pro Thr Gly Leu Gln Pro Gly Val His Ser Ala Val Ile Arg Ala Tyr
705                 710                 715                 720
Asp Thr Asp Cys Val Gln Lys Gly Ser Leu Phe Glu Ile Pro Val Thr
                725                 730                 735
Val Val Gln Pro His Val Leu Glu Ser Asp Gln Asn Thr Pro Val Phe
            740                 745                 750
Glu Pro Ala Ser Ser Lys Gly Asp Asn Ser Val Glu Phe Gln Pro Asn
        755                 760                 765
Thr Ile Gln Arg Asp Phe Ile Leu Val Pro Glu Arg Ala Thr Trp Ala
    770                 775                 780
Glu Leu Arg Met Arg Ile Thr Asp Pro Asn Arg Gly Glu Asp Ile Gly
785                 790                 795                 800
Lys Phe Phe Val His Thr Asn Gln Leu Leu Pro Lys Gln Ser Cys Arg
                805                 810                 815
Lys Leu Glu Thr Met Lys Ile Val Ser Val Gly Ser Glu Asn Glu Ser
            820                 825                 830
Ile Met Ala Phe Lys Val Lys Ser Gly Arg Ile Leu Glu Leu Cys Ile
        835                 840                 845
Ala Lys Tyr Trp Ser Asn Tyr Gly Gln Ser His Leu Lys Tyr Ser Leu
    850                 855                 860
Arg Phe Arg Gly Val Glu Ala His Asn Pro Asn Ala Tyr Val Met His
865                 870                 875                 880
Ala Gly Arg Gly Ile His Lys Leu Glu Ile Glu Ala Leu Val Ala Glu
                885                 890                 895
Asp Val Gln Pro Gln Leu Gln Leu Lys Asn Ala Glu Val Val Leu Lys
            900                 905                 910
Pro Thr Glu Ala Lys Ile Ser Pro Leu Ser Ala Thr Arg Asp Val Ile
        915                 920                 925
Pro Asp Gly Arg Gln Val Tyr Gln Asn Leu Leu Ala Phe Asn Leu Asn
    930                 935                 940
Val Ala Lys Ala Ala Asp Val Ser Ile Tyr Ala Pro Ile Phe Asn Asp
945                 950                 955                 960
Leu Leu Tyr Glu Ala Glu Phe Glu Ser Gln Met Trp Met Leu Phe Asp
                965                 970                 975
Ala Asn Lys Ala Leu Val Ala Thr Gly Asp Ala His Ser His Thr Ser
            980                 985                 990
Phe Thr Lys Leu Asp Lys Gly Glu Tyr Thr Ile Arg Leu Gln Val Arg
        995                 1000                1005
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His Glu Lys Arg Asp Leu Leu Glu Lys Ile Ser Glu Ala Asn Leu Val
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Ala Ser Phe Lys Leu Thr Ser Pro Leu Thr Leu Asp Phe Tyr Glu Asn
1025                1030                1035                1040
Tyr Asn Gln Cys Ile Val Gly Gly Arg Lys Tyr Val Ser Ser Pro Leu
                1045                1050                1055
Arg Leu Ser Thr Arg Val Leu Tyr Ile Ala Pro Ile Thr Gln Glu Arg
            1060                1065                1070
Leu Thr Lys Ala Asn Leu Pro Ala Gln Cys Ala Trp Leu Ser Gly Asn
        1075                1080                1085
Leu Val Phe Pro Gln Asp Glu Val Gly Arg Arg Val Ala Gln His Pro
    1090                1095                1100
Phe Thr Tyr Ile Leu Asn Pro Ala Glu Lys Lys Ser His Thr Asn Gly
1105                1110                1115                1120
Ser Ser Asn Gly Ser Ser Ala Ala Gly Ser Thr Ala Thr Ala Ala Ala
                1125                1130                1135
Val Thr Thr Ala Asn Gly Ala Lys Pro Lys Ala Pro Ala Thr Pro Gln
            1140                1145                1150
Ala Ala Thr Ser Val Thr Asn Pro Ala Ala Gly Asp Gly Ile Ser Val
        1155                1160                1165
Gln Asn Asp Pro Pro Val Asp Ser Ser Gly Ser Pro Ala Ser Pro Lys
    1170                1175                1180
Lys Gly Lys Ala Asn Ala Asp Asp Tyr Ala Glu Ser Phe Arg Asp Phe
1185                1190                1195                1200
Gln Cys Ser Gln Ile Val Lys Cys Glu Leu Glu Met Ala Glu Lys Ile
                1205                1210                1215
Tyr Asn Asp Val Val Ala Ala His Pro Lys His Leu Gln Ala Asn Leu
            1220                1225                1230
Leu Leu Ile Gln Asn Ile Glu Ser Asn Gln Leu Lys Ser Gln Leu Pro
        1235                1240                1245
Leu Thr Phe Val Asn Ala Gln Lys Thr Ser Pro Pro Glu Ala Gly Glu
    1250                1255                1260
Ser Ala Asp Lys Gln Lys Glu Asp Gln Lys Lys Val Arg Ser Ala Leu
1265                1270                1275                1280
Glu Arg Ile Val Lys Leu Ala Asp Lys Val Ile Gln Glu Thr Asp Ser
                1285                1290                1295
Glu Ala Leu Leu Ser Tyr Tyr Gly Leu Lys Asn Asp Thr Arg Ala Asp
            1300                1305                1310
Ala Ala Lys Ile Lys Thr Asn Met Asp Lys Gln Lys Asn Thr Leu Ile
        1315                1320                1325
Glu Ala Leu Ser Lys Lys Gly Ile Ala Val Ala Lys Leu Ala Val Leu
    1330                1335                1340
Asp Asp Cys Ile Lys Asp Ser Leu Ala Glu Ile Asn Glu Leu Tyr Thr
1345                1350                1355                1360
Glu Ile Ile Lys Phe Val Asp Ala Asn Asp Ser Lys Ala Ile Gln Phe
                1365                1370                1375
Ala Leu Trp His Ala Tyr Ala His Gly His Tyr Gly Arg Met Tyr Lys
            1380                1385                1390
Tyr Val Val Lys Leu Ile Glu Glu Lys Arg Thr Arg Asp His Phe Val
        1395                1400                1405
Glu Leu Ala Ala Ile Asn Gly Ala Leu Gly His Glu His Ile Arg Thr
    1410                1415                1420
Val Ile Asn Arg Met Met Ile Thr Ala Phe Pro Ser Ser Phe Arg Leu
1425                1430                1435                1440
Phe
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<210> 318
<211> 4309
<212> DNA
<213> Drosophila melanogaster

<220>
<223> Tripeptidyl-peptidase II (TPP-II) S08.090

<400> 318
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agcaggatgg ccaccagcgg tattgtcgag tcatttccca cgggcgcact ggtgcccaag 180
gcggagacgg gagtcctgaa ctttctgcag aagtacccgg agtacgatgg acgcgacgtc 240
accatagcca tcttcgattc cggcgtcgat ccccgggcaa cgggactgga gacgctgtgc 300
gatggaaaga ccgttaaagt aatagagcgg tacgactgtt ccggatgcgg cgacgtggac 360
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ggcctcaaga gcttcagcga tttgttgccc tccaaggtgc ggaacaacat tgtggcccag 540
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<210> 319
<211> 806
<212> PRT
<213> Bacillus subtilis

<220>
<223> Minor extracellular protease vpr precursor
S08.114

<400> 319

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            20                  25                  30
Ser Lys Thr Ser Ala Asp Leu Glu Lys Ala Glu Val Phe Gly Asp Ile
        35                  40                  45
Asp Met Thr Thr Ser Lys Lys Thr Thr Val Ile Val Glu Leu Lys Glu
    50                  55                  60
Lys Ser Leu Ala Glu Ala Lys Glu Ala Gly Glu Ser Gln Ser Lys Ser
65                  70                  75                  80
Lys Leu Lys Thr Ala Arg Thr Lys Ala Lys Asn Lys Ala Ile Lys Ala
                85                  90                  95
Val Lys Asn Gly Lys Val Asn Arg Glu Tyr Glu Gln Val Phe Ser Gly
            100                 105                 110
Phe Ser Met Lys Leu Pro Ala Asn Glu Ile Pro Lys Leu Leu Ala Val
        115                 120                 125
Lys Asp Val Lys Ala Val Tyr Pro Asn Val Thr Tyr Lys Thr Asp Asn
    130                 135                 140
Met Lys Asp Lys Asp Val Thr Ile Ser Glu Asp Ala Val Ser Pro Gln
```

```
145                 150                 155                 160
Met Asp Asp Ser Ala Pro Tyr Ile Gly Ala Asn Asp Ala Trp Asp Leu
                165                 170                 175
Gly Tyr Thr Gly Lys Gly Ile Lys Val Ala Ile Ile Asp Thr Gly Val
            180                 185                 190
Glu Tyr Asn His Pro Asp Leu Lys Lys Asn Phe Gly Gln Tyr Lys Gly
        195                 200                 205
Tyr Asp Phe Val Asp Asn Asp Tyr Asp Pro Lys Glu Thr Pro Thr Gly
    210                 215                 220
Asp Pro Arg Gly Glu Ala Thr Asp His Gly Thr His Val Ala Gly Thr
225                 230                 235                 240
Val Ala Ala Asn Gly Thr Ile Lys Gly Val Ala Pro Asp Ala Thr Leu
                245                 250                 255
Leu Ala Tyr Arg Val Leu Gly Pro Gly Gly Ser Gly Thr Thr Glu Asn
            260                 265                 270
Val Ile Ala Gly Val Glu Arg Ala Val Gln Asp Gly Ala Asp Val Met
        275                 280                 285
Asn Leu Ser Leu Gly Asn Ser Leu Asn Asn Pro Asp Trp Ala Thr Ser
    290                 295                 300
Thr Ala Leu Asp Trp Ala Met Ser Glu Gly Val Val Ala Val Thr Ser
305                 310                 315                 320
Asn Gly Asn Ser Gly Pro Asn Gly Trp Thr Val Gly Ser Pro Gly Thr
                325                 330                 335
Ser Arg Glu Ala Ile Ser Val Gly Ala Thr Gln Leu Pro Leu Asn Glu
            340                 345                 350
Tyr Ala Val Thr Phe Gly Ser Tyr Ser Ser Ala Lys Val Met Gly Tyr
        355                 360                 365
Asn Lys Glu Asp Asp Val Lys Ala Leu Asn Asn Lys Glu Val Glu Leu
    370                 375                 380
Val Glu Ala Gly Ile Gly Glu Ala Lys Asp Phe Glu Gly Lys Asp Leu
385                 390                 395                 400
Thr Gly Lys Val Ala Val Val Lys Arg Gly Ser Ile Ala Phe Val Asp
                405                 410                 415
Lys Ala Asp Asn Ala Lys Lys Ala Gly Ala Ile Gly Met Val Val Tyr
            420                 425                 430
Asn Asn Leu Ser Gly Glu Ile Glu Ala Asn Val Pro Gly Met Ser Val
        435                 440                 445
Pro Thr Ile Lys Leu Ser Leu Glu Asp Gly Glu Lys Leu Val Ser Ala
    450                 455                 460
Leu Lys Ala Gly Glu Thr Lys Thr Thr Phe Lys Leu Thr Val Ser Lys
465                 470                 475                 480
Ala Leu Gly Glu Gln Val Ala Asp Phe Ser Ser Arg Gly Pro Val Met
                485                 490                 495
Asp Thr Trp Met Ile Lys Pro Asp Ile Ser Ala Pro Gly Val Asn Ile
            500                 505                 510
Val Ser Thr Ile Pro Thr His Asp Pro Asp His Pro Tyr Gly Tyr Gly
        515                 520                 525
Ser Lys Gln Gly Thr Ser Met Ala Ser Pro His Ile Ala Gly Ala Val
    530                 535                 540
Ala Val Ile Lys Gln Ala Lys Pro Lys Trp Ser Val Glu Gln Ile Lys
545                 550                 555                 560
Ala Ala Ile Met Asn Thr Ala Val Thr Leu Lys Asp Ser Asp Gly Glu
                565                 570                 575
Val Tyr Pro His Asn Ala Gln Gly Ala Gly Ser Ala Arg Ile Met Asn
            580                 585                 590
Ala Ile Lys Ala Asp Ser Leu Val Ser Pro Gly Ser Tyr Ser Tyr Gly
        595                 600                 605
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Thr Phe Leu Lys Glu Asn Gly Asn Glu Thr Lys Asn Glu Thr Phe Thr
    610                 615                 620
Ile Glu Asn Gln Ser Ser Ile Arg Lys Ser Tyr Thr Leu Glu Tyr Ser
625                 630                 635                 640
Phe Asn Gly Ser Gly Ile Ser Thr Ser Gly Thr Ser Arg Val Val Ile
                645                 650                 655
Pro Ala His Gln Thr Gly Lys Ala Thr Ala Lys Val Lys Val Asn Thr
            660                 665                 670
Lys Lys Thr Lys Ala Gly Thr Tyr Glu Gly Thr Val Ile Val Arg Glu
        675                 680                 685
Gly Gly Lys Thr Val Ala Lys Val Pro Thr Leu Leu Ile Val Lys Glu
    690                 695                 700
Pro Asp Tyr Pro Arg Val Thr Ser Val Ser Val Ser Glu Gly Ser Val
705                 710                 715                 720
Gln Gly Thr Tyr Gln Ile Glu Thr Tyr Leu Pro Ala Gly Ala Glu Glu
                725                 730                 735
Leu Ala Phe Leu Val Tyr Asp Ser Asn Leu Asp Phe Ala Gly Gln Ala
            740                 745                 750
Gly Ile Tyr Lys Asn Gln Asp Lys Gly Tyr Gln Tyr Phe Asp Trp Asp
        755                 760                 765
Gly Thr Ile Asn Gly Gly Thr Lys Leu Pro Ala Gly Glu Tyr Tyr Leu
    770                 775                 780
Leu Ala Tyr Ala Ala Asn Lys Gly Lys Ser Ser Gln Val Leu Thr Glu
785                 790                 795                 800
Glu Pro Phe Thr Val Glu
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<210> 320
<211> 2931
<212> DNA
<213> Bacillus subtilis

<220>
<223> Minor extracellular protease vpr precursor S08.114

<400> 320
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S08.116

<400> 321

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Thr Ala Ala Thr Ala Lys Gln Ala Ala Thr Asp Thr Thr Ala Ala Thr
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Thr Asn Gln Ala Ile Ala Thr Gln Leu Ala Ala Lys Gly Ile Asp Tyr
65                  70                  75                  80
Asn Lys Leu Asn Lys Val Gln Gln Gln Asp Ile Tyr Val Asp Val Ile
                85                  90                  95
Val Gln Met Ser Ala Ala Pro Ala Ser Glu Asn Gly Ile Leu Arg Thr
            100                 105                 110
Asp Tyr Ser Ser Thr Ala Glu Ile Gln Gln Glu Thr Asn Lys Val Ile
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Thr Ala Gly Glu Ser Tyr Gly Tyr Val Val Asn Gly Phe Ser Thr Lys
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Val Arg Val Val Asp Ile Pro Lys Leu Lys Gln Ile Ala Gly Val Lys
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Thr Val Thr Leu Ala Lys Val Tyr Tyr Pro Thr Asp Ala Lys Ala Asn
            180                 185                 190
Ser Met Ala Asn Val Gln Ala Val Trp Ser Asn Tyr Lys Tyr Lys Gly
        195                 200                 205
Glu Gly Thr Val Val Ser Val Ile Asp Ser Gly Ile Asp Pro Thr His
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Lys Asp Met Arg Leu Ser Asp Asp Lys Asp Val Lys Leu Thr Lys Ser
225                 230                 235                 240
Asp Val Glu Lys Phe Thr Asp Thr Val Lys His Gly Arg Tyr Phe Asn
                245                 250                 255
Ser Lys Val Pro Tyr Gly Phe Asn Tyr Ala Asp Asn Asn Asp Thr Ile
            260                 265                 270
Thr Asp Asp Lys Val Asp Glu Gln His Gly Met His Val Ala Gly Ile
        275                 280                 285
Ile Gly Ala Asn Gly Thr Gly Asp Asp Pro Ala Lys Ser Val Val Gly
    290                 295                 300
Val Ala Pro Glu Ala Gln Leu Leu Ala Met Lys Val Phe Ser Asn Ser
305                 310                 315                 320
Asp Thr Ser Ala Lys Thr Gly Ser Ala Thr Val Val Ser Ala Ile Glu
                325                 330                 335
Asp Ser Ala Lys Ile Gly Ala Asp Val Leu Asn Met Ser Leu Gly Ser
            340                 345                 350
Asn Ser Gly Asn Gln Thr Leu Glu Asp Pro Glu Leu Ala Ala Val Gln
        355                 360                 365
Asn Ala Asn Glu Ser Gly Thr Ala Ala Val Ile Ser Ala Gly Asn Ser
    370                 375                 380
Gly Thr Ser Gly Ser Ala Thr Glu Gly Val Asn Lys Asp Tyr Tyr Gly
385                 390                 395                 400
Leu Gln Asp Asn Glu Met Val Gly Ser Pro Gly Thr Ser Arg Gly Ala
                405                 410                 415
Thr Thr Val Ala Ser Ala Glu Asn Thr Asp Val Ile Thr Gln Ala Val
            420                 425                 430
Thr Ile Thr Asp Gly Thr Gly Leu Gln Leu Gly Pro Glu Thr Ile Gln
        435                 440                 445
Leu Ser Ser His Asp Phe Thr Gly Ser Phe Asp Gln Lys Lys Phe Tyr
    450                 455                 460
Ile Val Lys Asp Ala Ser Gly Asn Leu Ser Lys Gly Ala Leu Ala Asp
465                 470                 475                 480
Tyr Thr Ala Asp Ala Lys Gly Lys Ile Ala Ile Val Lys Arg Gly Glu
                485                 490                 495
Phe Ser Phe Asp Asp Lys Gln Lys Tyr Ala Gln Ala Ala Gly Ala Ala
            500                 505                 510
Gly Leu Ile Ile Val Asn Thr Asp Gly Thr Ala Thr Pro Met Thr Ser
        515                 520                 525
Ile Ala Leu Thr Thr Thr Phe Pro Thr Phe Gly Leu Ser Ser Val Thr
    530                 535                 540
Gly Gln Lys Leu Val Asp Trp Val Thr Ala His Pro Asp Asp Ser Leu
545                 550                 555                 560
Gly Val Lys Ile Thr Leu Ala Met Leu Pro Asn Gln Lys Tyr Thr Glu
                565                 570                 575
Asp Lys Met Ser Asp Phe Thr Ser Tyr Gly Pro Val Ser Asn Leu Ser
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Phe Lys Pro Asp Ile Thr Ala Pro Gly Gly Asn Ile Trp Ser Thr Gln
        595                 600                 605
Asn Asn Asn Gly Tyr Thr Asn Met Ser Gly Thr Ser Met Ala Ser Pro
    610                 615                 620
Phe Ile Ala Gly Ser Gln Ala Leu Leu Lys Gln Ala Leu Asn Asn Lys
625                 630                 635                 640
Asn Asn Pro Phe Tyr Ala Tyr Tyr Lys Gln Leu Lys Gly Thr Ala Leu
                645                 650                 655
Thr Asp Phe Leu Lys Thr Val Glu Met Asn Thr Ala Gln Pro Ile Asn
            660                 665                 670
Asp Ile Asn Tyr Asn Asn Val Ile Val Ser Pro Arg Arg Gln Gly Ala
        675                 680                 685
Gly Leu Val Asp Val Lys Ala Ala Ile Asp Ala Leu Glu Lys Asn Pro
    690                 695                 700
Ser Thr Val Val Ala Glu Asn Gly Tyr Pro Ala Val Glu Leu Lys Asp
705                 710                 715                 720
Phe Thr Ser Thr Asp Lys Thr Phe Lys Leu Thr Phe Thr Asn Arg Thr
                725                 730                 735
Thr His Glu Leu Thr Tyr Gln Met Asp Ser Asn Thr Asp Thr Asn Ala
            740                 745                 750
Val Tyr Thr Ser Ala Thr Asp Pro Asn Ser Gly Val Leu Tyr Asp Lys
        755                 760                 765
Lys Ile Asp Gly Ala Ala Ile Lys Ala Gly Ser Asn Ile Thr Val Pro
    770                 775                 780
Ala Gly Lys Thr Ala Gln Ile Glu Phe Thr Leu Ser Leu Pro Lys Ser
785                 790                 795                 800
Phe Asp Gln Gln Gln Phe Val Glu Gly Phe Leu Asn Phe Lys Gly Ser
                805                 810                 815
Asp Gly Ser Arg Leu Asn Leu Pro Tyr Met Gly Phe Phe Gly Asp Trp
            820                 825                 830
Asn Asp Gly Lys Ile Val Asp Ser Leu Asn Gly Ile Thr Tyr Ser Pro
        835                 840                 845
Ala Gly Gly Asn Phe Gly Thr Val Pro Leu Leu Lys Asn Lys Asn Thr
    850                 855                 860
Gly Thr Gln Tyr Tyr Gly Gly Met Val Thr Asp Ala Asp Gly Asn Lys
865                 870                 875                 880
Thr Val Asp Asp Gln Ala Ile Ala Phe Ser Ser Asp Lys Asn Ala Leu
                885                 890                 895
Tyr Asn Asp Ile Ser Met Lys Tyr Tyr Leu Leu Arg Asn Ile Ser Asn
            900                 905                 910
Val Gln Val Asp Ile Leu Asp Gly Gln Gly Asn Lys Val Thr Thr Leu
        915                 920                 925
Ser Ser Ser Thr Asn Arg Lys Lys Thr Tyr Tyr Asn Ala His Ser Gln
    930                 935                 940
Gln Tyr Ile Tyr Tyr Asn Ala Pro Ala Trp Asp Gly Thr Tyr Tyr Asp
945                 950                 955                 960
Gln Arg Asp Gly Asn Ile Lys Thr Ala Asp Asp Gly Ser Tyr Thr Tyr
                965                 970                 975
Arg Ile Ser Gly Val Pro Glu Gly Gly Asp Lys Arg Gln Val Phe Asp
            980                 985                 990
Val Pro Phe Lys Leu Asp Ser Lys Ala Pro Thr Val Arg His Val Ala
        995                 1000                1005
Leu Ser Ala Lys Thr Glu Asn Gly Lys Thr Gln Tyr Tyr Leu Thr Ala
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Glu Ala Lys Asp Asp Leu Ser Gly Leu Asp Ala Thr Lys Ser Val Lys
1025                1030                1035                1040
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Gly Thr Thr Ala Asp Gly Tyr Thr Lys Ile Glu Thr Pro Leu Ser Asp
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Glu Gln Ala Gln Ala Leu Gly Asn Gly Asp Asn Ser Ala Glu Leu Tyr
        1075                1080                1085
Leu Thr Asp Asn Ala Ser Asn Ala Thr Asp Gln Asp Ala Ser Val Gln
    1090                1095                1100
Lys Pro Gly Ser Thr Ser Phe Asp Leu Ile Val Asn Gly Gly Gly Ile
1105                1110                1115                1120
Pro Asp Lys Ile Ser Ser Thr Thr Thr Gly Tyr Glu Ala Asn Thr Gln
                1125                1130                1135
Gly Gly Gly Thr Tyr Thr Phe Ser Gly Thr Tyr Pro Ala Ala Val Asp
            1140                1145                1150
Gly Thr Tyr Thr Asp Ala Gln Gly Lys Lys His Asp Leu Asn Thr Thr
        1155                1160                1165
Tyr Asp Ala Ala Thr Asn Ser Phe Thr Ala Ser Met Pro Val Thr Asn
    1170                1175                1180
Ala Asp Tyr Ala Ala Gln Val Asp Leu Tyr Ala Asp Lys Ala His Thr
1185                1190                1195                1200
Gln Leu Leu Lys His Phe Asp Thr Lys Val Arg Leu Met Ala Pro Thr
                1205                1210                1215
Phe Thr Asp Leu Lys Phe Asn Asn Gly Ser Asp Gln Thr Ser Glu Ala
            1220                1225                1230
Thr Ile Lys Val Thr Gly Thr Val Ser Ala Asp Thr Lys Thr Val Asn
        1235                1240                1245
Val Gly His Thr Val Ala Ala Leu Asp Ala Gln His His Phe Ser Val
    1250                1255                1260
Asp Val Pro Val Asn Tyr Gly Asp Asn Thr Ile Lys Val Thr Ala Thr
1265                1270                1275                1280
Asp Lys Asp Gly Asn Thr Thr Thr Glu Gln Lys Thr Ile Thr Ser Ser
                1285                1290                1295
Tyr Asp Pro Asp Met Leu Lys Lys Ser Val Thr Phe Asp Gln Gly Val
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Lys Phe Gly Thr Asn Lys Phe Asn Ala Thr Ser Ala Lys Phe Tyr Asp
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Pro Lys Thr Gly Ile Ala Thr Ile Thr Gly Lys Val Lys His Pro Thr
    1330                1335                1340
Thr Thr Leu Gln Val Asp Gly Lys Gln Ile Pro Ile Lys Asp Asp Leu
1345                1350                1355                1360
Thr Phe Ser Phe Thr Leu Asp Leu Gly Thr Leu Gly Gln Lys Pro Phe
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Gly Val Val Val Gly Asp Thr Thr Gln Asn Lys Thr Phe Gln Glu Ala
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Leu Ser Phe Ile Leu Asp Ala Val Ala Pro Thr Leu Ser Leu Asp Ser
        1395                1400                1405
Ser Thr Asp Ala Pro Val Tyr Thr Asn Asp Pro Asn Phe Gln Ile Thr
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Gly Thr Ala Thr Asp Asn Ala Gln Tyr Leu Ser Leu Ser Ile Asn Gly
1425                1430                1435                1440
Ser Ser Val Ala Ser Gln Tyr Glu Asp Ile Asn Ile Asn Ser Gly Lys
                1445                1450                1455
Pro Gly His Met Ala Ile Asp Gln Pro Val Lys Leu Leu Glu Gly Lys
            1460                1465                1470
Asn Val Leu Thr Val Ala Val Thr Asp Ser Glu Asp Asn Thr Thr Thr
        1475                1480                1485
Lys Asn Ile Thr Val Tyr Tyr Glu Pro Lys Lys Thr Leu Ala Ala Pro
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Gly Lys Thr Tyr Gln Asp Val Pro Ala Ala Gly Val Thr Ile Thr Ala
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Asn Gly Thr Phe Lys Phe Lys Ser Thr Asp Leu Tyr Gly Asn Glu Ser
        1555                1560                1565
Pro Ala Val Asp Tyr Val Val Thr Asn Ile Lys Ala Asp Asp Pro Ala
    1570                1575                1580
Gln Leu Gln Ala Ala Lys Gln Glu Leu Thr Asn Leu Ile Ala Ser Ala
1585                1590                1595                1600
Lys Thr Leu Ser Ala Ser Gly Lys Tyr Asp Asp Ala Thr Thr Thr Ala
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Ala Ser Val Asp Ser Leu Thr Gly Ala Asn Arg Asp Leu Gln Thr Ala
        1635                1640                1645
Ile Asn Gln Leu Ala Ala Lys Leu Pro Ala Asp Lys Lys Thr Ser Leu
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Leu Asn Gln Leu Gln Ser Val Lys Asp Ala Leu Gly Thr Asp Leu Gly
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Asn Gln Thr Asp Pro Ser Thr Gly Lys Thr Phe Thr Ala Ala Leu Asp
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Ala Leu Gln Ser Leu Lys Thr Lys Val Ala Ala Ala Val Glu Ala Ala
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Lys Gly Asp Glu Gly Ser Gln Pro Ser Ser Gly Gly Asn Ile Pro Thr
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Lys Pro Ala Thr Thr Thr Ser Thr Thr Thr Asp Asp Thr Thr Asp Arg
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Asn Gly Gln Leu Thr Ser Gly Lys Gly Ala Leu Pro Lys Thr Gly Glu
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Thr Thr Glu Arg Pro Ala Phe Gly Phe Leu Gly Val Ile Val Val Ser
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(Lactocepin) S08.116

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<210> 323
<211> 1101
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Furin-like protease 1, isoform 1-CRR precursor
(Furin-1) S08.048

<400> 323

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Thr Asn Ser Ser Ser Ser Ser Arg Ser Asp Ser Asn Ser Thr His Lys
            20                  25                  30
His Arg Ser Lys Ser Asn Lys Leu Asn Ala Arg Gln Leu Gly Ser Asn
        35                  40                  45
Ala Ala Arg Ser Cys Gln Gln Arg Ser Ser Val Ala Thr Thr Leu Glu
    50                  55                  60
Asp Glu Gln Gln Thr Ile Ile Glu Cys Asp Ile Gly Asn Phe Asn Phe
65                  70                  75                  80
Asp Cys Asn Leu Phe Lys Thr Ser Phe Leu Thr Gln His Lys Gln Lys
                85                  90                  95
Arg Ser Gly Lys Ser Ser Ser Lys Ser Lys Ser Asn Arg Ser Arg Pro
```

```
            100                 105                 110
Leu Ala Lys Thr Lys Ala Val Phe Leu Leu Ala Leu Gln Phe Ser Ala
        115                 120                 125
Val Val Phe Leu Cys Asn Ile Asn Val Gly Phe Val Ala Gly Ser Val
    130                 135                 140
Ala Thr Ala Ala Ser Ser Ala Gly Gly Ser Ser Pro Ala Ala Pro Ser
145                 150                 155                 160
Ser Ala Pro Ser Ser Pro Pro Thr Val Ala Val Pro Pro Pro Pro Pro
                165                 170                 175
Pro Ser Ser Ala Leu Lys Val Asp Pro Asn Gly Gln Ser Pro Val Leu
            180                 185                 190
Pro Pro Tyr Val Leu Asp Tyr Glu Thr Gly Gly Lys Ala Lys Leu Thr
        195                 200                 205
Pro Asn Asn Gly Lys Phe Gly Gln Ser Gly Ser Ser Gly Ser Asn Asn
    210                 215                 220
Asn His Ile Val Gly His Tyr Thr His Thr Trp Ala Val His Ile Pro
225                 230                 235                 240
Asn Gly Asp Asn Gly Met Ala Asp Ala Val Ala Lys Asp His Gly Phe
                245                 250                 255
Val Asn Leu Gly Lys Ile Phe Asp Asp His Tyr His Phe Ala His His
            260                 265                 270
Lys Val Ser Lys Arg Ser Leu Ser Pro Ala Thr His His Gln Thr Arg
        275                 280                 285
Leu Asp Asp Asp Asp Arg Val His Trp Ala Lys Gln Gln Arg Ala Lys
    290                 295                 300
Ser Arg Ser Lys Arg Asp Phe Ile Arg Met Arg Pro Ser Arg Thr Ser
305                 310                 315                 320
Ser Arg Ala Met Ser Met Val Asp Ala Met Ser Phe Asn Asp Ser Lys
                325                 330                 335
Trp Pro Gln Met Trp Tyr Leu Asn Arg Gly Gly Gly Leu Asp Met Asn
            340                 345                 350
Val Ile Pro Ala Trp Lys Met Gly Ile Thr Gly Lys Gly Val Val Val
        355                 360                 365
Thr Ile Leu Asp Asp Gly Leu Glu Ser Asp His Pro Asp Ile Gln Asp
    370                 375                 380
Asn Tyr Asp Pro Lys Ala Ser Tyr Asp Val Asn Ser His Asp Asp Asp
385                 390                 395                 400
Pro Met Pro His Tyr Asp Met Thr Asp Ser Asn Arg His Gly Thr Arg
                405                 410                 415
Cys Ala Gly Glu Val Ala Ala Thr Ala Asn Asn Ser Phe Cys Ala Val
            420                 425                 430
Gly Ile Ala Tyr Gly Ala Ser Val Gly Gly Val Arg Met Leu Asp Gly
        435                 440                 445
Asp Val Thr Asp Ala Val Glu Ala Arg Ser Leu Ser Leu Asn Pro Gln
    450                 455                 460
His Ile Asp Ile Tyr Ser Ala Ser Trp Gly Pro Asp Asp Asp Gly Lys
465                 470                 475                 480
Thr Val Asp Gly Pro Gly Glu Leu Ala Ser Arg Ala Phe Ile Glu Gly
                485                 490                 495
Thr Thr Lys Gly Arg Gly Gly Lys Gly Ser Ile Phe Ile Trp Ala Ser
            500                 505                 510
Gly Asn Gly Gly Arg Glu Gln Asp Asn Cys Asn Cys Asp Gly Tyr Thr
        515                 520                 525
Asn Ser Ile Trp Thr Leu Ser Ile Ser Ser Ala Thr Glu Glu Gly His
    530                 535                 540
Val Pro Trp Tyr Ser Glu Lys Cys Ser Ser Thr Leu Ala Thr Thr Tyr
545                 550                 555                 560
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Ser Ser Gly Gly Gln Gly Glu Lys Gln Val Val Thr Thr Asp Leu His
                565                 570                 575
His Ser Cys Thr Val Ser His Thr Gly Thr Ser Ala Ser Ala Pro Leu
            580                 585                 590
Ala Ala Gly Ile Ala Ala Leu Val Leu Gln Ser Asn Gln Asn Leu Thr
        595                 600                 605
Trp Arg Asp Leu Gln His Ile Val Val Arg Thr Ala Lys Pro Ala Asn
    610                 615                 620
Leu Lys Asp Pro Ser Trp Ser Arg Asn Gly Val Gly Arg Arg Val Ser
625                 630                 635                 640
His Ser Phe Gly Tyr Gly Leu Met Asp Ala Ala Glu Met Val Arg Val
                645                 650                 655
Ala Arg Asn Trp Lys Ala Val Pro Glu Gln Gln Arg Cys Glu Ile Asn
            660                 665                 670
Ala Pro His Val Asp Lys Val Ile Pro Pro Arg Thr His Ile Thr Leu
        675                 680                 685
Gln Leu Thr Val Asn His Cys Arg Ser Val Asn Tyr Leu Glu His Val
    690                 695                 700
Gln Ala Lys Ile Thr Leu Thr Ser Gln Arg Arg Gly Asp Ile Gln Leu
705                 710                 715                 720
Phe Leu Arg Ser Pro Ala Asn Thr Ser Val Thr Leu Leu Thr Pro Arg
                725                 730                 735
Ile His Asp Asn Ser Arg Ser Gly Phe Asn Gln Trp Pro Phe Met Ser
            740                 745                 750
Val His Thr Trp Gly Glu Ser Pro Gln Gly Asn Trp Gln Leu Glu Ile
        755                 760                 765
His Asn Glu Gly Arg Tyr Met Ala Gln Ile Thr Gln Trp Asp Met Ile
    770                 775                 780
Phe Tyr Gly Thr Glu Thr Pro Ala Gln Pro Asp Asp Val Ala Asn Pro
785                 790                 795                 800
Ser Gln Ser Asn Gln Phe Asn Leu Tyr Gly Asn Asp Met Ala His Asn
                805                 810                 815
Asp Val Glu Tyr Asp Ser Thr Gly Gln Trp Arg Asn Met Gln Gln Val
            820                 825                 830
Gly Glu Val Gly Met Thr Arg Asp His Ser Asn Thr Ala Ala Cys Leu
        835                 840                 845
Lys Trp Ser Asp Arg Lys Cys Leu Glu Cys Asn Asp Ser Ala Tyr Met
    850                 855                 860
Phe Glu Asp Gln Cys Tyr Asp Val Cys Pro Val His Thr Tyr Pro Leu
865                 870                 875                 880
Asp Lys Phe Gln Ala Glu Glu Asp Glu Gln Asp Asp Glu Val Thr Arg
                885                 890                 895
Gly Pro Val Asn Pro Tyr Ser Ser Ser Pro Met Asp His Ser Leu Leu
            900                 905                 910
Met Ser Asn Ser Leu Asp Asp Lys Gln Asp Pro Leu Gln Ala Glu Asp
        915                 920                 925
Arg Arg Arg Arg Ser Ser Leu Thr Gln Leu Val Glu Val Pro Ser Arg
    930                 935                 940
Val Cys Ala Ala Cys Asp Arg Ser Cys Leu Glu Cys Tyr Gly Ala Leu
945                 950                 955                 960
Ala Ser Gln Cys Ser Thr Cys Ser Pro Gly Ser Gln Leu Arg Lys Ile
                965                 970                 975
Leu Asn Glu Thr Phe Cys Tyr Ala Tyr Val Val Arg Ser Thr Gly Met
            980                 985                 990
Ala Ser Val Val Asp Ile Ser Lys Met Asp Asp Arg Asp Thr Gln Gln
        995                 1000                1005
Tyr Met Thr Gly Thr Thr Val Leu Leu Leu Val Ser Val Ile Phe Thr
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    1010                1015                1020
Leu Met Gly Val Ala Val Ala Gly Gly Ile Val Tyr His Arg Arg Ala
1025                1030                1035                1040
Met Ala Arg Ser Asn Glu Leu Tyr Ser Arg Val Ser Leu Val Pro Gly
                1045                1050                1055
Asp Glu Ser Asp Ser Asp Glu Asp Glu Leu Phe Thr Ala His Phe Pro
            1060                1065                1070
Ala Arg Lys Ser Gly Val Asn Ile Tyr Arg Asp Glu Ala Pro Ser Glu
        1075                1080                1085
Lys Ile Phe Glu Glu Asp Glu Ile Ser His Leu Val Pro
    1090                1095                1100
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<210> 324
<211> 3781
<212> DNA
<213> Drosophila melanogaster

<220>
<223> Furin-like protease 1, isoform 1-CRR precursor
(Furin-1) S08.048

<400> 324

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cttggcctca tctaacatcc acttaattga aatagaacat ttgcatctca gcctcacaac 180
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gaagatgaac aacaaacaat cattgaatgt gatataggaa atttcaattt cgattgcaat 480
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<210> 325
<211> 814
<212> PRT
<213> Saccharomyces cerevisiae

<220>
<223> Kexin precursor (KEX2 protease) S08.048

<400> 325

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            20                  25                  30
Ser Arg Gln Tyr Phe Ala Val Glu Ser Asn Glu Thr Leu Ser Arg Leu
        35                  40                  45
Glu Glu Met His Pro Asn Trp Lys Tyr Glu His Asp Val Arg Gly Leu
    50                  55                  60
Pro Asn His Tyr Val Phe Ser Lys Glu Leu Leu Lys Leu Gly Lys Arg
65                  70                  75                  80
Ser Ser Leu Glu Glu Leu Gln Gly Asp Asn Asn Asp His Ile Leu Ser
                85                  90                  95
Val His Asp Leu Phe Pro Arg Asn Asp Leu Phe Lys Arg Leu Pro Val
            100                 105                 110
Pro Ala Pro Pro Met Asp Ser Ser Leu Leu Pro Val Lys Glu Ala Glu
        115                 120                 125
```

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Asp Lys Leu Ser Ile Asn Asp Pro Leu Phe Glu Arg Gln Trp His Leu
    130                 135                 140
Val Asn Pro Ser Phe Pro Gly Ser Asp Ile Asn Val Leu Asp Leu Trp
145                 150                 155                 160
Tyr Asn Asn Ile Thr Gly Ala Gly Val Val Ala Ala Ile Val Asp Asp
                165                 170                 175
Gly Leu Asp Tyr Glu Asn Glu Asp Leu Lys Asp Asn Phe Cys Ala Glu
            180                 185                 190
Gly Ser Trp Asp Phe Asn Asp Asn Thr Asn Leu Pro Lys Pro Arg Leu
        195                 200                 205
Ser Asp Asp Tyr His Gly Thr Arg Cys Ala Gly Glu Ile Ala Ala Lys
    210                 215                 220
Lys Gly Asn Asn Phe Cys Gly Val Gly Val Gly Tyr Asn Ala Lys Ile
225                 230                 235                 240
Ser Gly Ile Arg Ile Leu Ser Gly Asp Ile Thr Thr Glu Asp Glu Ala
                245                 250                 255
Ala Ser Leu Ile Tyr Gly Leu Asp Val Asn Asp Ile Tyr Ser Cys Ser
            260                 265                 270
Trp Gly Pro Ala Asp Asp Gly Arg His Leu Gln Gly Pro Ser Asp Leu
        275                 280                 285
Val Lys Lys Ala Leu Val Lys Gly Val Thr Glu Gly Arg Asp Ser Lys
    290                 295                 300
Gly Ala Ile Tyr Val Phe Ala Ser Gly Asn Gly Gly Thr Arg Gly Asp
305                 310                 315                 320
Asn Cys Asn Tyr Asp Gly Tyr Thr Asn Ser Ile Tyr Ser Ile Thr Ile
                325                 330                 335
Gly Ala Ile Asp His Lys Asp Leu His Pro Pro Tyr Ser Glu Gly Cys
            340                 345                 350
Ser Ala Val Met Ala Val Thr Tyr Ser Ser Gly Ser Gly Glu Tyr Ile
        355                 360                 365
His Ser Ser Asp Ile Asn Gly Arg Cys Ser Asn Ser His Gly Gly Thr
    370                 375                 380
Ser Ala Ala Ala Pro Leu Ala Ala Gly Val Tyr Thr Leu Leu Leu Glu
385                 390                 395                 400
Ala Asn Pro Asn Leu Thr Trp Arg Asp Val Gln Tyr Leu Ser Ile Leu
                405                 410                 415
Ser Ala Val Gly Leu Glu Lys Asn Ala Asp Gly Asp Trp Arg Asp Ser
            420                 425                 430
Ala Met Gly Lys Lys Tyr Ser His Arg Tyr Gly Phe Gly Lys Ile Asp
        435                 440                 445
Ala His Lys Leu Ile Glu Met Ser Lys Thr Trp Glu Asn Val Asn Ala
    450                 455                 460
Gln Thr Trp Phe Tyr Leu Pro Thr Leu Tyr Val Ser Gln Ser Thr Asn
465                 470                 475                 480
Ser Thr Glu Glu Thr Leu Glu Ser Val Ile Thr Ile Ser Glu Lys Ser
                485                 490                 495
Leu Gln Asp Ala Asn Phe Lys Arg Ile Glu His Val Thr Val Thr Val
            500                 505                 510
Asp Ile Asp Thr Glu Ile Arg Gly Thr Thr Thr Val Asp Leu Ile Ser
        515                 520                 525
Pro Ala Gly Ile Ile Ser Asn Leu Gly Val Val Arg Pro Arg Asp Val
    530                 535                 540
Ser Ser Glu Gly Phe Lys Asp Trp Thr Phe Met Ser Val Ala His Trp
545                 550                 555                 560
Gly Glu Asn Gly Val Gly Asp Trp Lys Ile Lys Val Lys Thr Thr Glu
                565                 570                 575
Asn Gly His Arg Ile Asp Phe His Ser Trp Arg Leu Lys Leu Phe Gly
```

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            580                 585                 590
Glu Ser Ile Asp Ser Ser Lys Thr Glu Thr Phe Val Phe Gly Asn Asp
        595                 600                 605
Lys Glu Glu Val Glu Pro Ala Ala Thr Glu Ser Thr Val Ser Gln Tyr
    610                 615                 620
Ser Ala Ser Ser Thr Ser Ile Ser Ile Ser Ala Thr Ser Thr Ser Ser
625                 630                 635                 640
Ile Ser Ile Gly Val Glu Thr Ser Ala Ile Pro Gln Thr Thr Thr Ala
                645                 650                 655
Ser Thr Asp Pro Asp Ser Asp Pro Asn Thr Pro Lys Lys Leu Ser Ser
            660                 665                 670
Pro Arg Gln Ala Met His Tyr Phe Leu Thr Ile Phe Leu Ile Gly Ala
        675                 680                 685
Thr Phe Leu Val Leu Tyr Phe Met Phe Phe Met Lys Ser Arg Arg Arg
    690                 695                 700
Ile Arg Arg Ser Arg Ala Glu Thr Tyr Glu Phe Asp Ile Ile Asp Thr
705                 710                 715                 720
Asp Ser Glu Tyr Asp Ser Thr Leu Asp Asn Gly Thr Ser Gly Ile Thr
                725                 730                 735
Glu Pro Glu Glu Val Glu Asp Phe Asp Phe Asp Leu Ser Asp Glu Asp
            740                 745                 750
His Leu Ala Ser Leu Ser Ser Ser Glu Asn Gly Asp Ala Glu His Thr
        755                 760                 765
Ile Asp Ser Val Leu Thr Asn Glu Asn Pro Phe Ser Asp Pro Ile Lys
    770                 775                 780
Gln Lys Phe Pro Asn Asp Ala Asn Ala Glu Ser Ala Ser Asn Lys Leu
785                 790                 795                 800
Gln Glu Leu Gln Pro Asp Val Pro Pro Ser Ser Gly Arg Ser
                805                 810
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<210> 326
<211> 2848
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<223> Kexin precursor (KEX2 protease) S08.048

<400> 326
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ttgtttttg gcctcgtcac ataattataa actactaacc cattatcaga tgaaagtgag 180
gaaatatatt actttatgct tttggtgggc cttttcaaca tccgctcttg tatcatcaca 240
acaaattcca ttgaaggacc atacgtcacg acagtatttt gctgtagaaa gcaatgaaac 300
attatcccgc ttggaggaaa tgcatccaaa ttggaaatat gaacatgatg ttcgagggct 360
accaaaccat tatgtttttt caaaagagtt gctaaaattg ggcaaaagat catcattaga 420
agagttacag ggggataaca acgaccacat attatctgtc catgatttat tcccgcgtaa 480
cgacctattt aagagactac cggtgcctgc tccaccaatg gactcaagct tgttaccggt 540
aaaagaagct gaggataaac tcagcataaa tgatccgctt tttgagaggc agtggcactt 600
ggtcaatcca agttttcctg gcagtgatat aaatgttctt gatctgtggt acaataatat 660
tacaggcgca ggggtcgtgg ctgccattgt tgatgatggc cttgactacg aaaatgaaga 720
cttgaaggat aatttttgcg ctgaaggttc ttgggatttc aacgacaata ccaatttacc 780
taaaccaaga ttatctgatg actaccatgg tacgagatgt gcaggtgaaa tagctgccaa 840
aaaaggtaac aatttttgcg gtgtcggggt aggttacaac gctaaaatct caggcataag 900
aatcttatcc ggtgatatca ctacggaaga tgaagctgcg tccttgattt atggtctaga 960
```

```
cgtaaacgat atatattcat gctcatgggg tcccgctgat gacggaagac atttacaagg 1020
ccctagtgac ctggtgaaaa aggctttagt aaaaggtgtt actgagggaa gagattccaa 1080
aggagcgatt tacgtttttg ccagtggaaa tggtggaact cgtggtgata attgcaatta 1140
cgacggctat actaattcca tatattctat tactattggg gctattgatc acaaagatct 1200
acatcctcct tattccgaag gttgttccgc cgtcatggca gtcacgtatt cttcaggttc 1260
aggcgaatat attcattcga gtgatatcaa cggcagatgc agtaatagcc acggtggaac 1320
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cctaacttgg agagacgtac agtatttatc aatcttgtct gcggtagggt tagaaaagaa 1440
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gacattagaa tccgtcataa ccatatcaga aaaaagtctt caagatgcta acttcaagag 1680
aattgagcac gtcacggtaa ctgtagatat tgatacagaa attaggggaa ctacgactgt 1740
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gatcagaagg tcaagagcgg aaacgtatga attcgatatc attgatacag actctgagta 2340
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cgattttgat ttgtccgatg aagaccatct tgcaagtttg tcttcatcag aaaacggtga 2460
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gcaaaagttc ccaaatgacg ccaacgcaga atctgcttcc aataaattac aagaattaca 2580
gcctgatgtt cctccatctt ccggacgatc gtgattcgat atgtacagaa agcttcaaat 2640
tacaaaatag catttttttc ttatagatta taatactctc tcatacgtat acgtatatgt 2700
gtatatgata tataaacaaa cattaatatc ctattccttc cgtttgaaat ccctatgatg 2760
tactttgcat tgtttgcacc cgcgaataaa atgaaaactc cgaaccgata tatcaagcac 2820
ataaaagggg agggtccaat taatgcat                                    2848
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<210> 327
<211> 794
<212> PRT
<213> Homo sapiens

<220>
<223> Furin precursor S08.071

<400> 327

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Met Glu Leu Arg Pro Trp Leu Leu Trp Val Val Ala Ala Thr Gly Thr
 1               5                  10                  15
Leu Val Leu Leu Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn
            20                  25                  30
Thr Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn Ser Val
        35                  40                  45
Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln Ile Phe Gly Asp Tyr
    50                  55                  60
Tyr His Phe Trp His Arg Gly Val Thr Lys Arg Ser Leu Ser Pro His
65                  70                  75                  80
Arg Pro Arg His Ser Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu
                85                  90                  95
Glu Gln Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln Glu
            100                 105                 110
Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu Ser Gly Val Thr
```

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        115                 120                 125
Gln Arg Asp Leu Asn Val Lys Ala Ala Trp Ala Gln Gly Tyr Thr Gly
    130                 135                 140
His Gly Ile Val Val Ser Ile Leu Asp Asp Gly Ile Glu Lys Asn His
145                 150                 155                 160
Pro Asp Leu Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
                165                 170                 175
Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met Asn Asp Asn
            180                 185                 190
Arg His Gly Thr Arg Cys Ala Gly Glu Val Ala Ala Val Ala Asn Asn
        195                 200                 205
Gly Val Cys Gly Val Gly Val Ala Tyr Asn Ala Arg Ile Gly Gly Val
    210                 215                 220
Arg Met Leu Asp Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu
225                 230                 235                 240
Gly Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp Gly Pro
                245                 250                 255
Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala Arg Leu Ala Glu Glu
            260                 265                 270
Ala Phe Phe Arg Gly Val Ser Gln Gly Arg Gly Gly Leu Gly Ser Ile
        275                 280                 285
Phe Val Trp Ala Ser Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn
    290                 295                 300
Cys Asp Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser Ala
305                 310                 315                 320
Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala Cys Ser Ser Thr
                325                 330                 335
Leu Ala Thr Thr Tyr Ser Ser Gly Asn Gln Asn Glu Lys Gln Ile Val
            340                 345                 350
Thr Thr Asp Leu Arg Gln Lys Cys Thr Glu Ser His Thr Gly Thr Ser
        355                 360                 365
Ala Ser Ala Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
    370                 375                 380
Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val Val Gln Thr
385                 390                 395                 400
Ser Lys Pro Ala His Leu Asn Ala Asn Asp Trp Ala Thr Asn Gly Val
                405                 410                 415
Gly Arg Lys Val Ser His Ser Tyr Gly Tyr Gly Leu Leu Asp Ala Gly
            420                 425                 430
Ala Met Val Ala Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg
        435                 440                 445
Lys Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly Lys Arg
    450                 455                 460
Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu Gly Glu Pro Asn His
465                 470                 475                 480
Ile Thr Arg Leu Glu His Ala Gln Ala Arg Leu Thr Leu Ser Tyr Asn
                485                 490                 495
Arg Arg Gly Asp Leu Ala Ile His Leu Val Ser Pro Met Gly Thr Arg
            500                 505                 510
Ser Thr Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly Phe
        515                 520                 525
Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp Glu Asp Pro Ser
    530                 535                 540
Gly Glu Trp Val Leu Glu Ile Glu Asn Thr Ser Glu Ala Asn Asn Tyr
545                 550                 555                 560
Gly Thr Leu Thr Lys Phe Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu
                565                 570                 575
```

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Gly Leu Pro Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
            580                 585                 590
Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu His Gln Lys
        595                 600                 605
Ser Cys Val Gln His Cys Pro Pro Gly Phe Ala Pro Gln Val Leu Asp
    610                 615                 620
Thr His Tyr Ser Thr Glu Asn Asp Val Glu Thr Ile Arg Ala Ser Val
625                 630                 635                 640
Cys Ala Pro Cys His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu
                645                 650                 655
Thr Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro Val Glu
            660                 665                 670
Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg Glu Ser Pro Pro Gln
        675                 680                 685
Gln Gln Pro Pro Arg Leu Pro Pro Glu Val Glu Ala Gly Gln Arg Leu
    690                 695                 700
Arg Ala Gly Leu Leu Pro Ser His Leu Pro Glu Val Val Ala Gly Leu
705                 710                 715                 720
Ser Cys Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val Leu
                725                 730                 735
Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys Val Tyr Thr Met
            740                 745                 750
Asp Arg Gly Leu Ile Ser Tyr Lys Gly Leu Pro Pro Glu Ala Trp Gln
        755                 760                 765
Glu Glu Cys Pro Ser Asp Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg
    770                 775                 780
Thr Ala Phe Ile Lys Asp Gln Ser Ala Leu
785                 790
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<210> 328
<211> 4180
<212> DNA
<213> Homo sapiens

<220>
<223> Furin precursor S08.071

<400> 328
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ccgggccaca ggcagtgagc aggcacctgg gagccgaggc cctatgacca ggccaaggag 180
acgggcgctc cagggtccca gccacctgtc ccccccatgg agctgaggcc ctggttgcta 240
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gtcttcacca acacgtgggc tgtgcgcatc cctggaggcc cagcggtggc caacagtgtg 360
gcacggaagc atgggttcct caacctgggc cagatcttcg gggactatta ccacttctgg 420
catcgaggag tgacgaagcg gtccctgtcg cctcaccgcc cgcggcacag ccggctgcag 480
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gtgtaccagg agcccacaga ccccaagttt cctcagcagt ggtacctgtc tggtgtcact 600
cagcgggacc tgaatgtgaa ggcggcctgg gcgcagggct acacagggca cggcattgtg 660
gtctccattc tggacgatgg catcgagaag aaccacccgg acttggcagg caattatgat 720
cctggggcca gttttgatgt caatgaccag gaccctgacc cccagcctcg gtacacacag 780
atgaatgaca acaggcacgg cacacggtgt gcgggggaag tggctgcggt ggccaacaac 840
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ggcgaggtga cagatgcagt ggaggcacgc tcgctgggcc tgaaccccaa ccacatccac 960
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```

ctcgccgagg aggccttctt ccgtggggtt agccagggcc gaggggggct gggctccatc 1080
tttgtctggg cctcggggaa cgggggccgg gaacatgaca gctgcaactg cgacggctac 1140
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ttggacgcag gcgccatggt ggccctggcc cagaattgga ccacagtggc cccccagcgg 1560
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aggttttaaa gtgattaaac gtgcagacta tgcaaaccag 4180

<210> 329
<211> 969
<212> PRT

<213> Homo sapiens

<220>
<223> Subtilisin/kexin-like protease PACE4 S08.075

<400> 329
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20 25 30
Ala Gly Gly Ala Gly Gly Pro Gly Phe Arg Pro Leu Ala Pro Arg Pro
35 40 45
Trp Arg Trp Leu Leu Leu Leu Ala Leu Pro Ala Ala Cys Ser Ala Pro
50 55 60
Pro Pro Arg Pro Val Tyr Thr Asn His Trp Ala Val Gln Val Leu Gly
65 70 75 80
Gly Pro Ala Glu Ala Asp Arg Val Ala Ala Ala His Gly Tyr Leu Asn
85 90 95
Leu Gly Gln Ile Gly Asn Leu Glu Asp Tyr Tyr His Phe Tyr His Ser
100 105 110
Lys Thr Phe Lys Arg Ser Thr Leu Ser Ser Arg Gly Pro His Thr Phe
115 120 125
Leu Arg Met Asp Pro Gln Val Lys Trp Leu Gln Gln Gln Glu Val Lys
130 135 140
Arg Arg Val Lys Arg Gln Val Arg Ser Asp Pro Gln Ala Leu Tyr Phe
145 150 155 160
Asn Asp Pro Ile Trp Ser Asn Met Trp Tyr Leu His Cys Gly Asp Lys
165 170 175
Asn Ser Arg Cys Arg Ser Glu Met Asn Val Gln Ala Ala Trp Lys Arg
180 185 190
Gly Tyr Thr Gly Lys Asn Val Val Val Thr Ile Leu Asp Asp Gly Ile
195 200 205
Glu Arg Asn His Pro Asp Leu Ala Pro Asn Tyr Asp Ser Tyr Ala Ser
210 215 220
Tyr Asp Val Asn Gly Asn Asp Tyr Asp Pro Ser Pro Arg Tyr Asp Ala
225 230 235 240
Ser Asn Glu Asn Lys His Gly Thr Arg Cys Ala Gly Glu Val Ala Ala
245 250 255
Ser Ala Asn Asn Ser Tyr Cys Ile Val Gly Ile Ala Tyr Asn Ala Lys
260 265 270
Ile Gly Gly Ile Arg Met Leu Asp Gly Asp Val Thr Asp Val Val Glu
275 280 285
Ala Lys Ser Leu Gly Ile Arg Pro Asn Tyr Ile Asp Ile Tyr Ser Ala
290 295 300
Ser Trp Gly Pro Asp Asp Asp Gly Lys Thr Val Asp Gly Pro Gly Arg
305 310 315 320
Leu Ala Lys Gln Ala Phe Glu Tyr Gly Ile Lys Lys Gly Arg Gln Gly
325 330 335
Leu Gly Ser Ile Phe Val Trp Ala Ser Gly Asn Gly Gly Arg Glu Gly
340 345 350
Asp Tyr Cys Ser Cys Asp Gly Tyr Thr Asn Ser Ile Tyr Thr Ile Ser
355 360 365
Val Ser Ser Ala Thr Glu Asn Gly Tyr Lys Pro Trp Tyr Leu Glu Glu
370 375 380
Cys Ala Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Ala Phe Tyr Glu
385 390 395 400
Arg Lys Ile Val Thr Thr Asp Leu Arg Gln Arg Cys Thr Asp Gly His

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                405                 410                 415
Thr Gly Thr Ser Val Ser Ala Pro Met Val Ala Gly Ile Ile Ala Leu
            420                 425                 430
Ala Leu Glu Ala Asn Ser Gln Leu Thr Trp Arg Asp Val Gln His Leu
        435                 440                 445
Leu Val Lys Thr Ser Arg Pro Ala His Leu Lys Ala Ser Asp Trp Lys
    450                 455                 460
Val Asn Gly Ala Gly His Lys Val Ser His Phe Tyr Gly Phe Gly Leu
465                 470                 475                 480
Val Asp Ala Glu Ala Leu Val Val Glu Ala Lys Lys Trp Thr Ala Val
                485                 490                 495
Pro Ser Gln His Met Cys Val Ala Ala Ser Asp Lys Arg Pro Arg Ser
            500                 505                 510
Ile Pro Leu Val Gln Val Leu Arg Thr Thr Ala Leu Thr Ser Ala Cys
        515                 520                 525
Ala Glu His Ser Asp Gln Arg Val Val Tyr Leu Glu His Val Val Val
    530                 535                 540
Arg Thr Ser Ile Ser His Pro Arg Arg Gly Asp Leu Gln Ile Tyr Leu
545                 550                 555                 560
Val Ser Pro Ser Gly Thr Lys Ser Gln Leu Leu Ala Lys Arg Leu Leu
                565                 570                 575
Asp Leu Ser Asn Glu Gly Phe Thr Asn Trp Glu Phe Met Thr Val His
            580                 585                 590
Cys Trp Gly Glu Lys Ala Glu Gly Gln Trp Thr Leu Glu Ile Gln Asp
        595                 600                 605
Leu Pro Ser Gln Val Arg Asn Pro Glu Lys Gln Gly Lys Leu Lys Glu
    610                 615                 620
Trp Ser Leu Ile Leu Tyr Gly Thr Ala Glu His Pro Tyr His Thr Phe
625                 630                 635                 640
Ser Ala His Gln Ser Arg Ser Arg Met Leu Glu Leu Ser Ala Pro Glu
                645                 650                 655
Leu Glu Pro Pro Lys Ala Ala Leu Ser Pro Ser Gln Val Glu Val Pro
            660                 665                 670
Glu Asp Glu Glu Asp Tyr Thr Ala Gln Ser Thr Pro Gly Ser Ala Asn
        675                 680                 685
Ile Leu Gln Thr Ser Val Cys His Pro Glu Cys Gly Asp Lys Gly Cys
    690                 695                 700
Asp Gly Pro Asn Ala Asp Gln Cys Leu Asn Cys Val His Phe Ser Leu
705                 710                 715                 720
Gly Ser Val Lys Thr Ser Arg Lys Cys Val Ser Val Cys Pro Leu Gly
                725                 730                 735
Tyr Phe Gly Asp Thr Ala Ala Arg Arg Cys Arg Arg Cys His Lys Gly
            740                 745                 750
Cys Glu Thr Cys Ser Ser Arg Ala Ala Thr Gln Cys Leu Ser Cys Arg
        755                 760                 765
Arg Gly Phe Tyr His His Gln Glu Met Asn Thr Cys Val Thr Leu Cys
    770                 775                 780
Pro Ala Gly Phe Tyr Ala Asp Glu Ser Gln Lys Asn Cys Leu Lys Cys
785                 790                 795                 800
His Pro Ser Cys Lys Lys Cys Val Asp Glu Pro Glu Lys Cys Thr Val
                805                 810                 815
Cys Lys Glu Gly Phe Ser Leu Ala Arg Gly Ser Cys Ile Pro Asp Cys
            820                 825                 830
Glu Pro Gly Thr Tyr Phe Asp Ser Glu Leu Ile Arg Cys Gly Glu Cys
        835                 840                 845
His His Thr Cys Gly Thr Cys Val Gly Pro Gly Arg Glu Glu Cys Ile
    850                 855                 860
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His Cys Ala Lys Asn Phe His Phe His Asp Trp Lys Cys Val Pro Ala
865                 870                 875                 880
Cys Gly Glu Gly Phe Tyr Pro Glu Glu Met Pro Gly Leu Pro His Lys
                885                 890                 895
Val Cys Arg Arg Cys Asp Glu Asn Cys Leu Ser Cys Ala Gly Ser Ser
            900                 905                 910
Arg Asn Cys Ser Arg Cys Lys Thr Gly Phe Thr Gln Leu Gly Thr Ser
        915                 920                 925
Cys Ile Thr Asn His Thr Cys Ser Asn Ala Asp Glu Thr Phe Cys Glu
    930                 935                 940
Met Val Lys Ser Asn Arg Leu Cys Glu Arg Lys Leu Phe Ile Gln Phe
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Cys Cys Arg Thr Cys Leu Leu Ala Gly
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<210> 330
<211> 4403
<212> DNA
<213> Homo sapiens

<220>
<223> Subtilisin/kexin-like protease PACE4 S08.075

<400> 330

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<210> 331
<211> 662
<212> PRT
<213> Anabaena variabilis

<220>
<223> Calcium-dependent protease precursor (Trypsin)
S08.79

<400> 331
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Leu Ile Ser Asp Arg Pro Phe Glu Ala Ala Pro Val Ser Pro Gln Ala
        35                  40                  45
Arg Asn Ile Leu Asn Gln Phe Glu Leu Ser Thr Arg Phe Ser Gln Ala
    50                  55                  60
Gly Val Glu Val Leu His Val Lys Glu Pro Ser His Asp Gly Ala Leu
65                  70                  75                  80
Arg Asp Thr Ala Arg Glu Ile Leu Asn Gln Glu Pro Glu Val Gln Phe
                85                  90                  95
Ala Gly Arg Val Leu Ile Asp Pro Val Ser Gln Gln Pro Ile Val Tyr
            100                 105                 110
Thr Glu Asn Leu Phe Val Lys Phe Asp His Glu Glu Asp Val Ser Phe
        115                 120                 125
Cys Gln Glu Ile Leu Gly Arg Tyr Gly Leu Thr Ile Lys Arg Gln Leu
    130                 135                 140
Glu Tyr Ala Arg Asn Ala Tyr Phe Val Ser Ala Pro Ser Asn Thr Gly
145                 150                 155                 160
Leu Ala Ile Phe Asp Ile Ser Glu Arg Leu Leu Asn Glu Glu Ser Val
                165                 170                 175
Glu Leu Cys His Pro Glu Leu Val Arg Glu Phe Arg Gln Arg Gln Ala
            180                 185                 190
Phe Pro Pro Gln Trp His Leu Lys Gln Thr Thr Ile Gly Gly Lys Thr
        195                 200                 205
Ile Asn Ala His Ala Asn Val Glu Ala Ala Trp Lys Leu Ser Asp Gly
    210                 215                 220
Thr Gly Thr Ile Ile Ala Ile Ile Asp Asp Gly Val Asp Ile Asp His
225                 230                 235                 240
Glu Glu Phe Arg Ser Ser Gly Lys Ile Val Ala Pro Arg Asp Val Thr
                245                 250                 255
Arg Lys Thr Asn Phe Pro Thr Pro Gly Asn Arg Asp Asn His Gly Thr
            260                 265                 270
Ala Cys Ala Gly Val Ala Cys Gly Asn Gly Asn Phe Gly Ala Ser Gly
        275                 280                 285
Val Ala Pro Gly Ala Lys Leu Met Pro Ile Arg Phe Val Ser Ala Leu
    290                 295                 300
Gly Ser Gln Asp Glu Ala Asp Ser Phe Val Trp Ala Ala Gln Asn Gly
305                 310                 315                 320
Ala Asp Val Ile Ser Cys Ser Trp Gly Pro Pro Asp Gly Thr Trp Trp
                325                 330                 335
Asp Asp Lys Asp Pro Leu His Lys Gln Lys Val Pro Leu Pro Asp Ser
            340                 345                 350
Thr Arg Leu Ala Met Asp Tyr Ala Ile Asn Lys Gly Arg Asn Gly Lys
        355                 360                 365
Gly Cys Val Ile Leu Phe Ala Ala Gly Asn Gly Asn Glu Ser Val Asp
    370                 375                 380
Asn Asp Gly Tyr Ala Ser Tyr Glu Lys Val Ile Ala Val Ala Ala Cys
385                 390                 395                 400
Asn Asp Phe Gly Thr Arg Ser Ala Tyr Ser Asp Phe Gly Thr Ala Val
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Trp Cys Ala Phe Pro Ser Asn Asn Gly Asn Pro Ser Gln Thr Pro Gly
            420                 425                 430
Ile Trp Thr Ala Asp Arg Thr Gly Val Val Gly Tyr Asn Ser Gly Asn
        435                 440                 445
Thr Asn Leu Gly Asp Gln Ala Gly Asn Tyr Thr Asn Ser Phe Gly Gly
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Thr Ser Ser Ala Cys Pro Gly Ala Ala Gly Val Ala Ala Leu Ile Leu
465                 470                 475                 480
Ser Arg Asn Pro Asn Leu Arg Trp Asp Glu Val Arg Asp Ile Ile Lys
                485                 490                 495
Arg Ser Cys Asp Arg Ile Asp Pro Val Gly Gly Asn Tyr Asn Ala Glu
            500                 505                 510
Gly Arg Ser Pro Phe Tyr Gly Tyr Gly Arg Ile Asn Ala Leu Lys Ala
        515                 520                 525
Val Glu Leu Ala Leu Pro Ala Gln Pro Glu Pro Val Ser Ile Phe Thr
    530                 535                 540
Ala Val Gln Asp Val Pro Ile Asn Asp Leu Gln Ile Ser Gln Leu Ser
545                 550                 555                 560
Leu Ala Ile Ala Asn Thr Asn Pro Ile Lys Ser Ile Lys Val Thr Val
                565                 570                 575
Asp Ile Glu His Thr Tyr Ile Gly Asp Leu Val Val Ser Leu Asn Pro
            580                 585                 590
Pro Ala Glu Ser Gly Val Leu Pro Ile Ile Leu His Asp Arg Lys Gly
        595                 600                 605
Gly Gly Ala Asp Asp Ile Lys Gln Thr Tyr Asp Glu Val Ser Thr Pro
    610                 615                 620
Gly Leu Thr Ala Leu Lys Gly Lys Ile Pro Gln Gly Thr Trp Thr Leu
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Glu Val Ala Asp Lys Ala Gln Ala Asp Thr Gly Lys Ile Arg Ser Leu
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Thr Ile Glu Leu Gly Phe
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<210> 332
<211> 2187
<212> DNA
<213> Anabaena variabilis

<220>
<223> Calcium-dependent protease precursor
(Trypsin) S08.79

<400> 332
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<210> 333
<211> 402
<212> PRT
<213> Rattus norvegicus

<220>
<223> Caspase-1 precursor C14.001

<400> 333

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Arg Val Leu Asn Gln Glu Glu Met Asp Thr Ile Lys Leu Ala Asn Ile
        35                  40                  45
Thr Val Met Glu Lys Ala Arg Asp Leu Cys Asp His Val Thr Lys Lys
    50                  55                  60
Gly Pro Arg Ala Ser Gln Met Phe Ile Thr Tyr Ile Cys Asn Glu Asp
65                  70                  75                  80
Cys Tyr Leu Ala Glu Ile Leu Glu Leu Gln Ser Gly Pro Ser Ala Glu
                85                  90                  95
Thr Val Phe Val Thr Glu Asp Ser Lys Gly Gly His Pro Phe Ser Ser
            100                 105                 110
Glu Thr Lys Glu Lys Leu Asn Lys Glu Gly Gly Ala Phe Pro Gly Pro
        115                 120                 125
Ser Gly Ser Leu Lys Phe Cys Pro Leu Glu Ile Ala Gln Lys Leu Trp
    130                 135                 140
Lys Glu Asn His Ser Glu Ile Tyr Pro Ile Met Lys Thr Pro Thr Arg
145                 150                 155                 160
Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr Asp Phe Gln His Leu Ser
                165                 170                 175
Arg Arg Val Gly Ala Asp Val Asp Leu Arg Glu Met Lys Leu Leu Leu
            180                 185                 190
Gln Asp Leu Gly Tyr Thr Val Lys Val Lys Glu Asn Leu Thr Ala Leu
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        195                 200                 205
Glu Met Thr Lys Glu Leu Lys Glu Phe Ala Ala Cys Pro Glu His Lys
    210                 215                 220
Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Leu Gln Glu
225                 230                 235                 240
Gly Ile Cys Gly Ile Thr Tyr Ser Asn Glu Val Ala Asp Ile Leu Lys
                245                 250                 255
Val Asp Thr Ile Phe Gln Met Met Asn Thr Leu Lys Cys Pro Ser Leu
            260                 265                 270
Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Glu Lys
        275                 280                 285
Gln Gly Val Val Leu Leu Lys Asp Ser Val Gly Asn Ser Glu Glu Gly
    290                 295                 300
Phe Leu Thr Asp Ala Ile Phe Glu Asp Asp Gly Ile Lys Lys Ala His
305                 310                 315                 320
Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp Asn Val
                325                 330                 335
Ser Trp Arg His Pro Val Arg Gly Ser Leu Phe Ile Glu Ser Leu Ile
            340                 345                 350
Lys His Met Lys Glu Tyr Ala Trp Ser Cys Asp Leu Glu Asp Ile Phe
        355                 360                 365
Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Ser Arg Leu Gln Met
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Pro Thr Thr Glu Arg Val Thr Leu Thr Lys Arg Phe Tyr Leu Phe Pro
385                 390                 395                 400
Gly His
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<210> 334
<211> 1209
<212> DNA
<213> Rattus norvegicus

<220>
<223> Caspase-1 precursor C14.001

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<210> 335
<211> 503
<212> PRT
<213> Caenorhabditis elegans

<220>
<223> Cell death protein 3 precursor C14.002

<400> 335

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Lys	Gln	Val	Leu	Asn	Ser	Asp	Asn	Gly	Asp	Met	Ile	Asn	Ser	Cys	Gly
		35					40					45			
Thr	Val	Arg	Glu	Lys	Arg	Arg	Glu	Ile	Val	Lys	Ala	Val	Gln	Arg	Arg
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Gly	Asp	Val	Ala	Phe	Asp	Ala	Phe	Tyr	Asp	Ala	Leu	Arg	Ser	Thr	Gly
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His	Glu	Gly	Leu	Ala	Glu	Val	Leu	Glu	Pro	Leu	Ala	Arg	Ser	Val	Asp
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Ser	Asn	Ala	Val	Glu	Phe	Glu	Cys	Pro	Met	Ser	Pro	Ala	Ser	His	Arg
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Arg	Ser	Arg	Ala	Leu	Ser	Pro	Ala	Gly	Tyr	Thr	Ser	Pro	Thr	Arg	Val
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Gln	Pro	Ser	Ser	Ala	Asn	Ser	Ser	Phe	Thr	Gly	Cys	Ser	Ser	Leu	Gly
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Tyr	Ser	Ser	Ser	Arg	Asn	Arg	Ser	Phe	Ser	Lys	Ala	Ser	Gly	Pro	Thr
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	210					215					220				
Ile	Ser	Arg	Val	Phe	Asp	Glu	Lys	Thr	Met	Tyr	Arg	Asn	Phe	Ser	Ser
225					230					235					240
Pro	Arg	Gly	Met	Cys	Leu	Ile	Ile	Asn	Asn	Glu	His	Phe	Glu	Gln	Met
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Pro	Thr	Arg	Asn	Gly	Thr	Lys	Ala	Asp	Lys	Asp	Asn	Leu	Thr	Asn	Leu
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Phe	Arg	Cys	Met	Gly	Tyr	Thr	Val	Ile	Cys	Lys	Asp	Asn	Leu	Thr	Gly
		275					280					285			
Arg	Gly	Met	Leu	Leu	Thr	Ile	Arg	Asp	Phe	Ala	Lys	His	Glu	Ser	His
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<223> Cell death protein 3 precursor C14.002

<400> 336

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<211> 277
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-3 precursor C14.003

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Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
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Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
65   70   75   80
Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
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Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
            100   105   110
Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
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Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
    130   135   140
Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145   150   155   160
Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
                165   170   175
Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
            180   185   190
Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
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Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
    210   215   220
Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225   230   235   240
Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
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<210> 339
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<213> Homo sapiens

<220>

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Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
    50                  55                  60
Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
65                  70                  75                  80
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Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
145                 150                 155                 160
Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu
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Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
            180                 185                 190
Asp Gly Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn
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Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser
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225                 230                 235                 240
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ctcttaagcc atggagaaga aaatgtaatt tatgggaaag atggtgtcac accaataaag 480
gatttgacag cccactttag gggggataga tgcaaaaccc ttttagagaa acccaaactc 540
ttcttcattc aggcttgccg agggaccgag cttgatgatg ccatccaggc cgactcgggg 600
cccatcaatg acacagatgc taatcctcga tacaagatcc cagtggaagc tgacttcctc 660
ttcgcctatt ccacggttcc aggctattac tcgtggagga gcccaggaag aggctcctgg 720
tttgtgcaag ccctctgctc catcctggag gagcacggaa aagacctgga aatcatgcag 780
atcctcacca gggtgaatga cagagttgcc aggcactttg agtctcagtc tgatgaccca 840
cacttccatg agaagaagca gatcccctgt gtggtctcca tgctcaccaa ggaactctac 900
ttcagtcaat ag                                                    912
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<210> 341

<211> 293
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-6 precursor C14.005

<400> 341
Met Ser Ser Ala Ser Gly Leu Arg Arg Gly His Pro Ala Gly Gly Glu
1 5 10 15
Glu Asn Met Thr Glu Thr Asp Ala Phe Tyr Lys Arg Glu Met Phe Asp
20 25 30
Pro Ala Glu Lys Tyr Lys Met Asp His Arg Arg Arg Gly Ile Ala Leu
35 40 45
Ile Phe Asn His Glu Arg Phe Phe Trp His Leu Thr Leu Pro Glu Arg
50 55 60
Arg Gly Thr Cys Ala Asp Arg Asp Asn Leu Thr Arg Arg Phe Ser Asp
65 70 75 80
Leu Gly Phe Glu Val Lys Cys Phe Asn Asp Leu Lys Ala Glu Glu Leu
85 90 95
Leu Leu Lys Ile His Glu Val Ser Thr Val Ser His Ala Asp Ala Asp
100 105 110
Cys Phe Val Cys Val Phe Leu Ser His Gly Glu Gly Asn His Ile Tyr
115 120 125
Ala Tyr Asp Ala Lys Ile Glu Ile Gln Thr Leu Thr Gly Leu Phe Lys
130 135 140
Gly Asp Lys Cys His Ser Leu Val Gly Lys Pro Lys Ile Phe Ile Ile
145 150 155 160
Gln Ala Cys Arg Gly Asn Gln His Asp Val Pro Val Ile Pro Leu Asp
165 170 175
Val Val Asp Asn Gln Thr Glu Lys Leu Asp Thr Asn Ile Thr Glu Val
180 185 190
Asp Ala Ala Ser Val Tyr Thr Leu Pro Ala Gly Ala Asp Phe Leu Met
195 200 205
Cys Tyr Ser Val Ala Glu Gly Tyr Tyr Ser His Arg Glu Thr Val Asn
210 215 220
Gly Ser Trp Tyr Ile Gln Asp Leu Cys Glu Met Leu Gly Lys Tyr Gly
225 230 235 240
Ser Ser Leu Glu Phe Thr Glu Leu Leu Thr Leu Val Asn Arg Lys Val
245 250 255
Ser Gln Arg Arg Val Asp Phe Cys Lys Asp Pro Ser Ala Ile Gly Lys
260 265 270
Lys Gln Val Pro Cys Phe Ala Ser Met Leu Thr Lys Lys Leu His Phe
275 280 285
Phe Pro Lys Ser Asn
290

<210> 342
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-6 precursor C14.005

<400> 342
ccgagggcgg ggccgggccc gggagcctgt ggcttcagga agaggagggc aaggtgtctg 60
gctgcgcgtt tggctgcaat gagctcggcc tcggggctcc gcagggggca cccggcaggt 120
ggggaagaaa acatgacaga aacagatgcc ttctataaaa gagaaatgtt tgatccggca 180
gaaaagtaca aaatggacca caggaggaga ggaattgctt taatcttcaa tcatgagagg 240
ttcttttggc acttaacact gccagaaagg cggcgcacct gcgcagatag agacaatctt 300
acccgcaggt tttcagatct aggatttgaa gtgaaatgct ttaatgatct taaagcagaa 360
gaactactgc tcaaaattca tgaggtgtca actgttagcc acgcagatgc cgattgcttt 420
gtgtgtgtct tcctgagcca tggcgaaggc aatcacattt atgcatatga tgctaaaatc 480
gaaattcaga cattaactgg cttgttcaaa ggagacaagt gtcacagcct ggttggaaaa 540
cccaagatat ttatcatcca ggcatgtcgg ggaaaccagc acgatgtgcc agtcattcct 600
ttggatgtag tagataatca gacagagaag ttggacacca acataactga ggtggatgca 660
gcctccgttt acacgctgcc tgctggagct gacttcctca tgtgttactc tgttgcagaa 720
ggatattatt ctcaccggga aactgtgaac ggctcatggt acattcaaga tttgtgtgag 780
atgttgggaa aatatggctc ctccttagag ttcacagaac tcctcacact ggtgaacagg 840
aaagtttctc agcgccgagt ggacttttgc aaagacccaa gtgcaattgg aaagaagcag 900
gttccctgtt ttgcctcaat gctaactaaa aagctgcatt tctttccaaa atctaattaa 960
ttaatagagg ctatctaatt tcacactctg tattgaaaat ggctttctca gccaggcgtg 1020
gttactcaca cctgtaatcc cagcactttg ggagtccaag gtgggcggat cacctgaggt 1080
cgggagttcg agaccagcct gaccaacatg gcagaagccc cgcctctact aaaaatgcaa 1140
aaaaaaattt agctaggcat ggcggcgcat gcctgcaatc ccagctactt ggaaggctga 1200
ggcaggagaa tcacttgaac ccaggaggtg gaggctgcgg tgagccgagc attgcgccat 1260
tgcactccag cctgggcaac gagtgaaact ccgtctcaaa aaaaaagaaa atgtctttct 1320
cttccttta tataaatatc gttagggtga agcattatgg tctaatgatt caaatgtttt 1380
aaagtttaat gcctagcaga gaactgcctt aaaaaaaaaa agttcatgtt ggccatggtg 1440
aaagggtttg atatggagaa acaaaatcct caggaaatta gataaataaa aatttataag 1500
catttgtatt atttttaat aaactgcagg gttacacaaa aatct 1545

<210> 343
<211> 452
<212> PRT
<213> Mus musculus

<220>
<223> Caspase-2 precursor C14.006

<400> 343
Met Ala Ala Pro Ser Gly Arg Ser Gln Ser Ser Leu His Arg Lys Gly
 1   5   10   15
Leu Met Ala Ala Asp Arg Arg Ser Arg Ile Leu Ala Val Cys Gly Met
            20   25   30
His Pro Asp His Gln Glu Thr Leu Lys Lys Asn Arg Val Val Leu Ala
        35   40   45
Lys Gln Leu Leu Leu Ser Glu Leu Leu Glu His Leu Leu Glu Lys Asp
    50   55   60
Ile Ile Thr Leu Glu Met Arg Glu Leu Ile Gln Ala Lys Gly Gly Ser
65   70   75   80
Phe Ser Gln Asn Val Glu Leu Leu Asn Leu Leu Pro Lys Arg Gly Pro
                85   90   95
Gln Ala Phe Asp Ala Phe Cys Glu Ala Leu Arg Glu Thr Arg Gln Gly
            100   105   110
His Leu Glu Asp Leu Leu Leu Thr Thr Leu Ser Asp Ile Gln His Val
        115   120   125
Leu Pro Pro Leu Ser Cys Asp Tyr Asp Thr Ser Leu Pro Phe Ser Val
    130   135   140

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Cys Glu Ser Cys Pro Pro His Lys Gln Leu Arg Leu Ser Thr Asp Ala
145                 150                 155                 160
Thr Glu His Ser Leu Asp Asn Gly Asp Gly Pro Pro Cys Leu Leu Val
                165                 170                 175
Lys Pro Cys Thr Pro Glu Phe Tyr Gln Ala His Tyr Gln Leu Ala Tyr
            180                 185                 190
Arg Leu Gln Ser Gln Pro Arg Gly Leu Ala Leu Val Leu Ser Asn Val
        195                 200                 205
His Phe Thr Gly Glu Lys Asp Leu Glu Phe Arg Ser Gly Gly Asp Val
    210                 215                 220
Asp His Thr Thr Leu Val Thr Leu Phe Lys Leu Leu Gly Tyr Asn Val
225                 230                 235                 240
His Val Leu His Asp Gln Thr Ala Gln Glu Met Gln Glu Lys Leu Gln
                245                 250                 255
Asn Phe Ala Gln Leu Pro Ala His Arg Val Thr Asp Ser Cys Val Val
            260                 265                 270
Ala Leu Leu Ser His Gly Val Glu Gly Gly Ile Tyr Gly Val Asp Gly
        275                 280                 285
Lys Leu Leu Gln Leu Gln Glu Val Phe Arg Leu Phe Asp Asn Ala Asn
    290                 295                 300
Cys Pro Ser Leu Gln Asn Lys Pro Lys Met Phe Phe Ile Gln Ala Cys
305                 310                 315                 320
Arg Gly Asp Glu Thr Asp Arg Gly Val Asp Gln Gln Asp Gly Lys Asn
                325                 330                 335
His Thr Gln Ser Pro Gly Cys Glu Glu Ser Asp Ala Gly Lys Glu Glu
            340                 345                 350
Leu Met Lys Met Arg Leu Pro Thr Arg Ser Asp Met Ile Cys Gly Tyr
        355                 360                 365
Ala Cys Leu Lys Gly Asn Ala Ala Met Arg Asn Thr Lys Arg Gly Ser
    370                 375                 380
Trp Tyr Ile Glu Ala Leu Thr Gln Val Phe Ser Glu Arg Ala Cys Asp
385                 390                 395                 400
Met His Val Ala Asp Met Leu Val Lys Val Asn Ala Leu Ile Lys Glu
                405                 410                 415
Arg Glu Gly Tyr Ala Pro Gly Thr Glu Phe His Arg Cys Lys Glu Met
            420                 425                 430
Ser Glu Tyr Cys Ser Thr Leu Cys Gln Gln Leu Tyr Leu Phe Pro Gly
        435                 440                 445
Tyr Pro Pro Thr
    450
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<210> 344
<211> 3395
<212> DNA
<213> Mus musculus

<220>
<223> Caspase-2 precursor C14.006

<400> 344
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gcggctgaca ggaggagcag gattttggca gtgtgtggaa tgcatcctga ccaccaggaa 120
acactgaaaa agaatcgagt ggtgctggcc aagcagctgc tgctgagcga gctgttagaa 180
cacctcctag agaaggacat tatcactttg gaaatgaggg agctcatcca ggccaaaggg 240
ggcagtttca gccagaatgt ggaactcctc aacctgctgc caaagagagg accccaggct 300

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tttgatgcct tctgtgaagc cctgcgggag accaggcagg gtcacttgga agacttactg 360
ctcacaaccc tctcagatat tcagcacgta ctcccaccgt tgagctgtga ctatgacaca 420
agtctccctt tctcggtgtg tgagtcctgc cctcctcaca agcagctccg cctatccaca 480
gatgctacgg aacactcctt agataatggt gatggtcctc cctgtcttct ggtgaagcca 540
tgcactcctg agttttacca ggcacactac cagctggcct ataggttgca atctcagccc 600
cgtggcttgg cactggtgct gagcaatgtg cacttcactg gagagaaaga cctggaattc 660
cgctctggag gggatgtgga ccacactact ctagtcaccc tcttcaagct tttgggctac 720
aatgtccatg tgctacatga ccagaccgca caggaaatgc aagagaaact tcagaatttt 780
gcacagttac ctgcacaccg ggtcacagac tcctgcgtag tggcactcct ctcacatggt 840
gtggaaggtg gcatctatgg tgtagatggc aaactgcttc agctccaaga ggtttttcga 900
ctttttgaca atgctaactg tccaagtcta cagaacaagc caaaaatgtt cttcatccaa 960
gcatgtcgtg gagatgagac agatagaggt gtcgaccagc aagatggaaa gaaccacaca 1020

caatcccctg gatgtgagga gagtgatgct ggcaaagagg agttgatgaa gatgagactg 1080
cctactcgct cagacatgat atgtggctat gcttgcctta aaggtaatgc tgccatgcgg 1140
aacaccaaac ggggttcctg gtacattgag gccctcactc aggtgttctc tgaaagagct 1200
tgtgacatgc acgtggccga catgcttgtt aaggtgaatg cccttatcaa ggagcgtgaa 1260
ggctatgccc ctggcacaga attccaccga tgcaaggaga tgtctgagta ctgtagtact 1320
ctgtgccagc aactctacct gttcccaggc tacccaccca cgtgatgccg cctgctattc 1380
ctgctgttgg aggccactgg accactgggg gcacaatgga gacttctctt cagaatggtt 1440
tttgttctgt ctaccctctc agggatatga gattctccca ggcttgtttc ctgtcagcca 1500
tctctgtctt tgggtatgaa acataaggat ggctcctccg gtgtcgtgtt ctctacctat 1560
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attgtgaaca cagtattatt gtgggaagag ggcatttgga tttctcaatg tttgtgatat 1680
ttttgttccc aaggcatctt aggagtactt ggatcatagc ttttttttct tttcctaaat 1740
cagttaagga gtctcagaga tcatctcctt ttttttccat atctacaacc tcatttttcc 1800
cacagtggag atttggaaga tgtcccaatt taatgtaggt gttttcatct gtcatgaagg 1860
gacagatgag atcctactac ttgcgaagtt tctatgcata cctttaagtt caggccctag 1920
gtgaaggaca gtccctcagc ctttccattg gttcctttgt gttcagtgca cccagccttt 1980
gaacagagcc tagggtctgt atgccatgac actggaagtc atagaaattt ccctggtcat 2040
gctttgtttg aactgtcact gaatgaacct tatcgggcat aactacatga aaatgcagtg 2100
acagctgagt gtgctgtgtc tcacactatc acccgtcatc aggatgtctc tccttcctta 2160
ctgtggcttc tgcatgcact tacactgtac ttgacggctg gcctccaggg tctctcttgc 2220
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gtctctgatt tttgagtctg gcggaggcct cttgaccatg ctgcccatgc tgtctactgt 2820
gcctccttat gagggcatca tgttggtctc tgttgtgctt actgcaggct gtaatggcac 2880
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ttcttactta ctgatatcca gtaactggca cttactaggt cttcatgaat gtttcctgag 3000
taaaggaagg agaccagcag ctaaccttag ttagagccta ccttttgcag tttctaaatt 3060
gctattatag tgtacagttc aattagtata tgggtttttt tttccaggtg ttttatttct 3120
atccactgtt ttgttgttgt ttttttatat tttctacata tcacgtgtga gacaacttct 3180
ttcacatctc catagtgccc agcaaatttg aggcctatgg tagttgaggt gctcaactaa 3240
tgtttgttgt atgaaccaag tggtttgaag acttgctgcc aaattctgcc ttttgggtca 3300
gtataggatg cataagtggt agaatcttca cacttcccac tgccaagatt ttgtattgcc 3360
atcaggtgcc aaataaatgt tgatacttat tactg                          3395
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<210> 345
<211> 377

<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-4 precursor C14.007

<400> 345
Met Ala Glu Gly Asn His Arg Lys Lys Pro Leu Lys Val Leu Glu Ser
1 5 10 15
Leu Gly Lys Asp Phe Leu Thr Gly Val Leu Asp Asn Leu Val Glu Gln
20 25 30
Asn Val Leu Asn Trp Lys Glu Glu Glu Lys Lys Lys Tyr Tyr Asp Ala
35 40 45
Lys Thr Glu Asp Lys Val Arg Val Met Ala Asp Ser Met Gln Glu Lys
50 55 60
Gln Arg Met Ala Gly Gln Met Leu Leu Gln Thr Phe Phe Asn Ile Asp
65 70 75 80
Gln Ile Ser Pro Asn Lys Lys Ala His Pro Asn Met Glu Ala Gly Pro
85 90 95
Pro Glu Ser Gly Glu Ser Thr Asp Ala Leu Lys Leu Cys Pro His Glu
100 105 110
Glu Phe Leu Arg Leu Cys Lys Glu Arg Ala Glu Glu Ile Tyr Pro Ile
115 120 125
Lys Glu Arg Asn Asn Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr
130 135 140
Glu Phe Asp His Leu Pro Pro Arg Asn Gly Ala Asp Phe Asp Ile Thr
145 150 155 160
Gly Met Lys Glu Leu Leu Glu Gly Leu Asp Tyr Ser Val Asp Val Glu
165 170 175
Glu Asn Leu Thr Ala Arg Asp Met Glu Ser Ala Leu Arg Ala Phe Ala
180 185 190
Thr Arg Pro Glu His Lys Ser Ser Asp Ser Thr Phe Leu Val Leu Met
195 200 205
Ser His Gly Ile Leu Glu Gly Ile Cys Gly Thr Val His Asp Glu Lys
210 215 220
Lys Pro Asp Val Leu Leu Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn
225 230 235 240
Arg Asn Cys Leu Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Val Gln
245 250 255
Ala Cys Arg Gly Ala Asn Arg Gly Glu Leu Trp Val Arg Asp Ser Pro
260 265 270
Ala Ser Leu Glu Val Ala Ser Ser Gln Ser Ser Glu Asn Leu Glu Glu
275 280 285
Asp Ala Val Tyr Lys Thr His Val Glu Lys Asp Phe Ile Ala Phe Cys
290 295 300
Ser Ser Thr Pro His Asn Val Ser Trp Arg Asp Ser Thr Met Gly Ser
305 310 315 320
Ile Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys
325 330 335
Cys His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Thr
340 345 350
Pro Arg Ala Lys Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr
355 360 365
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
370 375

<210> 346
<211> 1291
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-4 precursor C14.007

<400> 346
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gaaaaaagcc acttaaggtg ttggaatccc tgggcaaaga tttcctcact ggtgttttgg 120
ataacttggt ggaacaaaat gtactgaact ggaaggaaga ggaaaaaaag aaatattacg 180
atgctaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaatctaca gatgccctca 360
agctttgtcc tcatgaagaa ttcctgagac tatgtaaaga aagagctgaa gagatctatc 420
caataaagga gagaaacaac cgcacacgcc tggctctcat catatgcaat acagagtttg 480
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540
agggtctgga ctatagtgta gatgtagaag agaatctgac agccagggat atggagtcag 600
cgctgagggc atttgctacc agaccagagc acaagtcctc tgacagcaca ttcttggtac 660
tcatgtctca tggcatcctg gagggaatct gcggaactgt gcatgatgag aaaaaaccag 720
atgtgctgct ttatgacacc atcttccaga tattcaacaa ccgcaactgc ctcagtctga 780
aggacaaacc caaggtcatc attgtccagg cctgcagagg tgcaaaccgt ggggaactgt 840
gggtcagaga ctctccagca tccttggaag tggcctcttc acagtcatct gagaacctgg 900
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgctttc tgctcttcaa 960
cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcatc acacaactca 1020
tcacatgctt ccagaaatat tcttggtgct gccacctaga ggaagtattt cggaaggtac 1080
agcaatcatt tgaaactcca agggccaaag ctcaaatgcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaa a 1291

<210> 347
<211> 418
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-5 precursor C14.008

<400> 347
Met Phe Lys Gly Ile Leu Gln Ser Gly Leu Asp Asn Phe Val Ile Asn
1 5 10 15
His Met Leu Lys Asn Asn Val Ala Gly Gln Thr Ser Ile Gln Thr Leu
20 25 30
Val Pro Asn Thr Asp Gln Lys Ser Thr Ser Val Lys Lys Asp Asn His
35 40 45
Lys Lys Lys Thr Val Lys Met Leu Glu Tyr Leu Gly Lys Asp Val Leu
50 55 60
His Gly Val Phe Asn Tyr Leu Ala Lys His Asp Val Leu Thr Leu Lys
65 70 75 80
Glu Glu Glu Lys Lys Lys Tyr Tyr Asp Ala Lys Ile Glu Asp Lys Ala
85 90 95
Leu Ile Leu Val Asp Ser Leu Arg Lys Asn Arg Val Ala His Gln Met
100 105 110
Phe Thr Gln Thr Leu Leu Asn Met Asp Gln Lys Ile Thr Ser Val Lys

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        115                 120                 125
Pro Leu Leu Gln Ile Glu Ala Gly Pro Pro Glu Ser Ala Glu Ser Thr
    130                 135                 140
Asn Ile Leu Lys Leu Cys Pro Arg Glu Glu Phe Leu Arg Leu Cys Lys
145                 150                 155                 160
Lys Asn His Asp Glu Ile Tyr Pro Ile Lys Lys Arg Glu Asp Arg Arg
                165                 170                 175
Arg Leu Ala Leu Ile Ile Cys Asn Thr Lys Phe Asp His Leu Pro Ala
            180                 185                 190
Arg Asn Gly Ala His Tyr Asp Ile Val Gly Met Lys Arg Leu Leu Gln
        195                 200                 205
Gly Leu Gly Tyr Thr Val Val Asp Glu Lys Asn Leu Thr Ala Arg Asp
    210                 215                 220
Met Glu Ser Val Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser
225                 230                 235                 240
Ser Asp Ser Thr Phe Leu Val Leu Met Ser His Gly Ile Leu Glu Gly
                245                 250                 255
Ile Cys Gly Thr Ala His Lys Lys Lys Lys Pro Asp Val Leu Leu Tyr
            260                 265                 270
Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu Lys
        275                 280                 285
Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Lys His
    290                 295                 300
Gly Glu Leu Trp Val Arg Asp Ser Pro Ala Ser Leu Ala Val Ile Ser
305                 310                 315                 320
Ser Gln Ser Ser Glu Asn Leu Glu Ala Asp Ser Val Cys Lys Ile His
                325                 330                 335
Glu Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro His Asn Val
            340                 345                 350
Ser Trp Arg Asp Arg Thr Arg Gly Ser Ile Phe Ile Thr Glu Leu Ile
        355                 360                 365
Thr Cys Phe Gln Lys Tyr Ser Cys Cys Cys His Leu Met Glu Ile Phe
    370                 375                 380
Arg Lys Val Gln Lys Ser Phe Glu Val Pro Gln Ala Lys Ala Gln Met
385                 390                 395                 400
Pro Thr Ile Glu Arg Ala Thr Leu Thr Arg Asp Phe Tyr Leu Phe Pro
                405                 410                 415
Gly Asn
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<210> 348
<211> 1400
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-5 precursor C14.008

<400> 348
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ccagacccta gtacctaata cggatcaaaa gtcgaccagt gtaaaaaaag acaaccacaa 180
aaaaaaaaca gttaagatgt tggaatacct gggcaaagat gttcttcatg gtgtttttaa 240
ttatttggca aaacacgatg ttctgacatt gaaggaagag gaaaagaaaa aatattatga 300

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tgccaaaatt gaagacaagg ccctgatctt ggtagactct ttgcgaaaga atcgcgtggc 360
tcatcaaatg tttacccaaa cacttctcaa tatggaccaa aagatcacca gtgtaaaacc 420
tcttctgcaa atcgaggctg gaccacctga gtcagcagaa tctacaaata tactcaaact 480
ttgtcctcgt gaagaattcc tgagactgtg taaaaaaaat catgatgaga tctatccaat 540
aaaaaagaga gaggaccgca gacgcctggc tctcatcata tgcaatacaa agtttgatca 600
cctgcctgca aggaatgggg ctcactatga catcgtgggg atgaaaaggc tgcttcaagg 660
cctgggctac actgtggttg acgaaaagaa tctcacagcc agggatatgg agtcagtgct 720
gagggcattt gctgccagac cagagcacaa gtcctctgac agcacgttct tggtactcat 780
gtctcatggc atcctagagg gaatctgcgg aactgcgcat aaaaagaaaa aaccggatgt 840
gctgctttat gacaccatct tccagatatt caacaaccgc aactgcctca gtctaaagga 900
caaacccaag gtcatcattg tccaggcctg cagaggtgaa aaacatgggg aactctgggt 960
cagagactct ccagcatcct tggcagtcat ctcttcacag tcatctgaga acctggaggc 1020
agattctgtt tgcaagatcc acgaggagaa ggacttcatt gctttctgtt cttcaacacc 1080
acataacgtg tcctggagag accgcacaag gggctccatc ttcattacgg aactcatcac 1140
atgcttccag aaatattctt gctgctgcca cctaatggaa atatttcgga aggtacagaa 1200
atcatttgaa gttccacagg ctaaagccca gatgcccacc atagaacgag caaccttgac 1260
aagagatttc tacctctttc ctggcaattg aaaatgaaac cacaggcagc ccagccctcc 1320
tctgtcaaca tcaaagagca catttaccag tatagcttgc atagtcaata tttggtattt 1380
caataaaagt aaagactgta                                            1400

<210> 349
<211> 479
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-8 precursor   C14.009

<400>  349
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Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu
        35                  40                  45
Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu
    50                  55                  60
Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr Leu Asn
65                  70                  75                  80
Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln Thr Pro Gly Arg Ala
                85                  90                  95
Gln Ile Ser Ala Tyr Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val
            100                 105                 110
Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile
        115                 120                 125
Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile
    130                 135                 140
Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu
145                 150                 155                 160
Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys Ile Ile Asn
                165                 170                 175
Asp Tyr Glu Glu Phe Ser Lys Glu Arg Ser Ser Ser Leu Glu Gly Ser
            180                 185                 190
Pro Asp Glu Phe Ser Asn Gly Glu Glu Leu Cys Gly Val Met Thr Ile
        195                 200                 205
Ser Asp Ser Pro Arg Glu Gln Asp Ser Glu Ser Gln Thr Leu Asp Lys
    210                 215                 220
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Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile Asn
225                 230                 235                 240
Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His Ser
                245                 250                 255
Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Ala Leu Thr Thr
            260                 265                 270
Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro His Asp Asp Cys Thr
        275                 280                 285
Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr Gln Leu Met Asp His
    290                 295                 300
Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu Ser His Gly Asp Lys
305                 310                 315                 320
Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala Pro Ile Tyr Glu Leu
                325                 330                 335
Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser Leu Ala Gly Lys Pro
            340                 345                 350
Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp Asn Tyr Gln Lys Gly
        355                 360                 365
Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met Asp
    370                 375                 380
Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp Glu Ala Asp Phe Leu
385                 390                 395                 400
Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser Tyr Arg Asn Pro Ala
                405                 410                 415
Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln Ser Leu Arg Glu Arg
            420                 425                 430
Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn Tyr
        435                 440                 445
Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met Pro
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Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Ser Asp
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<210> 350
<211> 2887
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-8 precursor C14.009

<400> 350

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cccacccccct tccctgctga gcacgtggag ttaggcaggt taggggactc ggagactgcg 240
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ttattccaga gactccagga aaagagaatg ttggaggaaa gcaatctgtc cttcctgaag 480
gagctgctct tccgaattaa tagactggat ttgctgatta cctacctaaa cactagaaag 540
gaggagatgg aaagggaact tcagacacca ggcagggctc aaatttctgc ctacagggtc 600
atgctctatc agatttcaga agaagtgagc agatcagaat tgaggtcttt taagtttctt 660
ttgcaagagg aaatctccaa atgcaaactg gatgatgaca tgaacctgct ggatattttc 720
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gagagaagca gcagccttga aggaagtcct gatgaatttt caaatgggga ggagttgtgt 900
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<210> 351
<211> 416
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-9 precursor
C14.010

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20 25 30
Glu Leu Phe Arg Pro His Met Ile Glu Asp Ile Gln Arg Ala Gly Ser
35 40 45
Gly Ser Arg Arg Asp Gln Ala Arg Gln Leu Ile Ile Asp Leu Glu Thr
50 55 60

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Arg Gly Ser Gln Ala Leu Pro Leu Phe Ile Ser Cys Leu Glu Asp Thr
65                  70                  75                  80
Gly Gln Asp Met Leu Ala Ser Phe Leu Arg Thr Asn Arg Gln Ala Ala
                85                  90                  95
Lys Leu Ser Lys Pro Thr Leu Glu Asn Leu Thr Pro Val Val Leu Arg
            100                 105                 110
Pro Glu Ile Arg Lys Pro Glu Val Leu Arg Pro Glu Thr Pro Arg Pro
        115                 120                 125
Val Asp Ile Gly Ser Gly Gly Phe Gly Asp Val Gly Ala Leu Glu Ser
    130                 135                 140
Leu Arg Gly Asn Ala Asp Leu Ala Tyr Ile Leu Ser Met Glu Pro Cys
145                 150                 155                 160
Gly His Cys Leu Ile Ile Asn Asn Val Asn Phe Cys Arg Glu Ser Gly
                165                 170                 175
Leu Arg Thr Arg Thr Gly Ser Asn Ile Asp Cys Glu Lys Leu Arg Arg
            180                 185                 190
Arg Phe Ser Ser Leu His Phe Met Val Glu Val Lys Gly Asp Leu Thr
        195                 200                 205
Ala Lys Lys Met Val Leu Ala Leu Leu Glu Leu Ala Gln Gln Asp His
    210                 215                 220
Gly Ala Leu Asp Cys Cys Val Val Val Ile Leu Ser His Gly Cys Gln
225                 230                 235                 240
Ala Ser His Leu Gln Phe Pro Gly Ala Val Tyr Gly Thr Asp Gly Cys
                245                 250                 255
Pro Val Ser Val Glu Lys Ile Val Asn Ile Phe Asn Gly Thr Ser Cys
            260                 265                 270
Pro Ser Leu Gly Gly Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gly
        275                 280                 285
Gly Glu Gln Lys Asp His Gly Phe Glu Val Ala Ser Thr Ser Pro Glu
    290                 295                 300
Asp Glu Ser Pro Gly Ser Asn Pro Glu Pro Asp Ala Thr Pro Phe Gln
305                 310                 315                 320
Glu Gly Leu Arg Thr Phe Asp Gln Leu Asp Ala Ile Ser Ser Leu Pro
                325                 330                 335
Thr Pro Ser Asp Ile Phe Val Ser Tyr Ser Thr Phe Pro Gly Phe Val
            340                 345                 350
Ser Trp Arg Asp Pro Lys Ser Gly Ser Trp Tyr Val Glu Thr Leu Asp
        355                 360                 365
Asp Ile Phe Glu Gln Trp Ala His Ser Glu Asp Leu Gln Ser Leu Leu
    370                 375                 380
Leu Arg Val Ala Asn Ala Val Ser Val Lys Gly Ile Tyr Lys Gln Met
385                 390                 395                 400
Pro Gly Cys Phe Asn Phe Leu Arg Lys Lys Leu Phe Phe Lys Thr Ser
                405                 410                 415
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<210> 352
<211> 1481
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-9 precursor C14.010

<400> 352
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atagatctgg agactcgagg gagtcaggct cttcctttgt tcatctcctg cttagaggac 240
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gttctcagac cggaaacacc cagaccagtg gacattggtt ctggaggatt cggtgatgtc 420
ggtgctcttg agagtttgag gggaaatgca gatttggctt acatcctgag catggagccc 480
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cgcactggct ccaacatcga ctgtgagaag ttgcggcgtc gcttctcctc gctgcatttc 600
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<210> 353
<211> 521
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-10 precursor C14.011

<400> 353

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            20                  25                  30
Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro
        35                  40                  45
Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His
    50                  55                  60
Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala
65                  70                  75                  80
Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln His Leu Asn
                85                  90                  95
Cys Thr Lys Glu Glu Val Glu Arg Leu Leu Pro Thr Arg Gln Arg Val
            100                 105                 110
Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp Ser
        115                 120                 125
Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro Lys
    130                 135                 140
Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln Gly
145                 150                 155                 160
Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys Thr
                165                 170                 175
Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys Arg Glu Lys
```

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            180                 185                 190
Ala Ile Gln Ile Val Thr Pro Pro Val Asp Lys Glu Ala Glu Ser Tyr
        195                 200                 205
Gln Gly Glu Glu Glu Leu Val Ser Gln Thr Asp Val Lys Thr Phe Leu
    210                 215                 220
Glu Ala Leu Pro Gln Glu Ser Trp Gln Asn Lys His Ala Gly Ser Asn
225                 230                 235                 240
Gly Asn Arg Ala Thr Asn Gly Ala Pro Ser Leu Val Ser Arg Gly Met
                245                 250                 255
Gln Gly Ala Ser Ala Asn Thr Leu Asn Ser Glu Thr Ser Thr Lys Arg
            260                 265                 270
Ala Ala Val Tyr Arg Met Asn Arg Asn His Arg Gly Leu Cys Val Ile

        275                 280                 285
Val Asn Asn His Ser Phe Thr Ser Leu Lys Asp Arg Gln Gly Thr His
    290                 295                 300
Lys Asp Ala Glu Ile Leu Ser His Val Phe Gln Trp Leu Gly Phe Thr
305                 310                 315                 320
Val His Ile His Asn Asn Val Thr Lys Val Glu Met Glu Met Val Leu
                325                 330                 335
Gln Lys Gln Lys Cys Asn Pro Ala His Ala Asp Gly Asp Cys Phe Val
            340                 345                 350
Phe Cys Ile Leu Thr His Gly Arg Phe Gly Ala Val Tyr Ser Ser Asp
        355                 360                 365
Glu Ala Leu Ile Pro Ile Arg Glu Ile Met Ser His Phe Thr Ala Leu
    370                 375                 380
Gln Cys Pro Arg Leu Ala Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala
385                 390                 395                 400
Cys Gln Gly Glu Glu Ile Gln Pro Ser Val Ser Ile Glu Ala Asp Ala
                405                 410                 415
Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln Asp Ser Ile Pro Ala
            420                 425                 430
Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val Pro Gly Tyr Val Ser
        435                 440                 445
Phe Arg His Val Glu Glu Gly Ser Trp Tyr Ile Gln Ser Leu Cys Asn
    450                 455                 460
His Leu Lys Lys Leu Val Pro Arg Met Leu Lys Phe Leu Glu Lys Thr
465                 470                 475                 480
Met Glu Ile Arg Gly Arg Lys Arg Thr Val Trp Gly Ala Lys Gln Ile
                485                 490                 495
Ser Ala Thr Ser Leu Pro Thr Ala Ile Ser Ala Gln Thr Pro Arg Pro
            500                 505                 510
Pro Met Arg Arg Trp Ser Ser Val Ser
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<210> 354
<211> 3536
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-10 precursor C14.011

<400> 354
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tttataatta tttatgtgaa agtcaaattc atgtacagta aatttgttat aagaat 3536

<210> 355
<211> 373
<212> PRT
<213> Mus musculus

<220>
<223> Caspase-11 C14.012

<400> 355

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            20                  25                  30
Asn Val Leu Lys Leu Lys Glu Glu Asp Lys Gln Lys Phe Asn Asn Ala
        35                  40                  45
Glu Arg Ser Asp Lys Arg Trp Val Phe Val Asp Ala Met Lys Lys Lys
    50                  55                  60
His Ser Lys Val Gly Glu Met Leu Leu Gln Thr Phe Phe Ser Val Asp
65                  70                  75                  80
Pro Gly Ser His His Gly Glu Ala Asn Leu Glu Met Glu Glu Pro Glu
                85                  90                  95
Glu Ser Leu Asn Thr Leu Lys Leu Cys Ser Pro Glu Glu Phe Thr Arg
            100                 105                 110
Leu Cys Arg Glu Lys Thr Gln Glu Ile Tyr Pro Ile Lys Glu Ala Asn
        115                 120                 125
Gly Arg Thr Arg Lys Ala Leu Ile Ile Cys Asn Thr Glu Phe Lys His
    130                 135                 140
Leu Ser Leu Arg Tyr Gly Ala Lys Phe Asp Ile Ile Gly Met Lys Gly
145                 150                 155                 160
Leu Leu Glu Asp Leu Gly Tyr Asp Val Val Val Lys Glu Glu Leu Thr
                165                 170                 175
Ala Glu Gly Met Glu Ser Glu Met Lys Asp Phe Ala Ala Leu Ser Glu
            180                 185                 190
His Gln Thr Ser Asp Ser Thr Phe Leu Val Leu Met Ser His Gly Thr
        195                 200                 205
Leu His Gly Ile Cys Gly Thr Met His Ser Glu Lys Thr Pro Asp Val
    210                 215                 220
Leu Gln Tyr Asp Thr Ile Tyr Gln Ile Phe Asn Asn Cys His Cys Pro
225                 230                 235                 240
Gly Leu Arg Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly
                245                 250                 255
Gly Asn Ser Gly Glu Met Trp Ile Arg Glu Ser Ser Lys Pro Gln Leu
            260                 265                 270
Cys Arg Gly Val Asp Leu Pro Arg Asn Met Glu Ala Asp Ala Val Lys
        275                 280                 285
Leu Ser His Val Glu Lys Asp Phe Ile Ala Phe Tyr Ser Thr Thr Pro
    290                 295                 300
His His Leu Ser Tyr Arg Asp Lys Thr Gly Gly Ser Tyr Phe Ile Thr
305                 310                 315                 320
Arg Leu Ile Ser Cys Phe Arg Lys His Ala Cys Ser Cys His Leu Phe
                325                 330                 335
Asp Ile Phe Leu Lys Val Gln Gln Ser Phe Glu Lys Ala Ser Ile His
            340                 345                 350
```

```
Ser Gln Met Pro Thr Ile Asp Arg Ala Thr Leu Thr Arg Tyr Phe Tyr
        355                 360                 365
Leu Phe Pro Gly Asn
    370
```

<210> 356
<211> 1350
<212> DNA
<213> Mus musculus

<220>
<223> Caspase-11 C14.012

<400> 356
tcttcacagt gcgaaagaac tgaggctttt tctcatggct gaaaacaaac accctgacaa 60
accacttaag gtgttggaac agctgggcaa agaagtcctt acggagtacc tagaaaaatt 120
agtacaaagc aatgtactga aattaaagga ggaagataaa caaaaattta acaatgctga 180
acgcagtgac aagcgttggg tttttgtaga tgccatgaaa aagaaacaca gcaaagtagg 240
tgaaatgctt ctccagacat tcttcagtgt ggacccaggc agccaccatg gtgaagctaa 300
tctggaaatg gaggaaccag aagaatcatt gaacactctc aagctttgtt cccctgaaga 360
gttcacaagg ctttgcagag aaaagacaca agaaatttac ccaataaagg aggccaatgg 420
ccgtacacga aaggctctta tcatatgcaa tacagagttc aaacatctct cactgaggta 480
tggggctaaa tttgacatca ttggtatgaa aggccttctt gaagacttag gctacgatgt 540
ggtggtgaaa gaggagctta cagcagaggg catggagtca gagatgaaag actttgctgc 600
actctcagaa caccagacat cagacagcac attcctggtg ctaatgtctc atggcacact 660
gcatggcatt tgtggaacaa tgcacagtga aaaaactcca gatgtgctac agtatgatac 720
catctatcag atattcaaca attgccactg tccaggtcta cgagacaaac ccaaagtcat 780
cattgtgcag gcctgcagag gtgggaactc tggagaaatg tggatcagag agtcttcaaa 840
accccagttg tgcagaggtg tagatctacc taggaatatg gaagctgatg ctgtcaagct 900
gagccacgtg gagaaggact tcattgcctt ctactctaca accccacatc acttgtccta 960
ccgagacaaa acaggaggct cttacttcat cactagactc atttcctgct tccggaaaca 1020
tgcttgctct tgtcatctct ttgatatatt cctgaaggtg caacaatcat ttgaaaaggc 1080
aagtattcat tcccagatgc ccaccattga tcgggcaacc ttgacaagat atttctacct 1140
ctttcctggc aactgagaac aaagcaacaa gcaactgaat ctcatttctt cagcttgaag 1200
aagtgatctt ggccaaggat cacattctat tcctgaaatt ccagaactag tgaaattaag 1260
gaaagaatac ttatgaattc aagaccagcc taagcaacac agtgggattc tgttccatag 1320
acaagcaaac aagcaaaaat aaaaaaaaaa   1350

<210> 357
<211> 419
<212> PRT
<213> Mus musculus

<220>
<223> Caspase-12 precursor
      C14.013

<400> 357
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Met Ala Ala Arg Arg Thr His Glu Arg Asp Pro Ile Tyr Lys Ile Lys
 1               5                  10                  15
Gly Leu Ala Lys Asp Met Leu Asp Gly Val Phe Asp Asp Leu Val Glu
            20                  25                  30
Lys Asn Val Leu Asn Gly Asp Glu Leu Leu Lys Ile Gly Glu Ser Ala
        35                  40                  45
Ser Phe Ile Leu Asn Lys Ala Glu Asn Leu Val Glu Asn Phe Leu Glu
```

```
     50                  55                  60
Lys Thr Asp Met Ala Gly Lys Ile Phe Ala Gly His Ile Ala Asn Ser
65                  70                  75                  80
Gln Glu Gln Leu Ser Leu Gln Phe Ser Asn Asp Glu Asp Asp Gly Pro
                85                  90                  95
Gln Lys Ile Cys Thr Pro Ser Ser Pro Ser Glu Ser Lys Arg Lys Val
            100                 105                 110
Glu Asp Asp Glu Met Glu Val Asn Ala Gly Leu Ala His Glu Ser His
        115                 120                 125
Leu Met Leu Thr Ala Pro His Gly Leu Gln Ser Ser Glu Val Gln Asp
    130                 135                 140
Thr Leu Lys Leu Cys Pro Arg Asp Gln Phe Cys Lys Ile Lys Thr Glu
145                 150                 155                 160
Arg Ala Lys Glu Ile Tyr Pro Val Met Glu Lys Glu Gly Arg Thr Arg
                165                 170                 175
Leu Ala Leu Ile Ile Cys Asn Lys Lys Phe Asp Tyr Leu Phe Asp Arg
            180                 185                 190
Asp Asn Ala Asp Thr Asp Ile Leu Asn Met Gln Glu Leu Leu Glu Asn
        195                 200                 205
Leu Gly Tyr Ser Val Val Leu Lys Glu Asn Leu Thr Ala Gln Glu Met
    210                 215                 220
Glu Thr Glu Leu Met Gln Phe Ala Gly Arg Pro Glu His Gln Ser Ser
225                 230                 235                 240
Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Glu Gly Ile
                245                 250                 255
Cys Gly Val Lys His Arg Asn Lys Lys Pro Asp Val Leu His Asp Asp
            260                 265                 270
Thr Ile Phe Lys Ile Phe Asn Asn Ser Asn Cys Arg Ser Leu Arg Asn
        275                 280                 285
Lys Pro Lys Ile Leu Ile Met Gln Ala Cys Arg Gly Arg Tyr Asn Gly
    290                 295                 300
Thr Ile Trp Val Ser Thr Asn Lys Gly Ile Ala Thr Ala Asp Thr Asp
305                 310                 315                 320
Glu Glu Arg Val Leu Ser Cys Lys Trp Asn Asn Ser Ile Thr Lys Ala
                325                 330                 335
His Val Glu Thr Asp Phe Ile Ala Phe Lys Ser Ser Thr Pro His Asn
            340                 345                 350
Ile Ser Trp Lys Val Gly Lys Thr Gly Ser Leu Phe Ile Ser Lys Leu
        355                 360                 365
Ile Asp Cys Phe Lys Lys Tyr Cys Trp Cys Tyr His Leu Glu Glu Ile
    370                 375                 380
Phe Arg Lys Val Gln His Ser Phe Glu Val Pro Gly Glu Leu Thr Gln
385                 390                 395                 400
Met Pro Thr Ile Glu Arg Val Ser Met Thr Arg Tyr Phe Tyr Leu Phe
                405                 410                 415
Pro Gly Asn
```

<210> 358
<211> 2228
<212> DNA
<213> Mus musculus

<220>
<223> Caspase-12 precursor C14.013

<400> 358
ggcacgagcg gcacgagcgg cacgagcaca gccatggcgg ccaggaggac acatgaaaga 60
gatccaatct acaagatcaa aggtttggcc aaggacatgc tggatggggt ttttgatgac 120
ctggtggaga agaatgtttt aaatggagat gagttactca aaatagggga aagtgcgagt 180
ttcatcctga acaaggctga gaatctggtt gagaacttct tagagaaaac agacatggca 240
ggaaaaatat ttgctggcca cattgccaat tcccaggaac agctgagttt acaatttttct 300
aatgatgagg atgatggacc tcagaagata tgtacacctt cttctccatc agaatccaag 360
agaaaagtag aggatgatga aatggaggta aatgctggat tggcccatga atcacatcta 420
atgctgacag ctcctcatgg actccagagc tcagaagtcc aagatacact gaagctttgt 480
ccacgtgatc agttttgtaa gataaagaca gaaagggcaa aagagatata tccagtgatg 540
gagaaggagg gacgaacacg tctggctctc atcatctgca acaaaaagtt tgactacctt 600
tttgatagag ataatgctga tactgacatt ttgaacatgc aagaactact tgaaaatctt 660
ggatactctg tggtgttaaa ggaaaacctt acagctcagg aaatggagac agagttaatg 720
cagtttgctg gccgtccaga gcaccagtcc tcagacagca cattcctggt gtttatgtcc 780
catggcatcc tggaaggaat ctgtggggtg aagcaccgaa acaaaaagcc agatgttctt 840
catgatgaca ctatcttcaa aattttcaac aactctaact gtcggagtct gagaaacaaa 900
cccaagattc tcatcatgca ggcctgcaga ggcagatata atggaactat ttgggtatcc 960
acaaacaaag ggatagccac tgctgataca gatgaggaac gtgtgttgag ctgtaaatgg 1020
aataatagta taacaaaggc ccatgtggag acagatttca ttgctttcaa atcttctacc 1080
ccacataata tttcttggaa ggtaggcaag actggttccc tcttcatttc caaactcatt 1140
gactgcttca aaaagtactg ttggtgttat catttggagg aaatttttcg aaaggttcaa 1200
cactcatttg aggtcccagg tgaactgacc cagatgccca ctattgagag agtatccatg 1260
acacgctatt tctacctttt tcccgggaat tagcacaggc aactctcatg cagttcccag 1320
tcaagtattg ctgtagctga gaagaaaaga aaattccaag atcccaggat ttttaaatgt 1380
gtaaaacttt tcagttagat attttataca atatcataag gctagataat ttccataggt 1440
tatttttagg ggaaacctga tacgtaaaat tttgcatgaa aagtatagat tcgttccttc 1500
cttccaaatc tgctcatctt ttactttatt ttattaaatt tatatttgca cattttttgta 1560
aaatgaataa aggaaaaaga cactaaagaa catgtctgaa catatcctgg aacttcttct 1620
ttgtaaaatg aataaaggaa aaagacacta aagaacaaag atgatacacc ttttgatgaa 1680
ccactttcac ctataaatta gtagtaagaa tttactcaca aggaagatct tatctacaat 1740
gtagctgaga aatgaaactg ttgcatatgt aggtaaaact aatcatcttt taggaataag 1800
ataaagaggt ttatgtccac tgtttgtctc tggcatacat ggttttcatg cctagtggct 1860
acctaccatt cctttcaatc aatttcttag gatataattg acaaatttat gctatgttta 1920
taatttttct cttaaatgcc tttgtaataa gatatactca cacatacaca tttaagattc 1980
tgtctattag tgttattgaa ataaatccta gaaacaaaaa ttaaaagttt aaagcattaa 2040
agacaatttt gagacaaaat attctatgaa attctatgca aaattgaatt cttctacaag 2100
tatgtgatga agcccaccta ccactatttt tgtcatcttg aggatgttat atcattattt 2160
ttacttaact gagctcaaat taaaatcttt gtttattctt tgttctataa aaaaaaaaaa 2220
aaaaaaaa 2228

<210> 359
<211> 339
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Caspase precursor (insect)
C14.015

<400> 359
Met Asp Ala Thr Asn Asn Gly Glu Ser Ala Asp Gln Val Gly Ile Arg
1 5 10 15
Val Gly Asn Pro Glu Gln Pro Asn Asp His Thr Asp Ala Leu Gly Ser
20 25 30
Val Gly Ser Gly Gly Ala Gly Ser Ser Gly Leu Val Ala Gly Ser Ser
35 40 45

```
His Pro Tyr Gly Ser Gly Ala Ile Gly Gln Leu Ala Asn Gly Tyr Ser
     50                  55                  60
Ser Pro Ser Ser Ser Tyr Arg Lys Asn Val Ala Lys Met Val Thr Asp
65                  70                  75                  80
Arg His Ala Ala Glu Tyr Asn Met Arg His Lys Asn Arg Gly Met Ala
                85                  90                  95
Leu Ile Phe Asn His Glu His Phe Glu Val Pro Thr Leu Lys Ser Arg
            100                 105                 110
Ala Gly Thr Asn Val Asp Cys Glu Asn Leu Thr Arg Val Leu Lys Gln
        115                 120                 125
Leu Asp Phe Glu Val Thr Val Tyr Lys Asp Cys Arg Tyr Lys Asp Ile
    130                 135                 140
Leu Arg Thr Ile Glu Tyr Ala Ala Ser Gln Asn His Ser Asp Ser Asp
145                 150                 155                 160
Cys Ile Leu Val Ala Ile Leu Ser His Gly Glu Met Gly Tyr Ile Tyr
                165                 170                 175
Ala Lys Asp Thr Gln Tyr Lys Leu Asp Asn Ile Trp Ser Phe Phe Thr
            180                 185                 190
Ala Asn His Cys Pro Ser Leu Ala Gly Lys Pro Lys Leu Phe Phe Ile
        195                 200                 205
Gln Ala Cys Gln Gly Asp Arg Leu Asp Gly Gly Val Thr Met Gln Arg
    210                 215                 220
Ser Gln Thr Glu Thr Asp Gly Asp Ser Ser Met Ser Tyr Lys Ile Pro
225                 230                 235                 240
Val His Ala Asp Phe Leu Ile Ala Tyr Ser Thr Val Pro Gly Phe Tyr
                245                 250                 255
Ser Trp Arg Asn Thr Thr Arg Gly Ser Trp Phe Met Gln Ser Leu Cys
            260                 265                 270
Ala Glu Leu Ala Ala Asn Gly Lys Arg Leu Asp Ile Leu Thr Leu Leu
        275                 280                 285
Thr Phe Val Cys Gln Arg Val Ala Val Asp Phe Glu Ser Cys Thr Pro
    290                 295                 300
Asp Thr Pro Glu Met His Gln Gln Lys Gln Ile Pro Cys Ile Thr Thr
305                 310                 315                 320
Met Leu Thr Arg Ile Leu Arg Phe Ser Asp Lys Gln Leu Ala Pro Ala

                325                 330                 335
Gly Arg Val
```

<210> 360
<211> 1020
<212> DNA
<213> Drosophila melanogaster

<220>
<223> Caspase precursor (insect) C14.015

<400> 360
atggacgcca ctaacaatgg agaatccgcc gaccaggtgg gcatcagggt gggcaatccg 60
gagcagccca acgatcacac agatgccctg ggctccgtgg gatccggagg agcgggtagc 120
agcggcctgg tcgcaggatc ctcgcatcct tacggcagcg gagccattgg gcagctggcc 180
aacgggtaca gctcaccctc gtccagctac cgaaagaatg tagccaaaat ggtcaccgac 240
cgccatgcag ccgagtacaa catgcgccac aagaaccgcg gaatggcact gatcttcaac 300
catgagcact tcgaggtgcc caccttgaag tcccgcgcgg gaaccaatgt ggactgcgag 360

```
aatctgactc gggtgctcaa gcagctggac ttcgaagtga ccgtgtacaa ggactgccgc 420
tacaaggaca ttttgaggac aatcgagtat tcagcgtcgc agaatcacag cgatagtgat 480
tgcatcctgg tcgccatcct gtcgcacggc gagatgggct acatctacgc caaggacaca 540
cagtacaagc tggataacat ctggagcttc ttcacggcca atcactgccc ctcgctagcc 600
ggcaaaccca agttgttctt catacaggcc tgccagggcg acagattgga tggcggagtg 660
accatgcagc gttctcagac ggaaaccgat ggcgactcct cgatgagcta caagattcca 720
gtgcacgccg actttctgat cgcctactcg acggttcctg gattctattc gtggcgcaac 780
accacccgcg gcacgtggtt catgcagagc ctgtgcgccg aactggcggc caatggcaag 840
cggctggaca tcctgaccct gctcacattc gtgtgccagc gggtggccgt ggactttgag 900
tcctgcaccc cggacactcc ggagatgcac cagcagaagc agataccctg catcaccacc 960
atgctgacgc gcattctgcg tttcagcgac aagcagttgg ctccagccgg acgggtttga 1020
```

<210> 361
<211> 323
<212> PRT
<213> Drosophila melanogaster

<220>
<223> Caspase-1 precursor (insect)
C14.016

<400> 361

```
Met Thr Asp Glu Cys Val Thr Arg Asn Tyr Gly Val Gly Ile Arg Ser
 1               5                  10                  15
Pro Asn Gly Ser Glu Asn Arg Gly Ser Phe Ile Met Ala Asp Asn Thr
            20                  25                  30
Asp Ala Lys Gly Cys Thr Pro Glu Ser Leu Val Val Gly Gly Ala Thr
        35                  40                  45
Ala Ala Ser Pro Leu Pro Ala Asn Lys Phe Val Ala Arg Met Pro Val
    50                  55                  60
Glu Arg Tyr Ala Ser Glu Tyr Asn Met Ser His Lys His Arg Gly Val
65                  70                  75                  80
Ala Leu Ile Phe Asn His Glu Phe Phe Asp Ile Pro Ser Leu Lys Ser
                85                  90                  95
Arg Thr Gly Thr Asn Val Asp Ala Gln Glu Leu Lys Lys Ala Phe Glu
            100                 105                 110
Asn Leu Gly Phe Ala Val Ser Val His Lys Asp Cys Lys Leu Arg Asp
        115                 120                 125
Ile Leu Lys His Val Gly Lys Ala Ala Glu Leu Asp His Thr Asp Asn
    130                 135                 140
Asp Cys Leu Ala Val Ala Ile Leu Ser His Gly Glu His Gly Tyr Leu
145                 150                 155                 160
Tyr Ala Lys Asp Thr Gln Tyr Lys Leu Asp Asn Ile Trp His Tyr Phe
                165                 170                 175
Thr Ala Thr Phe Cys Pro Ser Leu Ala Gly Lys Pro Lys Leu Phe Phe
            180                 185                 190
Ile Gln Ala Cys Gln Gly Asp Arg Leu Asp Gly Gly Ile Thr Leu Glu
        195                 200                 205
Lys Gly Val Thr Glu Thr Asp Gly Glu Ser Ser Thr Ser Tyr Lys Ile
    210                 215                 220
Pro Ile His Ala Asp Phe Leu Phe Ser Tyr Ser Thr Ile Pro Gly Tyr
225                 230                 235                 240
Phe Ser Trp Arg Asn Ile Asn Asn Gly Ser Trp Tyr Met Gln Ser Leu
                245                 250                 255
Ile Arg Glu Leu Asn Ala Asn Gly Lys Lys Tyr Asp Leu Leu Thr Leu
            260                 265                 270
```

```
Leu Thr Phe Val Asn Gln Arg Val Ala Leu Asp Phe Glu Ser Asn Val
        275                 280                 285
Pro Ala Thr Pro Met Met Asp Arg Gln Lys Gln Ile Pro Cys Leu Thr
    290                 295                 300
Ser Met Leu Thr Arg Ile Leu Arg Phe Gly Asp Lys Pro Asn Gly Asn
305                 310                 315                 320
Lys Ala Gly
```

<210> 362
<211> 1757
<212> DNA
<213> Drosophila melanogaster

<220>
<223> Caspase-1 precursor (insect) C14.016

<400> 362

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agtttgtttt cgccgctcag agcacgctta acctccgtta attgattgat taaacacgtc 60
cgactgtgag ccataaaagg acattcgctc gatcgaaagc cgacaaaagc tggctgagaa 120
gcgcaaaaca gctgcgctgc gcaaagtttg gccaacgcag agcaatagaa aacagaagca 180
gtgtcagaat aaaacaagaa tcagaccaaa aagggcgcaa caactgcgga gagagaaaag 240
gaaggaaaga gcagcgcgtg acgagggagg agcaggaggg agcgaacaaa aggcaagagg 300
aaacacaagg agaaacgcaa acaatcaaaa caagaactta agcaagaaaa ggggcgcaag 360
atgaccgacg agtgcgtaac cagaaactac ggagtaggca ttcgcagccc aaatggatcg 420
gaaaatcggg gcagctttat aatggctgat aataccgatg ccaagggctg tacgccggag 480
tctcttgttg ttggtggtgc aactgcagcg agccccttgc cggccaacaa gtttgtggct 540
cgaatgcccg tggaacgata tgcaagcgaa tacaacatga gtcacaagca ccgcggagtt 600
gcgctgatct tcaaccacga attcttcgac ataccctcgc tgaagagccg caccggaaca 660
aatgtcgatg cccaagagct gaaaaaggcc tttgaaaacc tgggattcgc ggtgtccgtg 720
cacaaggact gcaagttgag ggacatcctg aagcacgtgg ggaaggccgc cgagttggac 780
cacacggaca acgactgcct tgcggtggcc atactctcgc acggggagca cggctacctg 840
tacgccaagg atacgcagta caagctggac aacatctggc actacttcac tgccaccttc 900
tgcccctcgc tggcgggcaa gccgaagctg ttcttcatcc aagcctgcca gggcgatcgc 960
ttggacggag gcatcactct ggagaagggc gttaccgaga cggacgggga gtcctcgacg 1020
agctacaaga tacccataca cgccgacttt ctcttctcct actcgaccat tccgggctac 1080
ttctcctggc gcaacatcaa caatggctcc tggtacatgc aatcgctgat ccgcgagctg 1140
aacgccaatg gcaaaaagta cgacctgctc accctgctta cattcgttaa ccagcgcgta 1200
gccctagact ttgagtcgaa cgtgcccgcc acaccgatga tggatcgcca gaagcaaata 1260
ccgtgcctca cctccatgct gacgcgcata ctgcgcttcg gcgacaagcc gaacggcaat 1320
aaggctggct aggaagagat ctcccttcga agaagaactt tcaacagagg ttgtacaacc 1380
atcgcccgca atcattcacg ttggattcca attcacttca agtttagttt tagctgacgc 1440
gtgcgattaa cccgatggat attgaagcac ccgactccct ttcattcatt cccctgcctt 1500
tcccatgccc atttcggcct tatcattgac gaaattcgtt acccatttac ccactagatg 1560
acttccgtat gcataagcga gaccttgcca atagaaaacc cacaaatttg agataagata 1620
atacaatgaa gatttataca tacatacata cttttatgta cacgcaaaca tttatatttg 1680
atatgaataa aaatgaatta aaaacataaa aaaaaaaaaa aaaaaaaaaa aaaaaacaaa 1740
aaaaaaaaaa aaaaaaa                                                1757
```

<210> 363
<211> 377
<212> PRT
<213> Bos taurus

<220>
<223> Caspase-13 precursor C14.017

<400> 363
Met Ala Glu Asp Lys His Asn Lys Asn Pro Leu Lys Met Leu Glu Ser
1 5 10 15
Leu Gly Lys Glu Leu Ile Ser Gly Leu Leu Asp Asp Phe Val Glu Lys
20 25 30
Asn Val Leu Lys Leu Glu Glu Glu Glu Lys Lys Lys Ile Tyr Asp Ala
35 40 45
Lys Leu Gln Asp Lys Ala Arg Val Leu Val Asp Ser Ile Arg Gln Lys
50 55 60
Asn Gln Glu Ala Gly Gln Val Phe Val Gln Thr Phe Leu Asn Ile Asp
65 70 75 80
Lys Asn Ser Thr Ser Ile Lys Ala Pro Glu Glu Thr Val Ala Gly Pro
85 90 95
Asp Glu Ser Val Gly Ser Ala Ala Thr Leu Lys Leu Cys Pro His Glu
100 105 110
Glu Phe Leu Lys Leu Cys Lys Glu Arg Ala Gly Glu Ile Tyr Pro Ile
115 120 125
Lys Glu Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr
130 135 140
Glu Phe Asp His Met Pro Pro Arg Asn Gly Ala Ala Leu Asp Ile Leu
145 150 155 160
Gly Met Lys Gln Leu Leu Glu Gly Leu Gly Tyr Thr Val Glu Val Glu
165 170 175
Glu Lys Leu Thr Ala Arg Asp Met Glu Ser Val Leu Trp Lys Phe Ala
180 185 190
Ala Arg Glu Glu His Lys Ser Ser Asp Ser Thr Phe Leu Val Phe Met
195 200 205
Ser His Gly Ile Leu Asp Gly Ile Cys Gly Thr Met His Ser Glu Glu
210 215 220
Glu Pro Asp Val Leu Pro Tyr Asp Thr Ile Phe Arg Thr Phe Asn Asn
225 230 235 240
Arg Asn Cys Leu Ser Leu Lys Asp Lys Pro Lys Val Ile Ile Val Gln
245 250 255
Ala Cys Arg Gly Ala Asn Arg Gly Glu Leu Trp Val Ser Asp Ser Pro
260 265 270
Pro Ala Leu Ala Asp Ser Phe Ser Gln Ser Ser Glu Asn Leu Glu Glu
275 280 285
Asp Ala Val Tyr Lys Thr His Val Glu Lys Asp Phe Ile Ala Phe Cys
290 295 300
Ser Ser Thr Pro His Asn Val Ser Trp Arg Asp Ile Lys Lys Gly Ser
305 310 315 320
Leu Phe Ile Thr Arg Leu Ile Thr Cys Phe Gln Lys Tyr Ala Trp Cys
325 330 335
Cys His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys
340 345 350
Pro Asn Val Lys Ala Gln Met Pro Thr Val Glu Arg Leu Ser Met Thr
355 360 365
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn
370 375

<210> 364
<211> 2060
<212> DNA

<213> Homo sapiens

<220>
<223> Caspase-13 precursor C14.017

<400> 364
ccacgcgtcc gcggacgcgt gggctccttc aaggcagtag gaagatacta agcttattat 60
ctatggctga agacaaacac aacaaaaacc cacttaagat gttggaatct ttgggcaaag 120
aactcatttc tggccttttg gatgactttg tggaaaaaaa tgtcctgaaa ttggaggaag 180
aggagaagaa aaaaatttat gatgccaaac ttcaagacaa agcccgggtc ttggttgatt 240
ctatacgaca gaaaaaccaa gaggcaggtc aagtctttgt tcaaactttc ctaaacatag 300
acaaaaattc caccagtata aaagctcctg aggaaactgt ggctggacca gatgagtcag 360
tgggatctgc agctaccctc aagctttgcc ctcatgaaga attcctgaaa ctgtgtaaag 420
aaagggctgg agagatctat ccaataaagg agagaaagga ccgcactcgt ctggctctca 480
tcatatgcaa cacagagttt gatcatatgc ctcccaggaa tggggctgcc cttgacatcc 540
ttggaatgaa gcagctgctt gagggtcttg gctacactgt ggaagtggaa gagaaactca 600
cagccaggga catggaatca gtgctgtgga aatttgctgc acgtgaagag cacaaatcct 660
cagacagtac attcttggtg ttcatgtctc atggcatcct ggatgggatc tgtgggacta 720
tgcacagtga ggaagaacca gatgtgttac cttatgatac catcttccgg acattcaaca 780
accgtaattg cctcagtcta aaggacaaac ctaaagtcat cattgtccag gcctgcagag 840
gtgcaaatcg tggggaattg tgggtcagtg actctccacc agccttggca gacagctttt 900
cacagtcatc cgagaacctg gaagaggatg ctgtttacaa gacccatgta gagaaggact 960
tcattgcttt ctgttcctca actccacata atgtgtcctg gagagacata aaaaaaggtt 1020
ctctcttcat tacacgactc atcacatgct tccaaaaata tgcttggtgc tgtcatcttg 1080
aggaagtatt taggaaggta caacaatcat ttgaaaaacc aaatgttaaa gcccagatgc 1140
ccactgttga acgactctct atgacaagat atttctacct ctttcctggc aactgaaaat 1200

aaaaatcaca ggaaattcaa ccatttatca gcttcaagaa gcatttttat cagcacagca 1260
tccatgttta acctttttgtc tttcattaaa gtgaaaacat atgaactgtt ctttggggtc 1320
ctctaagaaa gaatagaatt tcaattaaaa caatggatgg atggaaataa agtagaagaa 1380
gaaaactgga ttttcttgtt atattgcata taatgcctgc actttactga gtgaagagaa 1440
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gaccaaaaac tgggtcacct gctcctttga tcactcatca aaccttgcaa ctagaattat 1560
ttggaagaat atttctaatt tattatttaa ccaacatcat aggtcaagtt caatttttttt 1620
tcagaaagtt gttatggtac ctatgcatct ttcttcttat ccataaatta atttgctttc 1680
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cacttggtaa ttgtctaaaa taaattgggc ctttgattta agatggtata attgggtgtg 1800
cttgtataga aagacagaca ttattagata cagaacatcc aagagtgtgg gaaatgtcag 1860
caatgggaaa gaaaatgtta aattttctgg aaagtgaatg tcagtagagg aattttagca 1920
acatggccat ctgagccact gactaaggag atgtaccact tcaattacat acatgcagaa 1980
tgctgaatag atatatcagg acatgctgaa ctgtattaca aataaaatga ttctctagat 2040
atcaaaaaaa aaaaaaaaaa 2060

<210> 365
<211> 242
<212> PRT
<213> Homo sapiens

<220>
<223> Caspase-14 precursor C14.018

<400> 365
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Ala Arg Leu Ala Leu Ile Leu Cys Val Thr Lys Ala Arg Glu Gly Ser
 20 25 30

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Glu Glu Asp Leu Asp Ala Leu Glu His Met Phe Arg Gln Leu Arg Phe
        35                  40                  45
Glu Ser Thr Met Lys Arg Asp Pro Thr Ala Glu Gln Phe Gln Glu Glu
    50                  55                  60
Leu Glu Lys Phe Gln Gln Ala Ile Asp Ser Arg Glu Asp Pro Val Ser
65                  70                  75                  80
Cys Ala Phe Val Val Leu Met Ala His Gly Arg Glu Gly Phe Leu Lys
                85                  90                  95
Gly Glu Asp Gly Glu Met Val Lys Leu Glu Asn Leu Phe Glu Ala Leu
            100                 105                 110
Asn Asn Lys Asn Cys Gln Ala Leu Arg Ala Lys Pro Lys Val Tyr Ile
        115                 120                 125
Ile Gln Ala Cys Arg Gly Glu Gln Arg Asp Pro Gly Glu Thr Val Gly
    130                 135                 140
Gly Asp Glu Ile Val Met Val Ile Lys Asp Ser Pro Gln Thr Ile Pro
145                 150                 155                 160
Thr Tyr Thr Asp Ala Leu His Val Tyr Ser Thr Val Glu Gly Tyr Ile
                165                 170                 175
Ala Tyr Arg His Asp Gln Lys Gly Ser Cys Phe Ile Gln Thr Leu Val
            180                 185                 190
Asp Val Phe Thr Lys Arg Lys Gly His Ile Leu Glu Leu Leu Thr Glu
        195                 200                 205
Val Thr Arg Arg Met Ala Glu Ala Glu Leu Val Gln Glu Gly Lys Ala
    210                 215                 220
Arg Lys Thr Asn Pro Glu Ile Gln Ser Thr Leu Arg Lys Arg Leu Tyr
225                 230                 235                 240
Leu Gln
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<210> 366
<211> 777
<212> DNA
<213> Homo sapiens

<220>
<223> Caspase-14 precursor C14.018

<400> 366
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gtcaccaaag cccgggaagg ttccgaagaa gacctggatg ctctggaaca catgtttcgg 180
cagctgagat tcgaaagcac catgaaaaga gaccccactg ccgagcaatt ccaggaagag 240
ctggaaaaat tccagcaggc catcgattcc cgggaagatc ccgtcagttg tgccttcgtg 300
gtactcatgg ctcacgggag ggaaggcttc ctcaagggag aagatgggga gatggtcaag 360
ctggagaatc tcttcgaggc cctgaacaac aagaactgcc aggccctgcg agctaagccc 420
aaggtgtaca tcatacaggc ctgtcgagga gaacaaaggg accccggtga aacagtaggt 480
ggagatgaga ttgtgatggt catcaaagac agcccacaaa ccatcccaac atacacagat 540
gccttgcacg tttattccac ggtagaggga tacatcgcct accgacatga tcagaaaggc 600
tcatgcttta tccagaccct ggtggatgtg ttcacgaaga ggaaaggaca tatcttggaa 660
cttctgacag aggtgacccg gcggatggca gaagcagagc tggttcaaga aggaaaagca 720
aggaaaacga accctgaaat ccaaagcacc ctccggaaac ggctgtatct gcagtag    777
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<210> 367
<211> 450
<212> PRT

<213> Drosophila melanogaster

<220>
<223> Caspase Nc precursor
C14.019

<400> 367

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 1               5                  10                  15
His Ile Arg Lys Asn Leu Asn Ile Leu Val Glu Trp Thr Asn Tyr Glu
            20                  25                  30
Arg Leu Ala Met Glu Cys Val Gln Gln Gly Ile Leu Thr Val Gln Met
        35                  40                  45
Leu Arg Asn Thr Gln Asp Leu Asn Gly Lys Pro Phe Asn Met Asp Glu
    50                  55                  60
Lys Asp Val Arg Val Glu Gln His Arg Arg Leu Leu Leu Lys Ile Thr
65                  70                  75                  80
Gln Arg Gly Pro Thr Ala Tyr Asn Leu Leu Ile Asn Ala Leu Arg Asn
                85                  90                  95
Ile Asn Cys Leu Asp Ala Ala Val Leu Leu Glu Ser Val Asp Glu Ser
            100                 105                 110
Asp Ser Arg Pro Pro Phe Ile Ser Leu Asn Glu Arg Arg Thr Ser Arg
        115                 120                 125
Lys Ser Ala Asp Ile Val Asp Thr Pro Ser Pro Glu Ala Ser Glu Gly
    130                 135                 140
Pro Cys Val Ser Lys Leu Arg Asn Glu Pro Leu Gly Ala Leu Thr Pro
145                 150                 155                 160
Tyr Val Gly Val Val Asp Gly Pro Glu Val Lys Lys Ser Lys Lys Ile
                165                 170                 175
His Gly Gly Asp Ser Ala Ile Leu Gly Thr Tyr Lys Met Gln Ser Arg
            180                 185                 190
Phe Asn Arg Gly Val Leu Leu Met Val Asn Ile Met Asp Tyr Pro Asp
        195                 200                 205
Gln Asn Arg Arg Arg Ile Gly Ala Glu Lys Asp Ser Lys Ser Leu Ile
    210                 215                 220
His Leu Phe Gln Glu Leu Asn Phe Thr Ile Phe Pro Tyr Gly Asn Val
225                 230                 235                 240
Asn Gln Asp Gln Phe Phe Lys Leu Leu Thr Met Val Thr Ser Ser Ser
                245                 250                 255
Tyr Val Gln Asn Thr Glu Cys Phe Val Met Val Leu Met Thr His Gly
            260                 265                 270
Asn Ser Val Glu Gly Lys Glu Lys Val Glu Phe Cys Asp Gly Ser Val
        275                 280                 285
Val Asp Met Gln Lys Ile Lys Asp His Phe Gln Thr Ala Lys Cys Pro
    290                 295                 300
Tyr Leu Val Asn Lys Pro Lys Val Leu Met Phe Pro Phe Cys Arg Gly
305                 310                 315                 320
Asp Glu Tyr Asp Leu Gly His Pro Lys Asn Gln Gly Asn Leu Met Glu
                325                 330                 335
Pro Val Tyr Thr Ala Gln Glu Glu Lys Trp Pro Asp Thr Gln Thr Glu
            340                 345                 350
Gly Ile Pro Ser Pro Ser Thr Asn Val Pro Ser Leu Ala Asp Thr Leu
        355                 360                 365
Val Cys Tyr Ala Asn Thr Pro Gly Tyr Val Thr His Arg Asp Leu Asp
    370                 375                 380
Thr Gly Ser Trp Tyr Ile Gln Lys Phe Cys Gln Val Met Ala Asp His
385                 390                 395                 400
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Ala His Asp Thr Asp Leu Glu Asp Ile Leu Lys Lys Thr Ser Glu Ala
                405                 410                 415
Val Gly Asn Lys Arg Thr Lys Lys Gly Ser Met Gln Thr Gly Ala Tyr
            420                 425                 430
Asp Asn Leu Gly Phe Asn Lys Lys Leu Tyr Phe Asn Pro Gly Phe Phe
        435                 440                 445
Asn Glu
    450
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<210> 368
<211> 2090
<212> DNA
<213> Drosophila melanogaster

<220>
<223> Caspase Nc precursor C14.019

<400> 368

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aataaggaca ccagcagggc cgccgatttg tgccccttc ttgaaagtcg caaaacaaaa 180
acaacgacga caacaacaaa gcggagacaa agaatcgaca agtagcgata aacgaaatca 240
ttcccgggaa aaccttggag acgggtgatt cactgccaat accactgcca attggagact 300
gatcacggca gccatccttg gcgcgcccaa taagcggagt caccggaacg cgtggaagcc 360
atatccggaa tgcagccgcc ggagctcgag attggaatgc cgaagaggca tcgcgagcat 420
atacgcaaga atctgaatat actggttgaa tggacgaact acgagcgtct ggccatggag 480
tgcgtgcaac agggcatcct aaccgttcag atgctaagaa atacgcagga tctcaatggc 540
aagccattca acatggacga gaaggatgtg cgtgtggagc agcatcgtag gctcctattg 600
aagatcaccc agcgtggtcc caccgcctat aacctgctga tcaatgcact gcgcaatatc 660
aattgtctgg atgcggccgt tctattggaa tccgtcgatg agtccgattc aaggccaccc 720
tttatctcgc taaacgaacg gagaaccagc cggaagtcgg ccgatattgt ggacacaccc 780
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ggtggggata gtgccatatt gggcacatat aagatgcaat cacgtttcaa ccgaggcgtt 960
ttgctaatgg ttaacataat ggactatccg gatcaaaacc gtcgacggat cggagccgaa 1020
aaggacagca agtcgttgat acacttgttt caagaactga attttacgat tttcccctat 1080
gggaacgtga atcaggatca gttctttaaa cttctgacaa tggtgacctc ctcgtcgtat 1140
gtgcagaata ccgagtgttt cgtaatggta ctgatgacac acggcaacag tgtggaggga 1200
aaagagaagg tggagttttg cgatggatct gtggtcgata tgcagaagat caaggaccat 1260
ttccagacgg ccaaatgtcc ttatttggtg aacaagccga aggtgcttat gtttcccttt 1320
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attcaagtat tcttctaata cgtattgcat acctcattta aaggtacgaa attatgtaat 1920
ttatgtgata actgccagaa atctacaaat attataatac agagttccag tatatacaca 1980
gccagatttt tgaaatcgaa catttaggca aaatgtaaag caattttcca gtctgatttt 2040
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<210> 369

<211> 824
<212> PRT
<213> Homo sapiens

<220>
<223> MALT lymphoma translocation protein 1
(paracaspase)
C14.026

<400> 369
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35 40 45
Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg
50 55 60
Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys
65 70 75 80
Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met
85 90 95
Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala
100 105 110
Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys
115 120 125
Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val
130 135 140
Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp
145 150 155 160
Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile
165 170 175
Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val
180 185 190
Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val
195 200 205
Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu
210 215 220
Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro
225 230 235 240
Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro
245 250 255
His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys
260 265 270
Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr
275 280 285
Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val
290 295 300
Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp
305 310 315 320
Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp
325 330 335
Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn
340 345 350
Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu
355 360 365
Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu

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    370                 375                 380
Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
385                 390                 395                 400
Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
                405                 410                 415
Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
            420                 425                 430
Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
        435                 440                 445
Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
    450                 455                 460
Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
465                 470                 475                 480
Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
                485                 490                 495
Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
            500                 505                 510
Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
        515                 520                 525
Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
    530                 535                 540
Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545                 550                 555                 560
Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
                565                 570                 575
Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
            580                 585                 590
Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
        595                 600                 605
Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
    610                 615                 620
Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
625                 630                 635                 640
Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
                645                 650                 655
Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
            660                 665                 670
Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
        675                 680                 685
Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu
    690                 695                 700
Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly
705                 710                 715                 720
Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro
                725                 730                 735
Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser
            740                 745                 750
Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro
        755                 760                 765
Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp
    770                 775                 780
Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg
785                 790                 795                 800
Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser
                805                 810                 815
Asp Arg Leu Arg Ile Ser Glu Lys
            820
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<210> 370
<211> 2828
<212> DNA
<213> Homo sapiens

<220>
<223> MALT lymphoma translocation protein 1
(paracaspase) C14.026

<400> 370
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gcccctgcct ccgcggctcg gaggcgagcg gaaggtgccc cggggccgag gcccgtgacg 120
gggcgggcgg gagccccggc agtccggggt cgccggcgag ggccatgtcg ctgttggggg 180
acccgctaca ggccctgccg ccctcggccg cccccacggg gccgctgctc gcccctccgg 240
ccggcgcgac cctcaaccgc ctgcgggagc cgctgctgcg gaggctcagc gagctcctgg 300
atcaggcgcc cgagggccgg ggctggagga gactggcgga gctggcgggg agtcgcgggc 360
gcctccgcct cagttgccta gacctggagc agtgttctct taaggtactg gagcctgaag 420
gaagccccag cctgtgtctg ctgaagttaa tgggtgaaaa aggttgcaca gtcacagaat 480
tgagtgattt cctgcaggct atggaacaca ctgaagttct tcagcttctc agccccccag 540
gaataaagat tactgtaaac ccagagtcaa aggcagtctt ggctggacag tttgtgaaac 600
tgtgttgccg ggcaactgga catccttttg ttcaatatca gtggttcaaa atgaataaag 660
agattccaaa tggaaataca tcagagctta tttttaatgc agtgcatgta aaagatgcag 720
gcttttatgt ctgtcgagtt aataacaatt tcacctttga attcagccag tggtcacagc 780
tggatgtttg cgacatccca gagagcttcc agagaagtgt tgatggcgtc tctgaatcca 840
agttgcaaat ctgtgttgaa ccaacttccc aaaagctgat gccaggcagc acattggttt 900
tacagtgtgt tgctgttgga agccctattc ctcactacca gtggttcaaa aatgaattac 960
cattaacaca tgagaccaaa aagctataca tggtgcctta tgtggatttg gaacaccaag 1020
gaacctactg gtgtcatgta tataatgatc gagacagtca agatagcaag aaggtagaaa 1080
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gtcatcctga taataaagag caaacaactg accagccttt ggcgaaggac aaggttgccc 1200
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tatatgggtt attatattat gcaggacatg gttatgaaaa ttttgggaac agcttcatgg 1440
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aggctctaga gattcgaagt agtttatctg agaagagagc acttactgat ccaatacagg 1860
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ctccttgttt ttgaaagtta gcataatttt agatgcctgt gaaatagtac tgcacttaca 2700
taaagtgaga cattgtgaaa aggcaaattt gtatatgtag agaaagaata gtagtaactg 2760
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ctctttct 2828

<210> 371
<211> 480
<212> PRT
<213> Homo sapiens

<220>
<223> CASP8 and FADD-like apoptosis regulator precursor
(c-FLIP)
C14.971

<400> 371
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20 25 30
Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly
35 40 45
Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg
50 55 60
Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu
65 70 75 80
Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg Val Leu
85 90 95
Met Ala Glu Ile Gly Glu Asp Leu Asp Lys Ser Asp Val Ser Ser Leu
100 105 110
Ile Phe Leu Met Lys Asp Tyr Met Gly Arg Gly Lys Ile Ser Lys Glu
115 120 125
Lys Ser Phe Leu Asp Leu Val Val Glu Leu Glu Lys Leu Asn Leu Val
130 135 140
Ala Pro Asp Gln Leu Asp Leu Leu Glu Lys Cys Leu Lys Asn Ile His
145 150 155 160
Arg Ile Asp Leu Lys Thr Lys Ile Gln Lys Tyr Lys Gln Ser Val Gln
165 170 175
Gly Ala Gly Thr Ser Tyr Arg Asn Val Leu Gln Ala Ala Ile Gln Lys
180 185 190
Ser Leu Lys Asp Pro Ser Asn Asn Phe Arg Leu His Asn Gly Arg Ser
195 200 205
Lys Glu Gln Arg Leu Lys Glu Gln Leu Gly Ala Gln Gln Glu Pro Val
210 215 220
Lys Lys Ser Ile Gln Glu Ser Glu Ala Phe Leu Pro Gln Ser Ile Pro
225 230 235 240
Glu Glu Arg Tyr Lys Met Lys Ser Lys Pro Leu Gly Ile Cys Leu Ile
245 250 255
Ile Asp Cys Ile Gly Asn Glu Thr Glu Leu Leu Arg Asp Thr Phe Thr
260 265 270
Ser Leu Gly Tyr Glu Val Gln Lys Phe Leu His Leu Ser Met His Gly
275 280 285
Ile Ser Gln Ile Leu Gly Gln Phe Ala Cys Met Pro Glu His Arg Asp
290 295 300
Tyr Asp Ser Phe Val Cys Val Leu Val Ser Arg Gly Gly Ser Gln Ser
305 310 315 320

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Val Tyr Gly Val Asp Gln Thr His Ser Gly Leu Pro Leu His His Ile
                325                 330                 335
Arg Arg Met Phe Met Gly Asp Ser Cys Pro Tyr Leu Ala Gly Lys Pro
            340                 345                 350
Lys Met Phe Phe Ile Gln Asn Tyr Val Val Ser Glu Gly Gln Leu Glu
        355                 360                 365
Asp Ser Ser Leu Leu Glu Val Asp Gly Pro Ala Met Lys Asn Val Glu
    370                 375                 380
Phe Lys Ala Gln Lys Arg Gly Leu Cys Thr Val His Arg Glu Ala Asp
385                 390                 395                 400
Phe Phe Trp Ser Leu Cys Thr Ala Asp Met Ser Leu Leu Glu Gln Ser
                405                 410                 415
His Ser Ser Pro Ser Leu Tyr Leu Gln Cys Leu Ser Gln Lys Leu Arg
            420                 425                 430
Gln Glu Arg Lys Arg Pro Leu Leu Asp Leu His Ile Glu Leu Asn Gly
        435                 440                 445
Tyr Met Tyr Asp Trp Asn Ser Arg Val Ser Ala Lys Glu Lys Tyr Tyr
    450                 455                 460
Val Trp Leu Gln His Thr Leu Arg Lys Lys Leu Ile Leu Ser Tyr Thr
465                 470                 475                 480
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<210> 372
<211> 1443
<212> DNA
<213> Homo sapiens

<220>
<223> CASP8 and FADD-like apoptosis regulator precursor (c-FLIP) C14.971

<400> 372
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ggcgagcggt atcagctcac tcaaaggcgg taatacggtt atccacagaa tcaggggata 2460
acgcaggaaa gaacatgtga gcaaaaggcc agcaaaaggc caggaaccgt aaaaaggccg 2520
cgttgctggc gtttttccat aggctccgcc cccctgacga gcatcacaaa aatcgacgct 2580
caagtcagag gtggcgaaac ccgacaggac tataaagata ccaggcgttt cccccctggaa 2640
gctccctcgt gcgctctcct gttccgaccc tgccgcttac cggatacctg tccgcctttc 2700
tcccttcggg aagcgtggcg ctttctcata gctcacgctg taggtatctc agttcggtgt 2760
aggtcgttcg ctccaagctg ggctgtgtgc acgaaccccc cgttcagccc gaccgctgcg 2820
ccttatccgg taactatcgt cttgagtcca acccggtaag acacgactta tcgccactgg 2880
cagcagccac tggtaacagg attagcagag cgaggtatgt aggcggtgct acagagttct 2940
tgaagtggtg gcctaactac ggctacacta gaaggacagt atttggtatc tgcgctctgc 3000
tgaagccagt taccttcgga aaaagagttg gtagctcttg atccggcaaa caaaccaccg 3060
ctggtagcgg tggtttttt gtttgcaagc agcagattac gcgcagaaaa aaaggatctc 3120
aagaagatcc tttgatcttt tctacggggt ctgacgctca gtggaacgaa aactcacgtt 3180
aagggatttt ggtcatgaga ttatcaaaaa ggatcttcac ctagatcctt ttaaattaaa 3240
aatgaagttt taaatcaatc taaagtatat atgagtaaac ttggtctgac agttaccaat 3300
gcttaatcag tgaggcacct atctcagcga tctgtctatt tcgttcatcc atagttgcct 3360
gactccccgt cgtgtagata actacgatac gggagggctt accatctggc cccagtgctg 3420
caatgatacc gcgagaccca cgctcaccgg ctccagattt atcagcaata aaccagccag 3480
ccggaagggc cgagcgcaga agtggtcctg caactttatc cgcctccatc cagtctatta 3540
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ccattgctgc aggcatcgtg gtgtcacgct cgtcgtttgg tatggcttca ttcagctccg 3660
gttcccaacg atcaaggcga gttacatgat cccccatgtt gtgcaaaaaa gcggttagct 3720
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tggcagcact gcataattct cttactgtca tgccatccgt aagatgcttt tctgtgactg 3840
gtgagtactc aaccaagtca ttctgagaat agtgtatgcg gcgaccgagt tgctcttgcc 3900
cggcgtcaac acgggataat accgcgccac atagcagaac tttaaaagtg ctcatcattg 3960
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tgtaacccac tcgtgcaccc aactgatctt cagcatcttt tactttcacc agcgtttctg 4080
ggtgagcaaa aacaggaagg caaaatgccg caaaaaaggg aataagggcg acacggaaat 4140
gttgaatact catactcttc ctttttcaat attattgaag catttatcag ggttattgtc 4200
tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaatagggg gttccgcgca 4260
catttccccg aaaagtgcca cctgacgtct aagaaaccat tattatcatg acattaacct 4320
ataaaaatag gcgtatcacg aggccctttc gtcttcaaga a 4361

<210> 378
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> wildtype RCL sequence from P4-P1

<400> 378
Val Ser Ala Arg Met
1 5

<210> 379
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> mutant RCL sequence from P4-P1'

<400> 379
Arg Arg Ala Arg Met
1 5

<210> 380
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> RRARM mutagenic primer

<400> 380
ccacagctgt cataaggagg gccagaatgg cccccgagga gatc 44

<210> 381
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 535

<400> 381
cagctatcgc gattgcag 18

<210> 382
<211> 17

<212> DNA
<213> Artificial Sequence

<220>
<223> primer 5542

<400> 382
gtgcgcagcc atcccgg 17

<210> 383
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<221> variation
<222> 8
<223> n = a, g, c, or t

<220>
<221> variation
<222> 9
<223> n = a, g, c, or t

<220>
<221> variation
<222> 10
<223> s = g or c

<220>
<223> Primer TC30

<400> 383
gccctggnns gcggccatc 19

<210> 384
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221> variation
<222> 8
<223> n = a, g, c, or t

<220>
<221> variation
<222> 9
<223> n = a, g, c, or t

<220>
<221> variation
<222> 10
<223> s = g or c

<220>
<223> Primer TC155

<400> 384
ggagcagnns aaaatgactg 20

<210> 385
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 717

<400> 385
tttcagtgtg gccaaaag 18

<210> 386
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 718

<400> 386
cagagtcttt tggccaca 18

<210> 387
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 850

<400> 387
ggggtaccgc caccatgaga gccctgctgg cgcgc 35

<210> 388
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer 851

<400> 388
gctctagatc atcagagggc caggccattc tct 33

<210> 389
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> mutant P4-P1' RCL loop sequence

<400> 389
Pro Phe Gly Arg Ser
1 5

<210> 390
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> PFGRS mutagenesis primer

<400> 390
ccacagctgt catacccttc ggcagaagcg cccccgagga gatc 44

<210> 391
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> mature chymotrypsin

<400> 391
Cys Gly Val Pro Ala Ile His Pro Val Leu Ser Gly Leu Ser Arg Ile
1 5 10 15
Val Asn Gly Glu Asp Ala Val Pro Gly Ser Trp Pro Trp Gln Val Ser
20 25 30
Leu Gln Asp Lys Thr Gly Phe His Phe Cys Gly Gly Ser Leu Ile Ser
35 40 45
Glu Asp Trp Val Val Thr Ala Ala His Cys Gly Val Arg Thr Ser Asp
50 55 60
Val Val Val Ala Gly Glu Phe Asp Gln Gly Ser Asp Glu Glu Asn Ile
65 70 75 80
Gln Val Leu Lys Ile Ala Lys Val Phe Lys Asn Pro Lys Phe Ser Ile
85 90 95
Leu Thr Val Asn Asn Asp Ile Thr Leu Leu Lys Leu Ala Thr Pro Ala
100 105 110
Arg Phe Ser Gln Thr Val Ser Ala Val Cys Leu Pro Ser Ala Asp Asp
115 120 125
Asp Phe Pro Ala Gly Thr Leu Cys Ala Thr Thr Gly Trp Gly Lys Thr
130 135 140
Lys Tyr Asn Ala Asn Lys Thr Pro Asp Lys Leu Gln Gln Ala Ala Leu
145 150 155 160
Pro Leu Leu Ser Asn Ala Glu Cys Lys Lys Ser Trp Gly Arg Arg Ile
165 170 175
Thr Asp Val Met Ile Cys Ala Gly Ala Ser Gly Val Ser Ser Cys Met
180 185 190
Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Lys Asp Gly Ala Trp Thr
195 200 205
Leu Val Gly Ile Val Ser Trp Gly Ser Asp Thr Cys Ser Thr Ser Ser
210 215 220
Pro Gly Val Tyr Ala Arg Val Thr Lys Leu Ile Pro Trp Val Gln Lys

225 230 235 240
Ile Leu Ala Ala Asn
245

<210> 392
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> AATTCTATGG

<400> 392
aattctatgg 10

<210> 393
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> tgcaccatag

<400> 393
tgcaccatag 10

<210> 394
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> ATGGAACCCTGAA

<400> 394
atggaaccct gaa 13

<210> 395
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> AGCTTCAGGGTTCCATCAC-

<400> 395
agcttcaggg ttccatcac 19

<210> 396
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> PAI-I with MET as cloned into pPAIST7HS

<400> 396
Met Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe
1 5 10 15
Gly Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn
20 25 30
Val Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln
35 40 45
Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln Ile Gln Ala Ala Met Gly
50 55 60
Phe Lys Ile Asp Asp Lys Gly Met Ala Pro Ala Leu Arg His Leu Tyr
65 70 75 80
Lys Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp
85 90 95
Ala Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro
100 105 110
His Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser
115 120 125
Glu Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His
130 135 140
Thr Lys Gly Met Ile Ser Asn Leu Leu Gly Lys Gly Ala Val Asp Gln
145 150 155 160
Leu Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp
165 170 175
Lys Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys
180 185 190
Ser Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys
195 200 205
Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile
210 215 220
Leu Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala
225 230 235 240
Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser
245 250 255
Ala Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg
260 265 270
Leu Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg
275 280 285
Lys Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln
290 295 300
Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Gln
305 310 315 320
Ala Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala
325 330 335
Ser Ser Ser Thr Ala Val Ile Val Ser Ala Arg Met Ala Pro Glu Glu
340 345 350
Ile Ile Met Asp Arg Pro Phe Leu Phe Val Val Arg His Asn Pro Thr
355 360 365
Gly Thr Val Leu Phe Met Gly Gln Val Met Glu Pro
370 375 380

<210> 397
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Manduca sexta serpin 1B RSL loop

<400> 397
Glu Gly Ala Glu Ala Ala Ala Ala Asn Ala Phe Gly Ile Val Pro Lys
 1   5   10   15
Ser Leu Ile Leu Tyr
            20

<210> 398
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Manduca sexta serpin 1K RSL loop

<400> 398
Glu Gly Ala Glu Ala Ala Ala Ala Asn Ala Phe Lys Ile Thr Thr Tyr
 1   5   10   15
Ser Phe His Phe Val
            20

<210> 399
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-antichymotrypsin RSL loop

<400> 399
Glu Gly Thr Glu Ala Ser Ala Ala Thr Ala Val Lys Ile Thr Leu Leu
 1   5   10   15
Ser Ala Leu Val Glu
            20

<210> 400
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Antithrombin-III RSL loop

<400> 400
Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg
 1   5   10   15
Ser Leu Asn Pro Asn
            20

<210> 401
<211> 21
<212> PRT

<213> Artificial Sequence

<220>
<223> PAI-II RSL loop

<400> 401
Glu Gly Thr Glu Ala Ala Ala Gly Thr Gly Gly Val Met Thr Gly Arg
 1   5   10   15
Thr Gly His Gly Gly
            20

<210> 402
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> 1-antitrypsin RSL loop

<400> 402
Lys Gly Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met
 1   5   10   15
Ser Ile Pro Pro Glu
            20

<210> 403
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> PAI-I RSL loop

<400> 403
Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala Arg
 1   5   10   15
Met Ala Pro Glu Glu
            20

<210> 404
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> PAI-III RSL loop

<400> 404
Ser Gly Thr Arg Ala Ala Ala Ala Thr Gly Thr Ile Phe Thr Phe Arg
 1   5   10   15
Ser Ala Arg Leu Asn
            20

<210> 405
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Ovalbumin RSL loop

<400> 405
Ala Gly Arg Glu Val Val Gly Ser Ala Glu Ala Gly Val Asp Ala Ala
 1   5   10   15
Ser Val Ser Glu Glu
            20

<210> 406
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> TNF- alpha cleavage sequence

<400> 406
Ala Glu Ala Lys
 1

<210> 407
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> TNF-R1 cleavage sequence (1)

<400> 407
Glu Asn Val Lys
 1

<210> 408
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> TNF-R1 cleavage sequence (2)

<400> 408
Gly Thr Glu Asp
 1

<210> 409
<211> 4
<212> PRT

<213> Artificial Sequence

<220>
<223> TNF-R2 cleavage sequence (1)

<400> 409
Ser Pro Thr Arg
 1

<210> 410
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> TNF-R2 cleavage sequence (2)

<400> 410
Val Ser Thr Arg
 1

<210> 411
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> TNF-R2 cleavage sequence (3)

<400> 411
Ser Thr Ser Phe
 1

<210> 412
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> HER-2 cleavage sequence (1)

<400> 412
Lys Phe Pro Asp
 1

<210> 413
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> HER-2 cleavage sequence (2)

<400> 413
Ala Glu Gln Arg
1

<210> 414
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR cleavage sequence (1)

<400> 414
Lys Tyr Ala Asp
1

<210> 415
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> EGFR cleavage sequence (2)

<400> 415
Asn Gly Pro Lys
1

<210> 416
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR-1 cleavage sequence (1)

<400> 416
Ser Ser Ala Tyr
1

<210> 417
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR-1 cleavage sequence (2)

<400> 417
Gly Thr Ser Asp
1

<210> 418
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR-2 cleavage sequence (1)

<400> 418
Ala Gln Glu Lys
1

<210> 419
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> VEGFR-2 cleavage sequence (2)

<400> 419
Arg Ile Asp Tyr
1

<210> 420
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (1)

<400> 420
Arg Glu Phe Lys
1

<210> 421
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (2)

<400> 421
Gly Leu Ala Arg
1

<210> 422
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (3)

<400> 422
Arg Leu Gly Arg
 1

<210> 423
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (4)

<400> 423
Ala Glu Gly Lys
 1

<210> 424
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (5)

<400> 424
Gln His Ala Arg
 1

<210> 425
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (6)

<400> 425
Leu Pro Ser Arg
 1

<210> 426
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (7)

<400> 426

Ser Leu Leu Arg
1

<210> 427
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (8)

<400> 427
Leu Gly Leu Ala
1

<210> 428
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C3 cleavage sequence (9)

<400> 428
Leu Ser Val Val
1

<210> 429
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C4 cleavage sequence (1)

<400> 429
His Arg Gly Arg
1

<210> 430
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C2 cleavage sequence (1)

<400> 430
Gly Ala Thr Arg
1

<210> 431

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

<220>
<223> C2 cleavage sequence (2)

<400> 431

Ser Leu Gly Arg
 1

<210> 432
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> C2 cleavage sequence (3)

<400> 432
Val Phe Ala Lys
 1

<210> 433
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> urokinase plasminogen activator (uPA) preproprotein

<400> 433
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1   5   10   15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20   25   30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35   40   45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50   55   60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65   70   75   80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85   90   95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100   105   110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115   120   125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130   135   140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145   150   155   160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165   170   175

```
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 434
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR73 F173I; F30I (CHYM SYSTEM)

<400> 434

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
```

```
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Ile Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 435
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR81 L224A, I240V; L73A, I89V (CHYM SYSTEM)

<400> 435

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
```

```
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 436
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR1 L224P; L73P (CHYM SYSTEM)

<400> 436

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
```

```
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Pro
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 437
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR3 R378C; R217C (CHYM SYSTEM)

<400> 437

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Cys Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 438

<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR4 L312P; L155P (CHYM SYSTEM)

<400> 438
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Pro Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
370 375 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg

385 390 395 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
405 410

<210> 439
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR7 S226P, I240V, I298T; S75P, I89V, I138T (CHYM SYSTEM)

<400> 439
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
210 215 220
Asn Pro Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Thr Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335

```
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 440
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR32 E294G; E137G (CHYM SYSTEM)

<400> 440

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
```

```
Phe Gly Thr Ser Cys Gly Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 441
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR36 R223G, L312P; R72G, L155P (CHYM SYSTEM)

<400> 441

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Gly Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
```

```
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Pro Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 442
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR37 G290D; G133D (CHYM SYSTEM)

<400> 442

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
```

```
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Asp Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 443
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR66 V317A; V160A (CHYM SYSTEM)

```
<400> 443
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1                5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
```

```
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Ala Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 444
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR24 V185D; V38D (CHYM SYSTEM)

<400> 444

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
```

```
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
                100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
            115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Asp Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 445
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> AR85 F289L, V317A; F132L, V160A (CHYM SYSTEM)

<400> 445

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1                5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
```

```
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
     50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu

                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Leu Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Ala Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 446
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF2 F173T, L224A, I240V; F30T, L73A, I189V (CHYM SYSTEM)

<400> 446
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Thr Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
370 375 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385 390 395 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
405 410

<210> 447
<211> 411

<212> PRT
<213> Artificial Sequence

<220>
<223> ARF6 F173L, L224A, I240V; F30L, L73A, I189V (CHYM SYSTEM)

<400> 447
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Leu Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
370 375 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385 390 395 400

Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
405 410

<210> 448
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF11 F173V, L224A, I240V; F30V, L73A, I189V (CHYM SYSTEM)

<400> 448
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350

```
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 449
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF17 F173G, L224A, I240V; F30G, L73A, I189V (CHYM SYSTEM)

<400> 449

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Gly Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
```

```
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410


<210> 450
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF16 F173L, L224A, I240V; F30L, L73A, I189V  (CHYM SYSTEM)

<400> 450
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125

His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Leu Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
```

```
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 451
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF33 L224A, I240V, L312V; L155V, L73A, I189V (CHYM SYSTEM)

<400> 451

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
```

```
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Val Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 452
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF35 F173M, L224A, I240V; F30M, L73A, I189V (CHYM SYSTEM)

<400> 452

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1                5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
```

```
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Met Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 453
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF36 L224A, L312M; L155M, L73A, I189V (CHYM SYSTEM)

<400> 453

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1                5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
```

```
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Met Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 454
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF37 F173M, L224A, I240V; F30M, L73A, I189V (CHYM SYSTEM)

<400> 454

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
```

```
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Met Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 455
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF43 F173L, L224A, I240V; F30L, L73A, I189V (CHYM SYSTEM)

<400> 455
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly

```
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Leu Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 456
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF47 F173V, L224A, I240V; F30V, L73A, I189V (CHYM SYSTEM)

<400> 456

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 457
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF48 F173L, L224A, I240V, L312M; F30L, L155M, L73A, I189V (CHYM SYSTEM)

<400> 457
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Leu Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Met Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365

```
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 458
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF103 F173L, L224A, I240V; F30L, L73A, I189V (CHYM SYSTEM)

<400> 458

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Leu Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
```

```
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 459
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> ARF115 F173G, L224A, I240V, L312M; F30G, L155M, L73A, I189V (CHYM SYSTEM)

<400> 459

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Gly Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Ala
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
```

```
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Met Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 460
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/Ia F164V; F21V (CHYM SYSTEM)

<400> 460

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Val Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
```

```
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 461
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/Ib I167L; I24L (CHYM SYSTEM)

<400> 461

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1                5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Leu Glu Asn Gln Pro Trp Phe Ala Ala Ile
```

```
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 462
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/Ic F173V; F30V (CHYM SYSTEM)

<400> 462

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
```

```
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu

    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 463
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/Id F173L; F30L (CHYM SYSTEM)

<400> 463

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
```

```
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Leu Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 464
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIa F173V, Y209H; F30V, Y61aH (CHYM SYSTEM)

<400> 464
```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
```

```
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
His Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 465
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIb F173V, K233E; F30V, K82E (CHYM SYSTEM)

<400> 465
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Glu Phe Glu Val Glu Asn Leu Ile
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
370 375 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385 390 395 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
405 410

<210> 466
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIc F173V, K313T; F30V, K156T (CHYM SYSTEM)

<400> 466
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
1 5 10 15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
20 25 30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
35 40 45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
50 55 60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65 70 75 80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
85 90 95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
100 105 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
115 120 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
130 135 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145 150 155 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
165 170 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
180 185 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
195 200 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
210 215 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225 230 235 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
245 250 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
260 265 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
275 280 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
290 295 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Thr Met Thr Val Val Lys Leu Ile
305 310 315 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
325 330 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
340 345 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
355 360 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp

```
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 467
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIIa F173V, K233E, V316A; F30V, K82E, V159A
(CHYM SYSTEM)

<400> 467

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Glu Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Ala Val Lys Leu Ile
305                 310                 315                 320
```

```
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 468
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIIb F173V, K233E, T186A, V316A; F30V, K82E, 39A, V159A (CHYM SYSTEM)

<400> 468

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Ala Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Glu Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
```

```
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Ala Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 469
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIIc F173V, K233E, T315A, V316A; F30V, K82E, T158A, V159A (CHYM SYSTEM)

<400> 469

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
```

```
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Glu Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Ala Ala Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 470
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IIId F173V, Y209H, K243E; F173V, Y61aH, K92E
(CHYM SYSTEM)

<400> 470

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
```

```
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
His Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile
225                 230                 235                 240
Leu His Glu Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 471
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IVa F173V, K233E, V316A, G231E, I240V, K348E; F173V, K82E, V159A, E80G, I89V, K187E (CHYM SYSTEM)

<400> 471

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
```

```
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Gly Met Glu Phe Glu Val Glu Asn Leu Val

225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Ala Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Glu Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 472
<211> 411
<212> PRT
<213> Artificial Sequence

<220>
<223> uPA/IVb F173V, K233E, V316A, G231E, E235K, I240V, K348E; F173V, K82E, V159A, E80G, E89K, I89V, K187E (CHYM SYSTEM)

<400> 472

```
Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
 1               5                  10                  15
```

```
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn
            20                  25                  30
Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys
        35                  40                  45
Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly Lys Ala Ser Thr
    50                  55                  60
Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser Ala Thr Val Leu
65                  70                  75                  80
Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu Gln Leu Gly Leu
                85                  90                  95
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg Pro Trp
            100                 105                 110
Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val
        115                 120                 125
His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu
    130                 135                 140
Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile
145                 150                 155                 160
Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Val Ala Ala Ile
                165                 170                 175
Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser
            180                 185                 190
Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp
        195                 200                 205
Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
    210                 215                 220
Asn Ser Asn Thr Gln Gly Gly Met Glu Phe Lys Val Glu Asn Leu Val
225                 230                 235                 240
Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile
                245                 250                 255
Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser
            260                 265                 270
Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln
        275                 280                 285
Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr
    290                 295                 300
Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Ala Val Lys Leu Ile
305                 310                 315                 320
Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr
                325                 330                 335
Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Glu Thr Asp Ser Cys
            340                 345                 350
Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met
        355                 360                 365
Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp
    370                 375                 380
Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg
385                 390                 395                 400
Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
                405                 410
```

<210> 473
<211> 299
<212> PRT
<213> Autographa californica nucleopolyhedrovirus

<220>
<223> P35 peptide

<400> 473
Met Cys Val Ile Phe Pro Val Glu Ile Asp Val Ser Gln Thr Ile Ile
 1   5   10   15
Arg Asp Cys Gln Val Asp Lys Gln Thr Arg Glu Leu Val Tyr Ile Asn
            20   25   30
Lys Ile Met Asn Thr Gln Leu Thr Lys Pro Val Leu Met Met Phe Asn
        35   40   45
Ile Ser Gly Pro Ile Arg Ser Val Thr Arg Lys Asn Asn Asn Leu Arg
    50   55   60
Asp Arg Ile Lys Ser Lys Val Asp Glu Gln Phe Asp Gln Leu Glu Arg
65   70   75   80
Asp Tyr Ser Asp Gln Met Asp Gly Phe His Asp Ser Ile Lys Tyr Phe
                85   90   95
Lys Asp Glu His Tyr Ser Val Ser Cys Gln Asn Gly Ser Val Leu Lys
            100   105   110
Ser Lys Phe Ala Lys Ile Leu Lys Ser His Asp Tyr Thr Asp Lys Lys
        115   120   125
Ser Ile Glu Ala Tyr Glu Lys Tyr Cys Leu Pro Lys Leu Val Asp Glu
    130   135   140
Arg Asn Asp Tyr Tyr Val Ala Val Cys Val Leu Lys Pro Gly Phe Glu
145   150   155   160
Asn Gly Ser Asn Gln Val Leu Ser Phe Glu Tyr Asn Pro Ile Gly Asn
                165   170   175
Lys Val Ile Val Pro Phe Ala His Glu Ile Asn Asp Thr Gly Leu Tyr
            180   185   190
Glu Tyr Asp Val Val Ala Tyr Val Asp Ser Val Gln Phe Asp Gly Glu
        195   200   205
Gln Phe Glu Glu Phe Val Gln Ser Leu Ile Leu Pro Ser Ser Phe Lys
    210   215   220
Asn Ser Glu Lys Val Leu Tyr Tyr Asn Glu Ala Ser Lys Asn Lys Ser
225   230   235   240
Met Ile Tyr Lys Ala Leu Glu Phe Thr Thr Glu Ser Ser Trp Gly Lys
                245   250   255
Ser Glu Lys Tyr Asn Trp Lys Ile Phe Cys Asn Gly Phe Ile Tyr Asp
            260   265   270
Lys Lys Ser Lys Val Leu Tyr Val Lys Leu His Asn Val Thr Ser Ala
        275   280   285
Leu Asn Lys Asn Val Ile Leu Asn Thr Ile Lys
    290   295

<210> 474
<211> 2105
<212> DNA
<213> Homo sapiens

<220>
<223> Full length u-PA

<400> 474
atgagagccc tgctggcgcg cctgcttctc tgcgtcctgg tcgtgagcga ctccaaaggc 60
agcaatgaac ttcatcaagt tccatcgaac tgtgactgtc taaatggagg aacatgtgtg 120
tccaacaagt acttctccaa cattcactgg tgcaactgcc caaagaaatt cggagggcag 180
cactggtgaa atagataagt caaaaacctg ctatgagggg aatggtcact tttaccgagg 240
aaaggccagc actgacacca gttgccggcc ctgcctgccc tggaactctg ccactgtcct 300

tcagcaaacg taccatgccc acagatctga tgctcttcag ctgggcctgg ggaaacataa 360
ttactgcagg aacccagaca accggaggcg accctggtgc tatgtgcagg tgggcctaaa 420
gccgcttgtc caagagtgca tggtgcatga ctgcgcagat ggaaaaaagc cctcctctcc 480
tccagaagaa ttaaaatttc agtgtggcca aaagactctg aggccccgct ttgagattat 540
tgggggagaa ttcaccacca tcgagaacca gccctggttt gcggccatct acaggaggca 600
ccgggggggc tctgtcacct acgtgtgtgg aggcagcctc atcagccctt gctgggtgat 660
cagcgccaca cactgcttca ttgattaccc aaagaaggag gactacatcg tctacctggg 720
tcgctcaagg cttaactcca acacgcaagg ggagatgaag tttgaggtgg aaaacctcat 780
cctacacaag gactacagcg ctgacacgct tgctcaccac aacgacattg ccttgctgaa 840
gatccgttcc aaggagggca ggtgtgcgca gccatcccgg actatacaga ccatctgcct 900
gccctcgatg tataacgatc cccagtttgg cacaagctgt gagatcactg gctttggaaa 960
agagaattct accgactatc tctatccgga gcagctgaaa atgactgttg tgaagctgat 1020
ttcccaccgg gagtgtcagc agccccacta ctacggctct gaagtcacca ccaaaatgct 1080
atgtgctgct gacccccaat ggaaaacaga ttcctgccag ggagactcag ggggacccct 1140
cgtctgttcc ctccaaggcc gcatgacttt gactggaatt gtgagctggg gccgtggatg 1200
tgccctgaag gacaagccag gcgtctacac gagagtctca cacttcttac cctggatccg 1260
cagtcacacc aaggaagaga atggcctggc cctctgaggg ttttcagtgt ggccaaaaga 1320
ctctgaggcc ccgctttaag attattgggg gagaattcac caccatcgag aaccagccct 1380
ggtttgcggc catctacagg aggcaccggg ggggctctgt cacctacgtg tgtggaggca 1440
gcctcatcag cccttgctgg gtgatcagcg ccacacactg cttcattgat tacccaaaga 1500
aggaggacta catcgtctac ctgggtcgct caaggcttaa ctccaacacg caaggggaga 1560
tgaagtttga ggtggaaaac ctcatcctac acaaggacta cagcgctgac acgcttgctc 1620
accacaacga cattgccttg ctgaagatcc gttccaagga gggcaggtgt gcgcagccat 1680
cccggactat acagaccatc tgcctgccct cgatgtataa cgatccccag tttggcacaa 1740
gctgtgagat cactggcttt ggaaaagaga attctaccga ctatctctat ccggagcagc 1800
tgaaaatgac tgttgtgaag ctgatttccc accgggagtg tcagcagccc cactactacg 1860
gctctgaagt caccaccaaa atgctatgtg ctgctgaccc ccaatggaaa acagattcct 1920
gccagggaga ctcaggggga cccctcgtct gttccctcca aggccgcatg actttgactg 1980
gaattgtgag ctggggccgt ggatgtgccc tgaaggacaa gccaggcgtc tacacgagag 2040
tctcacactt cttaccctgg atccgcagtc acaccaagga agagaatggc ctgccctctg 2100
agggt 2105

<210> 475
<211> 804
<212> DNA
<213> Homo sapiens

<220>
<223> uPA protease domain

<400> 475
tttcagtgtg gccaaaagac tctgaggccc cgctttaaga ttattggggg agaattcacc 60
accatcgaga accagccctg gtttgcggcc atctacagga ggcaccgggg gggctctgtc 120
acctacgtgt gtggaggcag cctcatcagc ccttgctggg tgatcagcgc cacacactgc 180
ttcattgatt acccaaagaa ggaggactac atcgtctacc tgggtcgctc aaggcttaac 240
tccaacacgc aaggggagat gaagtttgag gtggaaaacc tcatcctaca caaggactac 300
agcgctgaca cgcttgctca ccacaacgac attgccttgc tgaagatccg ttccaaggag 360
ggcaggtgtg cgcagccatc ccggactata cagaccatct gcctgccctc gatgtataac 420
gatccccagt ttggcacaag ctgtgagatc actggctttg gaaaagagaa ttctaccgac 480
tatctctatc cggagcagct gaaaatgact gttgtgaagc tgatttccca ccgggagtgt 540
cagcagcccc actactacgg ctctgaagtc accaccaaaa tgctatgtgc tgctgacccc 600
caatggaaaa cagattcctg ccagggagac tcaggggggac ccctcgtctg ttccctccaa 660
ggccgcatga ctttgactgg aattgtgagc tggggccgtg gatgtgccct gaaggacaag 720
ccaggcgtct acacgagagt ctcacacttc ttaccctgga tccgcagtca caccaaggaa 780
gagaatggcc tgccctctga gggt 804

<210> 476

<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer UPAF1

<400> 476
atgagagccc tgctggcgcg cc 22

<210> 477
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer UPAF2

<400> 477
ggaaaagaga attctaccg 19

<210> 478
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 478
Ile Ala Gly Arg Ser Leu
1 5

<210> 479
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 479
Ser Leu Gly Arg Lys Ile
1 5

<210> 480
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 480
Val Leu Lys Asp

1

<210> 481
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 481
Leu Val Glu Asp
1

<210> 482
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 482
Trp Phe Lys Asp
1

<210> 483
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 483
Arg Ile Tyr Asp
1

<210> 484
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 484
Lys Val Gly Arg
1

<210> 485
<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 485
Arg Val Arg Lys
 1

<210> 486
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 486
Arg Lys Thr Lys
 1

<210> 487
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 487
Lys Thr Lys Lys
 1

<210> 488
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 488
Thr Lys Lys Arg
 1

<210> 489
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site

<400> 489
Arg Arg Val Arg
1

<210> 490
<211> 1474
<212> PRT
<213> Homo sapiens

<220>
<223> Alpha-2-macroglobulin precursor (Alpha-2-M)

<400> 490
Met Gly Lys Asn Lys Leu Leu His Pro Ser Leu Val Leu Leu Leu Leu
1 5 10 15
Val Leu Leu Pro Thr Asp Ala Ser Val Ser Gly Lys Pro Gln Tyr Met
20 25 30
Val Leu Val Pro Ser Leu Leu His Thr Glu Thr Thr Glu Lys Gly Cys
35 40 45
Val Leu Leu Ser Tyr Leu Asn Glu Thr Val Thr Val Ser Ala Ser Leu
50 55 60
Glu Ser Val Arg Gly Asn Arg Ser Leu Phe Thr Asp Leu Glu Ala Glu
65 70 75 80
Asn Asp Val Leu His Cys Val Ala Phe Ala Val Pro Lys Ser Ser Ser
85 90 95
Asn Glu Glu Val Met Phe Leu Thr Val Gln Val Lys Gly Pro Thr Gln
100 105 110
Glu Phe Lys Lys Arg Thr Thr Val Met Val Lys Asn Glu Asp Ser Leu
115 120 125
Val Phe Val Gln Thr Asp Lys Ser Ile Tyr Lys Pro Gly Gln Thr Val
130 135 140
Lys Phe Arg Val Val Ser Met Asp Glu Asn Phe His Pro Leu Asn Glu
145 150 155 160
Leu Ile Pro Leu Val Tyr Ile Gln Asp Pro Lys Gly Asn Arg Ile Ala
165 170 175
Gln Trp Gln Ser Phe Gln Leu Glu Gly Gly Leu Lys Gln Phe Ser Phe
180 185 190
Pro Leu Ser Ser Glu Pro Phe Gln Gly Ser Tyr Lys Val Val Val Gln
195 200 205
Lys Lys Ser Gly Gly Arg Thr Glu His Pro Phe Thr Val Glu Glu Phe
210 215 220
Val Leu Pro Lys Phe Glu Val Gln Val Thr Val Pro Lys Ile Ile Thr
225 230 235 240
Ile Leu Glu Glu Glu Met Asn Val Ser Val Cys Gly Leu Tyr Thr Tyr
245 250 255
Gly Lys Pro Val Pro Gly His Val Thr Val Ser Ile Cys Arg Lys Tyr
260 265 270
Ser Asp Ala Ser Asp Cys His Gly Glu Asp Ser Gln Ala Phe Cys Glu
275 280 285
Lys Phe Ser Gly Gln Leu Asn Ser His Gly Cys Phe Tyr Gln Gln Val
290 295 300
Lys Thr Lys Val Phe Gln Leu Lys Arg Lys Glu Tyr Glu Met Lys Leu
305 310 315 320
His Thr Glu Ala Gln Ile Gln Glu Glu Gly Thr Val Val Glu Leu Thr
325 330 335

```
Gly Arg Gln Ser Ser Glu Ile Thr Arg Thr Ile Thr Lys Leu Ser Phe
            340                 345                 350
Val Lys Val Asp Ser His Phe Arg Gln Gly Ile Pro Phe Phe Gly Gln
        355                 360                 365
Val Arg Leu Val Asp Gly Lys Gly Val Pro Ile Pro Asn Lys Val Ile
    370                 375                 380
Phe Ile Arg Gly Asn Glu Ala Asn Tyr Tyr Ser Asn Ala Thr Thr Asp
385                 390                 395                 400
Glu His Gly Leu Val Gln Phe Ser Ile Asn Thr Thr Asn Val Met Gly
                405                 410                 415
Thr Ser Leu Thr Val Arg Val Asn Tyr Lys Asp Arg Ser Pro Cys Tyr
            420                 425                 430
Gly Tyr Gln Trp Val Ser Glu Glu His Glu Glu Ala His His Thr Ala
        435                 440                 445
Tyr Leu Val Phe Ser Pro Ser Lys Ser Phe Val His Leu Glu Pro Met
    450                 455                 460
Ser His Glu Leu Pro Cys Gly His Thr Gln Thr Val Gln Ala His Tyr
465                 470                 475                 480
Ile Leu Asn Gly Gly Thr Leu Leu Gly Leu Lys Lys Leu Ser Phe Tyr
                485                 490                 495
Tyr Leu Ile Met Ala Lys Gly Gly Ile Val Arg Thr Gly Thr His Gly
            500                 505                 510
Leu Leu Val Lys Gln Glu Asp Met Lys Gly His Phe Ser Ile Ser Ile
        515                 520                 525
Pro Val Lys Ser Asp Ile Ala Pro Val Ala Arg Leu Leu Ile Tyr Ala
    530                 535                 540
Val Leu Pro Thr Gly Asp Val Ile Gly Asp Ser Ala Lys Tyr Asp Val
545                 550                 555                 560
Glu Asn Cys Leu Ala Asn Lys Val Asp Leu Ser Phe Ser Pro Ser Gln
                565                 570                 575
Ser Leu Pro Ala Ser His Ala His Leu Arg Val Thr Ala Ala Pro Gln
            580                 585                 590
Ser Val Cys Ala Leu Arg Ala Val Asp Gln Ser Val Leu Leu Met Lys
        595                 600                 605
Pro Asp Ala Glu Leu Ser Ala Ser Ser Val Tyr Asn Leu Leu Pro Glu
    610                 615                 620
Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu Asn Asp Gln Asp Asp Glu
625                 630                 635                 640
Asp Cys Ile Asn Arg His Asn Val Tyr Ile Asn Gly Ile Thr Tyr Thr
                645                 650                 655
Pro Val Ser Ser Thr Asn Glu Lys Asp Met Tyr Ser Phe Leu Glu Asp
            660                 665                 670
Met Gly Leu Lys Ala Phe Thr Asn Ser Lys Ile Arg Lys Pro Lys Met
        675                 680                 685
Cys Pro Gln Leu Gln Gln Tyr Glu Met His Gly Pro Glu Gly Leu Arg
    690                 695                 700
Val Gly Phe Tyr Glu Ser Asp Val Met Gly Arg Gly His Ala Arg Leu
705                 710                 715                 720
Val His Val Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro
                725                 730                 735
Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala Gly Val Ala
            740                 745                 750
Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp Lys Ala Gly
        755                 760                 765
Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser Ser Thr Ala
    770                 775                 780
Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr Met Pro Tyr
```

785 790 795 800
Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr Val Leu Asn
805 810 815
Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu Ala Ser Pro
820 825 830
Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro His Cys Ile
835 840 845
Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr Pro Lys Ser
850 855 860
Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu Glu Ser Gln
865 870 875 880
Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His Gly Arg Lys
885 890 895
Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly Leu Glu Lys
900 905 910
Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly Glu Val Ser
915 920 925
Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu Glu Ser Ala
930 935 940
Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser Ala Met Gln
945 950 955 960
Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly Glu Gln Asn
965 970 975
Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr Leu Asn Glu
980 985 990
Thr Gln Gln Leu Thr Pro Glu Val Lys Ser Lys Ala Ile Gly Tyr Leu
995 1000 1005
Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr Asp Gly Ser
1010 1015 1020
Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly Asn Thr Trp
1025 1030 1035 1040
Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg Ala Tyr Ile
1045 1050 1055
Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp Leu Ser Gln
1060 1065 1070
Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser Leu Leu Asn
1075 1080 1085
Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu Ser Ala Tyr
1090 1095 1100
Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr His Pro Val
1105 1110 1115 1120
Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys Thr Ala Gln
1125 1130 1135
Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu Leu Ala Tyr
1140 1145 1150
Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu Val Leu Lys
1155 1160 1165
Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val His Trp Glu
1170 1175 1180
Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr Glu Pro Gln
1185 1190 1195 1200
Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu Leu Ala Tyr
1205 1210 1215
Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr Ser Ala Thr
1220 1225 1230
Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln Gly Gly Phe

```
        1235                1240                1245

Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu Ser Lys Tyr
    1250                1255                1260
Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln Val Thr Ile
1265                1270                1275                1280
Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp Asn Asn Asn
                1285                1290                1295
Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro Gly Glu Tyr
            1300                1305                1310
Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln Thr Ser Leu
        1315                1320                1325
Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe Ala Leu Gly
    1330                1335                1340
Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala His Thr Ser
1345                1350                1355                1360
Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg Ser Ala Ser
                1365                1370                1375
Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe Ile Pro Leu
            1380                1385                1390
Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val Ser Arg Thr
        1395                1400                1405
Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser Asn
    1410                1415                1420
Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val Pro Val Arg
1425                1430                1435                1440
Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr Glu Thr Asp
                1445                1450                1455
Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys Asp Leu Gly
            1460                1465                1470
Asn Ala
```

<210> 491
<211> 439
<212> PRT
<213> Spodoptera litura nucleopolyhedrovirus

<400> 491

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Met Cys Val Leu Ile Pro Thr Phe Asp Ala Ser Ala Thr Thr Ile Val
 1               5                  10                  15
Asp Cys Ala Asn Leu Ser Asp Ser Ser Leu Arg Asp Leu Ile Tyr Val
            20                  25                  30
Asn Asn Val Ala Val Ser Lys Thr Gly Asn Tyr Ile Asn Arg Ser Val
        35                  40                  45
Ile Met Ala Leu Asn Ile Ser Gly Pro Val Val Ser Val Asn Arg Val
    50                  55                  60
Ser Met His Ile Val His Met Tyr Arg Ser His Ile Asp Arg Ile Phe
65                  70                  75                  80
Asp Arg Phe Asn Arg Leu Thr Tyr Ser Ala Thr Val Thr Asp Gly Gly
                85                  90                  95
Asp Ile Asp Arg Val Leu Lys Ser Asp Asp Tyr Thr Val Val Cys Met
            100                 105                 110
Ser Arg Ser Glu Leu Leu Asp Asn Tyr Lys Lys Cys Leu Ile Asn Glu
        115                 120                 125
Met Gly Ala Thr Gln Asp Asp Val Glu Lys Phe Arg Lys Tyr Cys Leu
    130                 135                 140
Lys Pro Leu Val Glu Thr Glu Asn Asp Gly Gly Val Glu Asp Arg Lys
```

```
145                 150                 155                 160
Lys Pro Tyr Val Val Ile Cys Ser Leu Lys Pro Lys Leu Leu Asn Lys
                165                 170                 175
Asn Lys Thr Leu Cys Phe Thr Tyr Lys Pro Gln Thr Gly Gln Val Ile
            180                 185                 190
Val Pro Leu Met His Glu Ile Asn Glu Asn Gly Ser Asp Val Tyr Ser
        195                 200                 205
Tyr Glu Val Met Ala Met Ile Lys Asp Val Arg Leu Ser Asn Lys Pro
    210                 215                 220
Leu Ser Met Leu Glu Arg Leu Lys Arg Ser Met Asp Gln Ile Val Leu
225                 230                 235                 240
Asn His Asn Glu Asn Lys Tyr Met Met Thr Asn Gln Leu Glu Ser Leu
                245                 250                 255
Lys Tyr Tyr Leu Lys Ser Ile Asn Ser Asn Glu Asp Asp Asp Leu Asn
            260                 265                 270
Lys Leu Met Asn Val Leu Asn Asn Leu Ile Asp Gln Leu Glu Lys Val
        275                 280                 285
Leu His Lys Lys Ser Ile Cys Asp Phe Ser Asp Asp Asp Glu Asp Asp
    290                 295                 300
Asp Gly Leu Ile Asp Met Lys Tyr Tyr Asn Ser Ile Ile Glu Asp Asn
305                 310                 315                 320
Met Arg Ile Leu Leu Met Lys Ile Gln Gln Tyr Ile Asp Asp Arg His
                325                 330                 335
Met Phe Leu Ser Pro Pro Leu Ser Val Glu Lys Ser Thr Lys Ile Arg
            340                 345                 350
Leu Phe Glu Asn Val Met Ser Phe Met Lys Arg Phe Asn Leu Gly Glu
        355                 360                 365
Leu Tyr Ser Tyr Leu Lys Lys Ile Ile Asp Trp Lys Thr His Glu Asn
    370                 375                 380
Asn Gln Lys Leu Ala Trp Pro Glu Ile Val Asp Asp Lys Tyr Ala Phe
385                 390                 395                 400
Leu Lys Tyr Asp Tyr Phe Gly Thr Pro His Gly Phe Val Tyr Asp Gln
                405                 410                 415
Lys Asp Arg Thr Met Tyr Val Lys Leu His Cys Gly Ile Ala Ala Asn
            420                 425                 430
Arg Asn Ile Tyr Ile Asp Ile
        435
```

<210> 492
<211> 341
<212> PRT
<213> Cowpox virus

<400> 492

```
Met Asp Ile Phe Arg Glu Ile Ala Ser Ser Met Lys Gly Glu Asn Val
 1               5                  10                  15
Phe Ile Ser Pro Pro Ser Ile Ser Ser Val Leu Thr Ile Leu Tyr Tyr
            20                  25                  30
Gly Ala Asn Gly Ser Thr Ala Glu Gln Leu Ser Lys Tyr Val Glu Lys
        35                  40                  45
Glu Ala Asp Lys Asn Lys Asp Asp Ile Ser Phe Lys Ser Met Asn Lys
    50                  55                  60
Val Tyr Gly Arg Tyr Ser Ala Val Phe Lys Asp Ser Phe Leu Arg Lys
65                  70                  75                  80
Ile Gly Asp Asn Phe Gln Thr Val Asp Phe Thr Asp Cys Arg Thr Val
                85                  90                  95
```

```
Asp Ala Ile Asn Lys Cys Val Asp Ile Phe Thr Glu Gly Lys Ile Asn
            100                 105                 110
Pro Leu Leu Asp Glu Pro Leu Ser Pro Asp Thr Cys Leu Leu Ala Ile
        115                 120                 125
Ser Ala Val Tyr Phe Lys Ala Lys Trp Leu Met Pro Phe Glu Lys Glu
    130                 135                 140
Phe Thr Ser Asp Tyr Pro Phe Tyr Val Ser Pro Thr Glu Met Val Asp
145                 150                 155                 160
Val Ser Met Met Ser Met Tyr Gly Glu Ala Phe Asn His Ala Ser Val
                165                 170                 175
Lys Glu Ser Phe Gly Asn Phe Ser Ile Ile Glu Leu Pro Tyr Val Gly
            180                 185                 190
Asp Thr Ser Met Val Val Ile Leu Pro Asp Asn Ile Asp Gly Leu Glu
        195                 200                 205
Ser Ile Glu Gln Asn Leu Thr Asp Thr Asn Phe Lys Lys Trp Cys Asp
    210                 215                 220
Ser Met Asp Ala Met Phe Ile Asp Val His Ile Pro Lys Phe Lys Val
225                 230                 235                 240
Thr Gly Ser Tyr Asn Leu Val Asp Ala Leu Val Lys Leu Gly Leu Thr
                245                 250                 255
Glu Val Phe Gly Ser Thr Gly Asp Tyr Ser Asn Met Cys Asn Ser Asp
            260                 265                 270
Val Ser Val Asp Ala Met Ile His Lys Thr Tyr Ile Asp Val Asn Glu
        275                 280                 285
Glu Tyr Thr Glu Ala Ala Ala Ala Thr Cys Ala Leu Val Ala Asp Cys
    290                 295                 300
Ala Ser Thr Val Thr Asn Glu Phe Cys Ala Asp His Pro Phe Ile Tyr
305                 310                 315                 320
Val Ile Arg His Val Asp Gly Lys Ile Leu Phe Val Gly Arg Tyr Cys
                325                 330                 335
Ser Pro Thr Thr Asn
            340
```

<210> 493
<211> 432
<212> PRT
<213> Homo sapiens

<220>
<223> antithrombin III mature

<400> 493

```
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1               5                  10                  15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20                  25                  30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35                  40                  45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50                  55                  60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65                  70                  75                  80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85                  90                  95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100                 105                 110
```

```
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115                 120                 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130                 135                 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145                 150                 155                 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165                 170                 175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180                 185                 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195                 200                 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210                 215                 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225                 230                 235                 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
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Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
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<223> AT3/RRVRKE

<400> 497
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            20   25   30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35   40   45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50   55   60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65   70   75   80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85   90   95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100   105   110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115   120   125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130   135   140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145   150   155   160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165   170   175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180   185   190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195   200   205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210   215   220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225   230   235   240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly

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                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355                 360                 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370                 375                 380
Ser Thr Ala Val Val Arg Arg Val Arg Lys Glu Asn Pro Asn Arg Val
385                 390                 395                 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
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Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
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<210> 498
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> replacement cleavage site RRVRKE

<400> 498
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<210> 499
<211> 432
<212> PRT
<213> Homo sapiens

<220>
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<223> AT3/SLGRKI

<400> 499
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            20                  25                  30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35                  40                  45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
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65                  70                  75                  80
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                85                  90                  95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100                 105                 110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115                 120                 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130                 135                 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145                 150                 155                 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165                 170                 175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180                 185                 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195                 200                 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210                 215                 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225                 230                 235                 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355                 360                 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370                 375                 380
Ser Thr Ala Val Val Ser Leu Gly Arg Lys Ile Asn Pro Asn Arg Val
385                 390                 395                 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
                405                 410                 415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430
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<210> 500
<211> 432
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant AT3 sequence

<223> SKGRSL

<400> 500

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His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1               5                  10                  15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20                  25                  30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35                  40                  45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50                  55                  60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65                  70                  75                  80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85                  90                  95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100                 105                 110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115                 120                 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130                 135                 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145                 150                 155                 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165                 170                 175

Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180                 185                 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195                 200                 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210                 215                 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225                 230                 235                 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355                 360                 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370                 375                 380
Ser Thr Ala Val Val Ser Lys Gly Arg Ser Leu Asn Pro Asn Arg Val
385                 390                 395                 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
                405                 410                 415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
```

420 425 430

<210> 501
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> replacement cleavage site SKGRSL

<400> 501
Ser Lys Gly Arg Ser Leu
1 5

<210> 502
<211> 432
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant AT3 sequence

<223> AT3/PRFKII

<400> 502
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
1 5 10 15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
20 25 30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
35 40 45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
50 55 60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65 70 75 80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
85 90 95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
100 105 110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
115 120 125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
130 135 140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145 150 155 160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
165 170 175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
180 185 190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
195 200 205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
210 215 220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr

```
225                 230                 235                 240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
                245                 250                 255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260                 265                 270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275                 280                 285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290                 295                 300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305                 310                 315                 320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325                 330                 335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340                 345                 350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355                 360                 365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370                 375                 380
Ser Thr Ala Val Val Pro Arg Phe Lys Ile Ile Asn Pro Asn Arg Val
385                 390                 395                 400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
                405                 410                 415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430
```

<210> 503
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> replacement cleavage site PRFKII

<400> 503
Pro Arg Phe Lys Ile Ile
 1   5

<210> 504
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<223> MT-SP1 protease domain

<400> 504
gttgttgggg gcacggatgc ggatgagggc gagtggccct ggcaggtaag cctgcatgct 60
ctgggccagg gccacatctg cggtgcttcc ctcatctctc ccaactggct ggtctctgcc 120
gcacactgct acatcgatga cagaggattc aggtactcag accccacgca gtggacggcc 180
ttcctgggct tgcacgacca gagccagcgc agcgcccctg gggtgcagga gcgcaggctc 240
aagcgcatca tctcccaccc cttcttcaat gacttcacct tcgactatga catcgcgctg 300
ctggagctgg agaaaccggc agagtacagc tccatggtgc ggcccatctg cctgccggac 360
gcctcccatg tcttccctgc cggcaaggcc atctgggtca cgggctgggg acacacccag 420

tatggaggca ctggcgcgct gatcctgcaa aagggtgaga tccgcgtcat caaccagacc 480
acctgcgaga acctcctgcc gcagcagatc acgccgcgca tgatgtgcgt gggcttcctc 540
agcggcggcg tggactcctg ccagggtgat tccgggggac ccctgtccag cgtggaggcg 600
gatgggcgga tcttccaggc cggtgtggtg agctggggag acggctgcgc tcagaggaac 660
aagccaggcg tgtacacaag gctccctctg tttcgggact ggatcaaaga gaacactggg 720
gta 723

<210> 505
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> MT-SP1 protease domain

<400> 505
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165   170   175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 506
<211> 444
<212> PRT
<213> Homo sapiens

<220>
<223> MT-SP1 protease domain fusion

<223> STII/MT-SP1/GeneII

<400> 506

```
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
 1               5                  10                  15
Ile Ala Thr Asn Ala Tyr Ala Val Val Gly Gly Thr Asp Ala Asp Glu
            20                  25                  30
Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His
        35                  40                  45
Ile Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala
    50                  55                  60
His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln
65                  70                  75                  80
Trp Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro
                85                  90                  95
Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe
            100                 105                 110
Asn Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys
        115                 120                 125
Pro Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala
    130                 135                 140
Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly
145                 150                 155                 160
His Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu
                165                 170                 175
Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln
            180                 185                 190
Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp
        195                 200                 205
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp
    210                 215                 220
Gly Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala
225                 230                 235                 240
Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp
                245                 250                 255
Trp Ile Lys Glu Asn Thr Gly Val Ser Gly Ser Ser Gly Gly Gly Ser
            260                 265                 270
Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser Gly
        275                 280                 285
Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala
    290                 295                 300
Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser
305                 310                 315                 320
Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala
                325                 330                 335
Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly
            340                 345                 350

Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly
        355                 360                 365
Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro
    370                 375                 380
Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Ser Ala Gly
385                 390                 395                 400
```

```
Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg
                405                 410                 415
Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe
            420                 425                 430
Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
        435                 440
```

<210> 507
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutated MT-SP1 protease domain

<223> CB496

<400> 507

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 508
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> MT-SP1 forward primer

<400> 508
gcgcagatat cgtaccgcat atgaaaaaga atatcgcatt tctt 44

<210> 509
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> MT-SP1 reverse primer

<400> 509
gtgcatgctg actgactgag ctcccgctta ccccagtgtt ctc 43

<210> 510
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<223> MT-SP1 protease domain fusion

<223> STII/MT-SP1/GeneIII

<400> 510
atgaaaaaga atatcgcatt tcttcttgca tctatgttcg ttttttctat tgctacaaat 60
gcctatgcag ttgttggggg cacggatgcg gatgagggcg agtggccctg gcaggtaagc 120
ctgcatgctc tgggccaggg ccacatctgc ggtgcttccc tcatctctcc caactggctg 180
gtctctgccg cacactgcta catcgatgac agaggattca ggtactcaga ccccacgcag 240
tggacggcct tcctgggctt gcacgaccag agccagcgca gcgcccctgg ggtgcaggag 300
cgcaggctca agcgcatcat ctcccacccc ttcttcaatg acttcacctt cgactatgac 360
atcgcgctgc tggagctgga gaaaccggca gagtacagct ccatggtgcg gcccatctgc 420
ctgccggacg cctcccatgt cttccctgcc ggcaaggcca tctgggtcac gggctgggga 480
cacacccagt atggaggcac tggcgcgctg atcctgcaaa agggtgagat ccgcgtcatc 540
aaccagacca cctgcgagaa cctcctgccg cagcagatca cgccgcgcat gatgtgcgtg 600
ggcttcctca gcggcggcgt ggactcctgc cagggtgatt ccgggggacc cctgtccagc 660
gtggaggcgg atgggcggat cttccaggcc ggtgtggtga gctggggaga cggctgcgct 720
cagaggaaca agccaggcgt gtacacaagg ctccctctgt ttcgggactg gatcaaagag 780
aacactgggg taagcgggag ctccggtggt ggctctgagg gtggcggttc tgagggtggc 840
ggctctgagg gaggcggttc cggtggtggc tctggttccg gtgattttga ttatgaaaag 900
atggcaaacg ctaataaggg ggctatgacc gaaaatgccg atgaaaacgc gctacagtct 960
gacgctaaag gcaaacttga ttctgtcgct actgattacg gtgctgctat cgatggtttc 1020
attggtgacg tttccggcct tgctaatggt aatggtgcta ctggtgattt tgctggctct 1080
aattcccaaa tggctcaagt cggtgacggt gataattcac ctttaatgaa taatttccgt 1140
caatatttac cttccctccc tcaatcggtt gaatgtcgcc cttttgtctt tagcgctggt 1200
aaaccatatg aattttctat tgattgtgac aaaataaact tattccgtgg tgtctttgcg 1260
tttcttttat atgttgccac ctttatgtat gtattttcta cgtttgctaa catactgcgt 1320
aataaggagt cttaa 1335

<210> 511
<211> 23
<212> PRT
<213> Escherichia coli

<220>
<223> STII leader sequence

<400> 511
Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe Ser
 1   5   10   15
Ile Ala Thr Asn Ala Tyr Ala
            20

<210> 512
<211> 180
<212> PRT
<213> M13 phage

<220>
<223> GeneIII

<400> 512
Ser Gly Ser Ser Gly Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly Gly
 1   5   10   15
Gly Ser Glu Gly Gly Gly Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe
            20   25   30
Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn
        35   40   45
Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser
    50   55   60
Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val
65   70   75   80
Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser
                85   90   95
Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met
            100   105   110
Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys
        115   120   125
Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp
    130   135   140
Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr
145   150   155   160
Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg
                165   170   175
Asn Lys Glu Ser
            180

<210> 513
<211> 4
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized protease cleavage site RQAR

<400> 513
Arg Gln Ala Arg
1

<210> 514
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized protease cleavage site SLGR

<400> 514
Ser Leu Gly Arg
1

<210> 515
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CB469

<400> 515
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
1 5 10 15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
20 25 30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
35 40 45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
50 55 60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65 70 75 80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
85 90 95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100 105 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115 120 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130 135 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145 150 155 160

```
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
```

```
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 516
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP-1 protease domain

<223> CPC-0019595

<400> 516

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1                5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
```

```
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Thr Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asp Gln Ala
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Leu Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 517
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0023085

<400> 517

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr

                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
```

```
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 518
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0024153

<400> 518

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Thr Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Gly
```

<210> 519

<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0025366

<400> 519
Val Val Gly Gly Thr Asp Ala Glu Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Pro Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Ile Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165   170   175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 520
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0025387

<400> 520
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15

```
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 521
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0025582

```
<400> 521
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
```

```
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Gly
```

<210> 522
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP-1 protease domain

<223> CPC-0025720

<400> 522

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly Arg Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
```

```
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 523
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0025876

<400> 523

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 524
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0025974

<400> 524
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165   170   175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 525
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0026100

<400> 525
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg

```
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Val Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Gly
```

<210> 526
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0026323

```
<400> 526
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Met Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Asp Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
```

```
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Leu Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 527
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0027399

<400> 527

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Leu Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
```

225 230 235 240
Val

<210> 528
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0027706

<400> 528
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Tyr Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Val Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys His Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ile Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 529
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0027797

<400> 529
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
Arg Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Ser Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165   170   175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 530
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0028017

<400> 530
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45

```
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
     50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly

        195                 200                 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 531
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0028333

```
<400> 531
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Lys Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Leu Phe Asn Asp Tyr Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
```

```
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 532
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0028341

<400> 532

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Thr Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Ser Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Leu Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
```

```
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 533
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0033634

<400> 533

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Leu Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Leu Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 534
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0028791

<400> 534
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165   170   175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 535
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0027484

<400> 535
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15

```
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Lys Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 536
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 protease domain

<223> CPC-0028993

```
<400> 536
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Ser Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
```

```
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Ser Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 537
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0019595

<400> 537

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
```

```
                180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
```

```
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Thr Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asp Gln Ala Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Leu Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 538
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0023085

<400> 538

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15

Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
```

```
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp

        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
```

```
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 539
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length


<223> CPC-0024153

<400> 539
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
```

```
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140

Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
```

```
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Thr Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Gly
    850                 855
```

<210> 540
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0025366

<400> 540

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270

Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
```

```
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Glu Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Pro Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Ile Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 541
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0025387

<400> 541
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1   5   10   15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20   25   30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35   40   45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50   55   60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65   70   75   80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85   90   95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100   105   110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115   120   125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130   135   140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145   150   155   160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165   170   175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180   185   190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195   200   205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210   215   220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225   230   235   240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245   250   255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260   265   270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275   280   285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290   295   300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305   310   315   320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325   330   335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn

```
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400

Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His

            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
```

```
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 542
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length


<223> CPC-0025582

<400> 542
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
```

```
                260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525

Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
```

```
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Gly
    850                 855
```

<210> 543
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0025720

<400> 543

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
```

Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
340 345 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
355 360 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
370 375 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385 390 395 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
405 410 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
420 425 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
435 440 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
450 455 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465 470 475 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
485 490 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
500 505 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
515 520 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
530 535 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545 550 555 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
565 570 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
580 585 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
595 600 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
610 615 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625 630 635 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His

```
                645                 650                 655

Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly Arg
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 544
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0025876

```
<400> 544
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
```

```
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
```

```
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile
    770                 775                 780

Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 545
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0025974

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<400> 545
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
```

```
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
     50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
```

```
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 546
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0026100

<400> 546
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1   5   10   15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20   25   30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35   40   45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50   55   60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65   70   75   80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85   90   95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100   105   110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115   120   125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130   135   140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145   150   155   160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165   170   175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180   185   190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195   200   205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210   215   220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225   230   235   240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245   250   255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260   265   270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275   280   285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290   295   300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305   310   315   320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325   330   335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340   345   350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355   360   365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370   375   380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385   390   395   400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405   410   415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420   425   430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp

```
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Val Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Gly
    850                 855
```

<210> 547
<211> 855

<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0026323

<400> 547

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
```

```
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Met Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Asp Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Leu
            820                 825                 830
```

```
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 548
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length


<223> CPC-002739

<400> 548
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
```

```
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Leu Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
```

```
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 549
<211> 855

<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length


<223> CPC-0027706

<400> 549
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
```

```
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
```

```
     690                 695                 700
Asp Tyr Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Val Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys His Gly Asp Ser Gly Gly Pro Leu Ser Ile Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 550
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length


<223> CPC-0027797

<400> 550
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
```

```
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
```

```
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu Arg Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Ser Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 551
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0028017

```
<400> 551
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
```

```
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
```

```
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 552
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0028333

<400> 552

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
```

```
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
```

```
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Lys Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Leu Phe Asn
    690                 695                 700
Asp Tyr Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 553
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0028341

<400> 553
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
1 5 10 15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
20 25 30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
35 40 45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
50 55 60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65 70 75 80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
85 90 95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100 105 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115 120 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130 135 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145 150 155 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165 170 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180 185 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
340 345 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
355 360 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
370 375 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385 390 395 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
405 410 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
420 425 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp

```
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Thr
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Ser Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Leu Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 554
<211> 855

<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0033634

<400> 554
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1   5   10   15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20   25   30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35   40   45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50   55   60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65   70   75   80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85   90   95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100   105   110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115   120   125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130   135   140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145   150   155   160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165   170   175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180   185   190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195   200   205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210   215   220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225   230   235   240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245   250   255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260   265   270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275   280   285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290   295   300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305   310   315   320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325   330   335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340   345   350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355   360   365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe

```
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Leu Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
```

```
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Leu Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 555
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0028791

<400> 555

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Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
```

```
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
```

```
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 556
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0027484

<400> 556

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Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
```

```
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Lys
    690                 695                 700
```

```
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 557
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MT-SP1 full length

<223> CPC-0028993

<400> 557

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Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
```

```
                180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
```

```
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Ser Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Ser Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 558
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> N-terminal sequence of pIVEX 2.3d MTSP

<400> 558

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Met Glu Lys Thr Arg His His His His His His Ser Gly Ser Asp Cys
 1               5                  10                  15
Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg
            20                  25
```

<210> 559
<211> 3560
<212> DNA
<213> Artificial Sequence

<220>
<223> pIVEX 2.3d vector

<400> 559

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tcgcgcgttt cggtgatgac ggtgaaaacc tctgacacat gcagctcccg gagacggtca 60
cagcttgtct gtaagcggat gccgggagca gacaagcccg tcagggcgcg tcagcgggtg 120
ttggcgggtg tcggggctgg cttaactatg cggcatcaga gcagattgta ctgagagtgc 180
```

accatatatg cggtgtgaaa taccgcacag atgcgtaagg agaaaatacc gcatcaggcg 240
ccattcgcca ttcaggctgc gcaactgttg ggaagggcga tcggtgcggg cctcttcgct 300
attacgccag ctggcgaaag ggggatgtgc tgcaaggcga ttaagttggg taacgccagg 360
gttttcccag tcacgacgtt gtaaaacgac ggccagtgcc aagcttgcat gcaaggagat 420
ggcgcccaac agtcccccgg ccacggggcc tgccaccata cccacgccga aacaagcgct 480
catgagcccg aagtggcgag cccgatcttc cccatcggtg atgtcggcga tataggcgcc 540
agcaaccgca cctgtggcgc cggtgatgcc ggccacgatg cgtccggcgt agaggatcga 600
gatctcgatc ccgcgaaatt aatacgactc actataggga gaccacaacg gtttccctct 660
agaaataatt ttgtttaact ttaagaagga gatataccat ggcacatatg agcggccgcg 720
tcgactcgag cgagctcccg gggggggttc tcatcatcat catcatcatt aataaaaggg 780
cgaattccag cacactggcg gccgttacta gtggatccgg ctgctaacaa agcccgaaag 840
gaagctgagt tggctgctgc caccgctgag caataactag cataacccct tggggcctct 900
aaacgggtct tgaggggttt tttgctgaaa ggaggaacta tatccggata tccacaggac 960
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tgggcggcgg ccaaagcggt cggacagtgc tccgagaacg ggtgcgcata gaaattgcat 1080
caacgcatat agcgctagca gcacgccata gtgactggcg atgctgtcgg aatggacgat 1140
atcccgcaag aggcccggca gtaccggcat aaccaagcct atgcctacag catccagggt 1200
gacggtgccg aggatgacga tgagcgcatt gttagatttc atacacggtg cctgactgcg 1260
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atgagaattc gtaatcatgt catagctgtt tcctgtgtga aattgttatc cgctcacaat 1380
tccacacaac atacgagccg gaagcataaa gtgtaaagcc tggggtgcct aatgagtgag 1440
ctaactcaca ttaattgcgt tgcgctcact gcccgctttc cagtcgggaa acctgtcgtg 1500
ccagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc 1560
ttccgcttcc tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc 1620
agctcactca aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa 1680
catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt 1740
tttccatagg ctccgccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg 1800
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cgtggcgctt tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc 1980
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taacaggatt agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc 2160
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cttcggaaaa agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcggtgg 2280
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aaggcgagtt acatgatccc ccatgttgtg caaaaaagcg gttagctcct tcggtcctcc 2940
gatcgttgtc agaagtaagt tggccgcagt gttatcactc atggttatgg cagcactgca 3000
taattctctt actgtcatgc catccgtaag atgcttttct gtgactggtg agtactcaac 3060
caagtcattc tgagaatagt gtatgcggcg accgagttgc tcttgcccgg cgtcaatacg 3120
ggataatacc gcgccacata gcagaacttt aaaagtgctc atcattggaa aacgttcttc 3180
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tgcacccaac tgatcttcag catcttttac tttcaccagc gtttctgggt gagcaaaaac 3300
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<223> pQE-Insert-F2 forward primer

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<223> pQE-Linear-F2 primer

<400> 562
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<210> 563
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> pQE-Linear-R1 primer

<400> 563
taataagctt aattagctga gcttggactc c 31

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<213> Artificial Sequence

<220>
<223> forward primer: MTSP-5F

<400> 564
ggagaaaccg gcagagtac 19

<210> 565
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<212> DNA
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<220>
<223> reverse primer MTSP-5R

<400> 565
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<212> DNA
<213> Artificial Sequence

<220>
<223> pET21a vector

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atttagagct tgacggggaa agccggcgaa cgtggcgaga aaggaaggga agaaagcgaa 5340
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<210> 567

<211> 379
<212> PRT
<213> Homo sapiens

<220>
<223> PAI-1 stable

<400> 567
Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly
 1   5   10   15
Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val
            20   25   30
Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu
        35   40   45
Thr Thr Gly Gly Glu Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe
    50   55   60
Lys Ile Asp Asp Lys Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys
65   70   75   80
Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala
                85   90   95
Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro His
            100   105   110
Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser Glu
        115   120   125
Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr
    130   135   140
Lys Gly Met Ile Ser His Leu Leu Gly Thr Gly Ala Val Asp Gln Leu
145   150   155   160
Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys
                165   170   175
Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys Ser
            180   185   190
Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe
        195   200   205
Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu
    210   215   220
Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro
225   230   235   240
Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser Ala
                245   250   255
Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu
            260   265   270
Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys
        275   280   285
Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala
    290   295   300
Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Leu Ala
305   310   315   320
Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser
                325   330   335
Ser Ser Thr Ala Val Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile
            340   345   350
Ile Ile Asp Arg Pro Phe Leu Phe Val Val Arg His Asn Pro Thr Gly
        355   360   365
Thr Val Leu Phe Met Gly Gln Val Met Glu Pro
    370   375

<210> 568
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I136T/N164D/T166A/F184(A)L/D217V

<400> 568
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Thr Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asp Gln Ala
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Leu Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 569
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41F

<400> 569
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165   170   175

Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 570
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41F/A126T/V244G

<400> 570
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60

```
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met

            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Thr Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Gly
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<210> 571
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> D23E/I41F/T98P/T144I

<400> 571

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Val Val Gly Gly Thr Asp Ala Glu Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Pro Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Ile Gln Tyr Gly Gly Thr
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    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
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<210> 572
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41F

<400> 572

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Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
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Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 573
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41F/L171F/V244G

<400> 573
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Gly

<210> 574
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> H143R/Q175R

<400> 574
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20   25   30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35   40   45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50   55   60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65   70   75   80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85   90   95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100   105   110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115   120   125
Lys Ala Ile Trp Val Thr Gly Trp Gly Arg Thr Gln Tyr Gly Gly Thr
    130   135   140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145   150   155   160
Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile Thr Pro Arg Met Met Cys
                165   170   175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180   185   190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195   200   205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210   215   220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225   230   235   240
Val

<210> 575
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41F/L171F

<400> 575
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1   5   10   15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile

```
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 576
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> R230W

```
<400> 576
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
```

```
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140

Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 577
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41F/I154V/V244G

<400> 577

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu

65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Val Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
```

```
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Gly
```

<210> 578
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I141F/L52M/V129D/Q221(A)L

<400> 578

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Phe Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Met Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Asp Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Leu Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 579
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> F99L

<400> 579
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Leu Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 580
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> F97Y/I136V/Q192H/S201I

<400> 580
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Tyr Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Val Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys His Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ile Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 581
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> H71R/P131S/D217V

<400> 581
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60

```
Arg Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Ser Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 582
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> D217V

<400> 582

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
```

```
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 583
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> T65K/F93L/F97Y/D217V

<400> 583

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Lys Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Leu Phe Asn Asp Tyr Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Val Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
```

Val

<210> 584
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> I41T/P173S/Q209L

<400> 584
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Thr Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Ser Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Leu Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 585
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> F97L//F234L

<400> 585
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
50 55 60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65 70 75 80
Lys Arg Ile Ile Ser His Pro Leu Phe Asn Asp Phe Thr Phe Asp Tyr
85 90 95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
100 105 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Leu Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 586
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> Q175R

<400> 586
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
1 5 10 15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
20 25 30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
35 40 45

```
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 587
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> N95K

<400> 587

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Lys Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
```

```
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225                 230                 235                 240
Val
```

<210> 588
<211> 241
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 protease domain

<223> Y60(G)S

<400> 588

```
Val Val Gly Gly Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val
 1               5                  10                  15
Ser Leu His Ala Leu Gly Gln Gly His Ile Cys Gly Ala Ser Leu Ile
            20                  25                  30
Ser Pro Asn Trp Leu Val Ser Ala Ala His Cys Tyr Ile Asp Asp Arg
        35                  40                  45
Gly Phe Arg Ser Ser Asp Pro Thr Gln Trp Thr Ala Phe Leu Gly Leu
    50                  55                  60
His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu
65                  70                  75                  80
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
                85                  90                  95
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met
            100                 105                 110
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
        115                 120                 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
    130                 135                 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145                 150                 155                 160
Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile Thr Pro Arg Met Met Cys
                165                 170                 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
            180                 185                 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
        195                 200                 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
    210                 215                 220
```

Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

<210> 589
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> I136T/N164D/T166A/F184(A)L/D217V

<400> 589
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
1 5 10 15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
20 25 30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
35 40 45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
50 55 60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65 70 75 80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
85 90 95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100 105 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115 120 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130 135 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145 150 155 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165 170 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180 185 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr

305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335

Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
340 345 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
355 360 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
370 375 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385 390 395 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
405 410 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
420 425 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
435 440 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
450 455 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465 470 475 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
485 490 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
500 505 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
515 520 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
530 535 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545 550 555 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
565 570 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
580 585 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
595 600 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
610 615 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625 630 635 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
645 650 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
660 665 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
675 680 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
690 695 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705 710 715 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
725 730 735
His Val Phe Pro Ala Gly Lys Ala Thr Trp Val Thr Gly Trp Gly His
740 745 750

```
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asp Gln Ala Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Leu Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 590
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length


<223> I41F

<400> 590
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
```

```
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
```

```
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 591
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> I41F/A126T/V244G

```
<400> 591
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
```

Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165 170 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180 185 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
340 345 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
355 360 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
370 375 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385 390 395 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
405 410 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
420 425 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
435 440 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
450 455 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465 470 475 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
485 490 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
500 505 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
515 520 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
530 535 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545 550 555 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
565 570 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
580 585 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
595 600 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly

```
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Thr Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Gly
    850                 855
```

<210> 592
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> D23E/I41F/T98P/T144I

```
<400> 592
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
```

```
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
                100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
```

```
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Glu Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Pro Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Ile Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 593
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> I41F

<400> 593

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
```

```
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
```

```
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 594
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> I41F/L171F/V244G

<400> 594

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
```

```
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Gly
    850                 855
```

<210> 595
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> H143R/Q175R

<400> 595
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
1 5 10 15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
20 25 30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
35 40 45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
50 55 60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65 70 75 80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
85 90 95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100 105 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115 120 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130 135 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145 150 155 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165 170 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180 185 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
340 345 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp

```
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly Arg
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
```

```
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 596
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length


<223>  I41F/L171F

<400> 596
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
```

```
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
```

```
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Phe Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 597

<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> R230W

<400> 597

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
```

```
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
```

```
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 598
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> I41F/I154V/V244G

<400> 598

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1                  5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
```

```
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
```

```
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Val Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830

Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Gly
    850                 855


<210> 599
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length


<223>  I141F/L52M/V129D/Q221(A)L

<400> 599
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
```

```
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
```

```
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Phe
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Met Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Asp Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Leu
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 600
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> F99L

<400> 600

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
```

```
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
```

```
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Leu Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 601
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> F97Y/I136V/Q192H/S201I

<400> 601

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
```

```
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Tyr Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Val Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys His Gly Asp Ser Gly Gly Pro Leu Ser Ile Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 602
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> H71R/P131S/D217V

<400> 602
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
1 5 10 15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
20 25 30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
35 40 45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
50 55 60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65 70 75 80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
85 90 95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100 105 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115 120 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130 135 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145 150 155 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165 170 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180 185 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn

```
                340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu Arg Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Ser Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
```

```
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 603
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length


<223> D217V

<400> 603
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
```

```
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720

Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
```

```
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 604
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> T65K/F93L/F97Y/D217V

<400> 604

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
```

```
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
```

```
            660                 665                 670
Lys Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Leu Phe Asn
    690                 695                 700
Asp Tyr Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Val Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 605
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length


<223> I41T/P173S/Q209L

<400> 605
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1                   5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
```

```
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
```

```
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Thr
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Ser Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Leu Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 606
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length


<223> F97L//F234L

<400> 606
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
```

```
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
```

```
     530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Leu Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Leu Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 607
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> Q175R

<400> 607

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
```

```
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
```

```
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 608
<211> 855
<212> PRT
<213> Homo sapiens

<220>

<223> Mutant MTSP1 full length

<223> N95K

<400> 608

```
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
 1               5                  10                  15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
            20                  25                  30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
        35                  40                  45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
    50                  55                  60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65                  70                  75                  80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
                85                  90                  95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
            100                 105                 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
        115                 120                 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
    130                 135                 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145                 150                 155                 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
                165                 170                 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
            180                 185                 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
        195                 200                 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
    210                 215                 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225                 230                 235                 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
                245                 250                 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
            260                 265                 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
        275                 280                 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
    290                 295                 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305                 310                 315                 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
                325                 330                 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn
            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
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                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Lys
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855
```

<210> 609
<211> 855
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant MTSP1 full length

<223> Y60(G)S

<400> 609
Met Gly Ser Asp Arg Ala Arg Lys Gly Gly Gly Gly Pro Lys Asp Phe
1 5 10 15
Gly Ala Gly Leu Lys Tyr Asn Ser Arg His Glu Lys Val Asn Gly Leu
20 25 30
Glu Glu Gly Val Glu Phe Leu Pro Val Asn Asn Val Lys Lys Val Glu
35 40 45
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly
50 55 60
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln
65 70 75 80
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile
85 90 95
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu
100 105 110
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr
115 120 125
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr
130 135 140
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser
145 150 155 160
Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val Met Ala Glu Glu
165 170 175
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val
180 185 190
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg
195 200 205
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu
210 215 220
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala
225 230 235 240
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu
245 250 255
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly
260 265 270
Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro Met Glu Pro His
275 280 285
Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser Tyr Asn Leu Thr
290 295 300
Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu Ile Thr Asn Thr
305 310 315 320
Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe Gln Leu Pro Arg
325 330 335
Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln Gly Thr Phe Asn

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            340                 345                 350
Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile Asp Cys Thr Trp
        355                 360                 365
Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val Arg Phe Lys Phe
    370                 375                 380
Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr Cys Pro Lys Asp
385                 390                 395                 400
Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu Arg Ser Gln Phe
                405                 410                 415
Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg Phe His Ser Asp
            420                 425                 430
Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr Leu Ser Tyr Asp
        435                 440                 445
Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg Thr Gly Arg Cys
    450                 455                 460
Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp Cys Thr Asp His
465                 470                 475                 480
Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His Gln Phe Thr Cys
                485                 490                 495
Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys Asp Ser Val Asn
            500                 505                 510
Asp Cys Gly Asp Asn Ser Asp Glu Gln Gly Cys Ser Cys Pro Ala Gln
        515                 520                 525
Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys Ser Gln Gln Cys
    530                 535                 540
Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu Ala Ser Cys Pro
545                 550                 555                 560
Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr Arg Cys Leu Asn
                565                 570                 575
Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp Gly Lys Glu Asp
            580                 585                 590
Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys Gly Leu Arg Ser
        595                 600                 605
Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp Ala Asp Glu Gly
    610                 615                 620
Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly Gln Gly His Ile
625                 630                 635                 640
Cys Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val Ser Ala Ala His
                645                 650                 655
Cys Tyr Ile Asp Asp Arg Gly Phe Arg Ser Ser Asp Pro Thr Gln Trp
            660                 665                 670
Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg Ser Ala Pro Gly
        675                 680                 685
Val Gln Glu Arg Arg Leu Lys Arg Ile Ile Ser His Pro Phe Phe Asn
    690                 695                 700
Asp Phe Thr Phe Asp Tyr Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro
705                 710                 715                 720
Ala Glu Tyr Ser Ser Met Val Arg Pro Ile Cys Leu Pro Asp Ala Ser
                725                 730                 735
His Val Phe Pro Ala Gly Lys Ala Ile Trp Val Thr Gly Trp Gly His
            740                 745                 750
Thr Gln Tyr Gly Gly Thr Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile
        755                 760                 765
Arg Val Ile Asn Gln Thr Thr Cys Glu Asn Leu Leu Pro Gln Arg Ile
    770                 775                 780
Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
785                 790                 795                 800
```

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Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
                805                 810                 815
Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
            820                 825                 830
Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp
        835                 840                 845
Ile Lys Glu Asn Thr Gly Val
    850                 855


<210> 610
<211> 380
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant mature PAI-1

<223> PAI-1/RRAR

<400> 610
Met Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe
 1               5                  10                  15
Gly Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn
            20                  25                  30
Val Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln
        35                  40                  45
Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln Ile Gln Ala Ala Met Gly
    50                  55                  60
Phe Lys Ile Asp Asp Lys Gly Met Ala Pro Ala Leu Arg His Leu Tyr
65                  70                  75                  80
Lys Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp
                85                  90                  95
Ala Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro
            100                 105                 110
His Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser
        115                 120                 125
Glu Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His
    130                 135                 140
Thr Lys Gly Met Ile Ser Asn Leu Leu Gly Lys Gly Ala Val Asp Gln
145                 150                 155                 160
Leu Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp
                165                 170                 175
Lys Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys
            180                 185                 190
Ser Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys
        195                 200                 205
Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile
    210                 215                 220
Leu Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala
225                 230                 235                 240
Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser
                245                 250                 255
Ala Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg
            260                 265                 270
Leu Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg
        275                 280                 285
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Lys Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln
    290                 295                 300
Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Gln
305                 310                 315                 320
Ala Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala
                325                 330                 335
Ser Ser Ser Thr Ala Val Ile Arg Arg Ala Arg Met Ala Pro Glu Glu
            340                 345                 350
Ile Ile Met Asp Arg Pro Phe Leu Phe Val Val Arg His Asn Pro Thr
        355                 360                 365
Gly Thr Val Leu Phe Met Gly Gln Val Met Glu Pro
    370                 375                 380


<210> 611
<211> 380
<212> PRT
<213> Homo sapiens

<220>
<223> Mutant mature PAI-1

<223> PAI-1/69 (containing PFGRS)

<400> 611
Met Val His His Pro Pro Ser Tyr Val Ala His Leu Ala Ser Asp Phe
 1               5                  10                  15
Gly Val Arg Val Phe Gln Gln Val Ala Gln Ala Ser Lys Asp Arg Asn
            20                  25                  30
Val Val Phe Ser Pro Tyr Gly Val Ala Ser Val Leu Ala Met Leu Gln
        35                  40                  45
Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln Ile Gln Ala Ala Met Gly
    50                  55                  60
Phe Lys Ile Asp Asp Lys Gly Met Ala Pro Ala Leu Arg His Leu Tyr
65                  70                  75                  80
Lys Glu Leu Met Gly Pro Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp
                85                  90                  95
Ala Ile Phe Val Gln Arg Asp Leu Lys Leu Val Gln Gly Phe Met Pro
            100                 105                 110
His Phe Phe Arg Leu Phe Arg Ser Thr Val Lys Gln Val Asp Phe Ser
        115                 120                 125
Glu Val Glu Arg Ala Arg Phe Ile Ile Asn Asp Trp Val Lys Thr His
    130                 135                 140
Thr Lys Gly Met Ile Ser Asn Leu Leu Gly Lys Gly Ala Val Asp Gln
145                 150                 155                 160
Leu Thr Arg Leu Val Leu Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp
                165                 170                 175
Lys Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His Lys
            180                 185                 190
Ser Asp Gly Ser Thr Val Ser Val Pro Met Met Ala Gln Thr Asn Lys
        195                 200                 205
Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile
    210                 215                 220
Leu Glu Leu Pro Tyr His Gly Asp Thr Leu Ser Met Phe Ile Ala Ala
225                 230                 235                 240
Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala Leu Thr Asn Ile Leu Ser
                245                 250                 255
```

```
Ala Gln Leu Ile Ser His Trp Lys Gly Asn Met Thr Arg Leu Pro Arg
            260                 265                 270
Leu Leu Val Leu Pro Lys Phe Ser Leu Glu Thr Glu Val Asp Leu Arg
        275                 280                 285
Lys Pro Leu Glu Asn Leu Gly Met Thr Asp Met Phe Arg Gln Phe Gln
    290                 295                 300
Ala Asp Phe Thr Ser Leu Ser Asp Gln Glu Pro Leu His Val Ala Gln
305                 310                 315                 320
Ala Leu Gln Lys Val Lys Ile Glu Val Asn Glu Ser Gly Thr Val Ala
                325                 330                 335
Ser Ser Ser Thr Ala Val Ile Pro Phe Gly Arg Ser Ala Pro Glu Glu
            340                 345                 350
Ile Ile Met Asp Arg Pro Phe Leu Phe Val Val Arg His Asn Pro Thr
        355                 360                 365
Gly Thr Val Leu Phe Met Gly Gln Val Met Glu Pro
    370                 375                 380
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<210> 612
<211> 1395
<212> DNA
<213> Homo sapiens

<220>
<223> ATIII

<400> 612

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atgtattcca atgtgatagg aactgtaacc tctggaaaaa ggaaggttta tcttttgtcc 60
ttgctgctca ttggcttctg ggactgcgtg acctgtcacg ggagccctgt ggacatctgc 120
acagccaagc cgcgggacat tcccatgaat cccatgtgca tttaccgctc cccggagaag 180
aaggcaactg aggatgaggg ctcagaacag aagatcccgg aggccaccaa ccggcgtgtc 240
tgggaactgt ccaaggccaa ttcccgcttt gctaccactt tctatcagca cctggcagat 300
tccaagaatg acaatgataa cattttcctg tcacccctga gtatctccac ggcttttgct 360
atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggaggt atttaagttt 420
gacaccatat ctgagaaaac atctgatcag atccacttct tctttgccaa actgaactgc 480
cgactctatc gaaaagccaa caaatcctcc aagttagtat cagccaatcg ccttttgga 540
gacaaatccc ttaccttcaa tgagacctac caggacatca gtgagttggt atatggagcc 600
aagctccagc ccctggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa 660
tgggtgtcca ataagaccga aggccgaatc accgatgtca ttccctcgga agccatcaat 720
gagctcactg ttctggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaag 780
ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca 840
gcatctatga tgtaccagga aggcaagttc cgttatcggc gcgtggctga aggcacccag 900
gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tcctcatctt gcccaagcct 960
gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgctgca ggagtggctg 1020
gatgaattgg aggagatgat gctggtggtc cacatgcccc gcttccgcat tgaggacggc 1080
ttcagtttga aggagcagct gcaagacatg ggccttgtcg atctgttcag ccctgaaaag 1140
tccaaactcc caggtattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc 1200
cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt 1260
gtgattgctg gccgttcgct aaaccccaac agggtgactt tcaaggccaa caggcctttc 1320
ctggttttta taagagaagt tcctctgaac actattatct tcatgggcag agtagccaac 1380
ccttgtgtta agtaa                                                  1395
```

<210> 613
<211> 1458
<212> DNA
<213> Artificial Sequence

<220>
<223> AT3 His tag fusion protein

<400> 613
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agcgctattg ttttatatgt gcttttggcg gcggcggcgc attctgcctt tgcggcggat 120
cttggatccc acgggagccc tgtggacatc tgcacagcca agccgcggga cattcccatg 180
aatcccatgt gcatttaccg ctccccggag aagaaggcaa ctgaggatga gggctcagaa 240
cagaagatcc cggaggccac caaccggcgt gtctgggaac tgtccaaggc caattcccgc 300
tttgctacca ctttctatca gcacctggca gattccaaga atgacaatga taacattttc 360
ctgtcacccc tgagtatctc cacggctttt gctatgacca agctgggtgc ctgtaatgac 420
accctccagc aactgatgga ggtatttaag tttgacacca tatctgagaa aacatctgat 480
cagatccact tcttctttgc caaactgaac tgccgactct atcgaaaagc caacaaatcc 540
tccaagttag tatcagccaa tcgccttttt ggagacaaat cccttacctt caatgagacc 600
taccaggaca tcagtgagtt ggtatatgga gccaagctcc agcccctgga cttcaaggaa 660
aatgcagagc aatccagagc ggccatcaac aaatgggtgt ccaataagac cgaaggccga 720
atcaccgatg tcattccctc ggaagccatc aatgagctca ctgttctggt gctggttaac 780
accatttact tcaagggcct gtggaagtca aagttcagcc ctgagaacac aaggaaggaa 840
ctgttctaca aggctgatgg agagtcgtgt tcagcatcta tgatgtacca ggaaggcaag 900
ttccgttatc ggcgcgtggc tgaaggcacc caggtgcttg agttgccctt caaaggtgat 960
gacatcacca tggtcctcat cttgcccaag cctgagaaga gcctggccaa ggtagagaag 1020
gaactcaccc cagaggtgct gcaagagtgg ctggatgaat tggaggagat gatgctggtg 1080
gtccacatgc cccgcttccg cattgaggac ggcttcagtt tgaaggagca gctgcaagac 1140
atgggccttg tcgatctgtt cagccctgaa aagtccaaac tcccaggtat tgttgcagaa 1200
ggccgagatg acctctatgt ctcagatgca ttccataagg catttcttga ggtaaatgaa 1260
gaaggcagtg aagcagctgc aagtaccgct gttgtgattg ctggccgttc gctaaacccc 1320
aacagggtga ctttcaaggc caacaggcct ttcctggttt ttataagaga agttcctctg 1380
aacactatta tcttcatggg cagagtagcc aacccttgtg ttaagggagg cggaagccat 1440
caccaccatc accactaa 1458

<210> 614
<211> 485
<212> PRT
<213> Artificial Sequence

<220>
<223> AT3 His tag fusion protein

<400> 614
Met Leu Leu Val Asn Gln Ser His Gln Gly Phe Asn Lys Glu His Thr
 1   5   10   15
Ser Lys Met Val Ser Ala Ile Val Leu Tyr Val Leu Leu Ala Ala Ala
            20   25   30
Ala His Ser Ala Phe Ala Ala Asp Leu Gly Ser His Gly Ser Pro Val
        35   40   45
Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys
    50   55   60
Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu
65   70   75   80
Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu Leu Ser Lys
                85   90   95
Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu Ala Asp Ser
            100   105   110
Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser Thr
        115   120   125
Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln

```
    130                 135                 140
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp
145                 150                 155                 160
Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys
                165                 170                 175
Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp
            180                 185                 190
Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser Glu Leu Val
        195                 200                 205
Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn Ala Glu Gln
    210                 215                 220
Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr Glu Gly Arg
225                 230                 235                 240
Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu
                245                 250                 255
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe
            260                 265                 270
Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu
        275                 280                 285
Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg
    290                 295                 300
Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe Lys Gly Asp
305                 310                 315                 320
Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys Ser Leu Ala
                325                 330                 335
Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu Trp Leu Asp
            340                 345                 350
Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg Ile
        355                 360                 365
Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val
    370                 375                 380
Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu
385                 390                 395                 400
Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu
                405                 410                 415
Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Val
            420                 425                 430
Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe Lys Ala Asn
        435                 440                 445
Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn Thr Ile Ile
    450                 455                 460
Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys Gly Gly Gly Ser His
465                 470                 475                 480
His His His His His
                485
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<210> 615
<211> 6644
<212> DNA
<213> Artificial Sequence

<220>
<223> pMal2c vector

<400> 615
ccgacaccat cgaatggtgc aaaacctttc gcggtatggc atgatagcgc ccggaagaga 60

gtcaattcag ggtggtgaat gtgaaaccag taacgttata cgatgtcgca gagtatgccg 120
gtgtctctta tcagaccgtt tcccgcgtgg tgaaccaggc cagccacgtt tctgcgaaaa 180
cgcgggaaaa agtggaagcg gcgatggcgg agctgaatta cattcccaac cgcgtggcac 240
aacaactggc gggcaaacag tcgttgctga ttggcgttgc cacctccagt ctggccctgc 300
acgcgccgtc gcaaattgtc gcggcgatta aatctcgcgc cgatcaactg ggtgccagcg 360
tggtggtgtc gatggtagaa cgaagcggcg tcgaagcctg taaagcggcg gtgcacaatc 420
ttctcgcgca acgcgtcagt gggctgatca ttaactatcc gctggatgac caggatgcca 480
ttgctgtgga agctgcctgc actaatgttc cggcgttatt tcttgatgtc tctgaccaga 540
cacccatcaa cagtattatt ttctcccatg aagacggtac gcgactgggc gtggagcatc 600
tggtcgcatt gggtcaccag caaatcgcgc tgttagcggg cccattaagt tctgtctcgg 660
cgcgtctgcg tctggctggc tggcataaat atctcactcg caatcaaatt cagccgatag 720
cggaacggga aggcgactgg agtgccatgt ccggttttca acaaaccatg caaatgctga 780
atgagggcat cgttcccact gcgatgctgg ttgccaacga tcagatggcg ctgggcgcaa 840
tgcgcgccat taccgagtcc gggctgcgcg ttggtgcgga tatctcggta gtgggatacg 900
acgataccga agacagctca tgttatatcc cgccgttaac caccatcaaa caggattttc 960
gcctgctggg gcaaaccagc gtggaccgct tgctgcaact ctctcagggc aggcggtga 1020
agggcaatca gctgttgccc gtctcactgg tgaaaagaaa aaccaccctg gcgcccaata 1080
cgcaaaccgc ctctccccgc gcgttggccg attcattaat gcagctggca cgacaggttt 1140
cccgactgga aagcgggcag tgagcgcaac gcaattaatg taagttagct cactcattag 1200
gcacaattct catgtttgac agcttatcat cgactgcacg gtgcaccaat gcttctggcg 1260
tcaggcagcc atcggaagct gtggtatggc tgtgcaggtc gtaaatcact gcataattcg 1320
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Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly
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Asp Gln Glu Pro Leu His Val Ala Leu Ala Leu Gln Lys Val Lys Ile
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Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His Arg Arg Leu Phe His
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